of proteins involved in the synaptic plasticity in neurons (34) and cellular proliferation and migration in multiple cell types (28) through an interaction with G3BP. USP10, another SG-associated molecule, also interacts with G3BP and forms the G3BP/USP10 complex (29), suggesting that several SG-associated RBPs participate in the formation of a protein-protein network. In this study, the JEV core protein was shown to directly interact with Caprin-1, to sequester several key molecule complexes involved in SG formation to the perinuclear region in cells infected with JEV, and to facilitate viral propagation through the suppression of SG formation.

Flaviviruses replicate at a relatively low rate in comparison with most of the other positive-stranded RNA viruses, and thus rapid shutdown of host cellular protein synthesis would be deleterious for the viral life cycle. In cells infected with JEV, several SG components were colocalized with the core protein in the perinuclear region, while in those infected with WNV or DENV, SG components were accumulated in a replication complex composed of viral RNA and nonstructural proteins. In addition, the phosphorylation of eIF2α induced by arsenite was completely canceled by the infection with WNV or DENV, whereas the suppression of the phosphorylation was limited in JEV infection (15). Incorporation of the nascent viral RNA into the membranous structure induced by viral nonstructural proteins prevents PKR activation and inhibits SG formation in cells infected with WNV (17). In cells infected with hepatitis C virus (HCV), which belongs to the genus *Hepacivirus* in the family *Flaviviridae*, induction of SG formation was observed in the early stage of infection, in contrast to the inhibition of the arsenite-induced SG formation in the late stage (35). Several SG components, such as G3BP1, PABP1, and ataxin-2, were colocalized with HCV core protein around lipid droplets (35), and G3BP1 was also associated with the NS5B protein and the 5′ terminus of the minus-strand viral RNA (36) to mediate efficient viral replication. Collectively, these data suggest that flaviviruses have evolved to regulate cellular processes involved in SG formation through various strategies.

PKR is one of the interferon-stimulated genes and plays a crucial role in antiviral defense through phosphorylation of eIF2α, which leads to host translational shutoff (37, 38). In the early stage of flavivirus infection, both positive- and negative-stranded RNAs transcribe at low levels, while genomic RNA predominantly synthesizes in the late stage of infection (39). It was shown that activation of PKR was suppressed (40) or only induced in the late stage of WNV infection (41) and impaired by the expression of HCV NS5A (42–44). Very recently, JEV NS2A was shown to suppress PKR activation through inhibition of dimerization of PKR in the early stage but not in the late stage of infection (45). In this study, we have shown that JEV core protein interacts with Caprin-1 and inhibits SG formation downstream of the phosphorylation of eIF2α in the late stage of infection, suggesting that JEV has evolved to escape from host antiviral responses in the multiple stages of viral replication by using structural and nonstructural proteins.

The flavivirus core protein is a multifunctional protein involved in many aspects of the viral life cycle. In addition to the formation of viral nucleocapsid through the interaction with viral RNA (as a structural protein) (46), flavivirus core proteins interact with various host factors, such as B23 (47), Jab1 (48), hnRNP K (49), and hnRNP A2 (23), and regulate viral replication and/or modify the host cell environment (as a nonstructural protein). Although further investigations are needed to clarify the precise mechanisms underlying the circumvention of SG formation through the interaction of JEV core protein with Caprin-1, leading to efficient propagation *in vitro* and pathogenicity in mice, these findings could help not only to provide new insight into strategies by which viruses escape host stress responses but also to develop novel antiviral agents for flavivirus infection.

ACKNOWLEDGMENTS

We thank M. Tomiyama for secretarial assistance. We also thank K. Saito and T. Wakita for technical advice and the infectious clone of JEV, respectively.

This work was supported in part by grants-in-aid from the Ministry of Health, Labor, and Welfare, the Ministry of Education, Culture, Sports, Science, and Technology, and the Osaka University Global Center of Excellence Program. H. Katoh is a research fellow of the Japanese Society for the Promotion of Science.

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Signal Peptidase Complex Subunit 1 Participates in the Assembly of Hepatitis C Virus through an Interaction with E2 and NS2

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Abstract

Hepatitis C virus (HCV) nonstructural protein 2 (NS2) is a hydrophobic, transmembrane protein that is required not only for NS2-NS3 cleavage, but also for infectious virus production. To identify cellular factors that interact with NS2 and are important for HCV propagation, we screened a human liver cDNA library by split-ubiquitin membrane yeast two-hybrid assay using full-length NS2 as a bait, and identified signal peptidase complex subunit 1 (SPCS1), which is a component of the microsomal signal peptidase complex. Silencing of endogenous SPCS1 resulted in markedly reduced production of infectious HCV, whereas neither processing of structural proteins, cell entry, RNA replication, nor release of virus from the cells was impaired. Propagation of Japanese encephalitis virus was not affected by knockdown of SPCS1, suggesting that SPCS1 does not widely modulate the viral lifecycles of the *Flaviviridae* family. SPCS1 was found to interact with both NS2 and E2. A complex of NS2, E2, and SPCS1 was formed in cells as demonstrated by co-immunoprecipitation assays. Knockdown of SPCS1 impaired interaction of NS2 with E2. Our findings suggest that SPCS1 plays a key role in the formation of the membrane-associated NS2-E2 complex via its interaction with NS2 and E2, which leads to a coordinating interaction between the structural and non-structural proteins and facilitates the early step of assembly of infectious particles.

Citation: Suzuki R, Matsuda M, Watashi K, Aizaki H, Matsuura Y, et al. (2013) Signal Peptidase Complex Subunit 1 Participates in the Assembly of Hepatitis C Virus through an Interaction with E2 and NS2. PLoS Pathog 9(8): e1003589. doi:10.1371/journal.ppat.1003589

Editor: Aleem Siddiqui, University of California, San Diego, United States of America

Received February 1, 2013; **Accepted** July 19, 2013; **Published** August 29, 2013

Funding: This work was supported by a grant-in-aid for Scientific Research from the Japan Society for the Promotion of Science, from the Ministry of Health, Labour and Welfare of Japan and from the Ministry of Education, Culture, Sports, Science and Technology of Japan. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

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Introduction

Over 170 million people worldwide are chronically-infected with hepatitis C virus (HCV), and are at risk of developing chronic hepatitis, cirrhosis, and hepatocellular carcinoma [1]. HCV is an enveloped virus of the family *Flaviviridae*, and its genome is an uncapped 9.6-kb positive-strand RNA consisting of the 5′ untranslated region (UTR), an open reading frame encoding viral proteins, and the 3′ UTR [2]. A precursor polyprotein is further processed into structural proteins (Core, E1, and E2), followed by p7 and nonstructural (NS) proteins (NS2, NS3, NS4A, NS4B, NS5A, and NS5B), by cellular and viral proteases. The structural proteins (Core to E2) and p7 reside in the N-terminal region, and are processed by signal peptidase from the polyprotein. NS2, NS3, and NS4A are prerequisites for proteolytic processing of the NS proteins. NS3 to NS5B are considered to assemble into a membrane-associated HCV RNA replicase complex. NS3 also possesses activities of helicase and nucleotide triphosphatase. NS4 is a cofactor that activates the NS3 protease. NS4B induces vesicular membrane alteration. NS5A is considered to play an important but undefined role in viral RNA replication. NS5B is the RNA-dependent RNA polymerase. It is now accepted that NS proteins, such as NS2, NS3, and NS5A, contribute to the assembly or release of infectious HCV [3–9].

NS2 protein is a transmembrane protein of 21–23 kDa, with highly hydrophobic N-terminal residues forming transmembrane helices that insert into the endoplasmic reticulum (ER) membrane [5,10]. The C-terminal part of NS2 resides in the cytoplasm, enabling zinc-stimulated NS2/3 autoprotease activity together with the N-terminal domain of NS3. The crystal structure of the C-terminal region of NS2 reveals a dimeric cysteine protease containing two composite active sites [11]. Prior work showed that NS2 is not essential for RNA replication of subgenomic replicons [12]; however, the protein is required for virus assembly independently of protease activity [5,6]. Several adaptive mutations in NS2 that increase virus production have been reported [13–17]. In addition, there is increasing evidence for genetic and biochemical interaction of NS2 with other HCV proteins, including E1, E2, p7, NS3-4A, and NS5A [10,18–25]. Thus, NS2 is now suggested to act as a scaffold to coordinate interactions between the structural and NS proteins for viral assembly. However, the molecular mechanism by which NS2 is involved in virus assembly remains unclear.

In this study, we identified signal peptidase complex subunit 1 (SPCS1) as a host factor that interacts with NS2 by yeast two-hybrid screening with a split-ubiquitin system. SPCS1 is a component of the microsomal signal peptidase complex which is

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

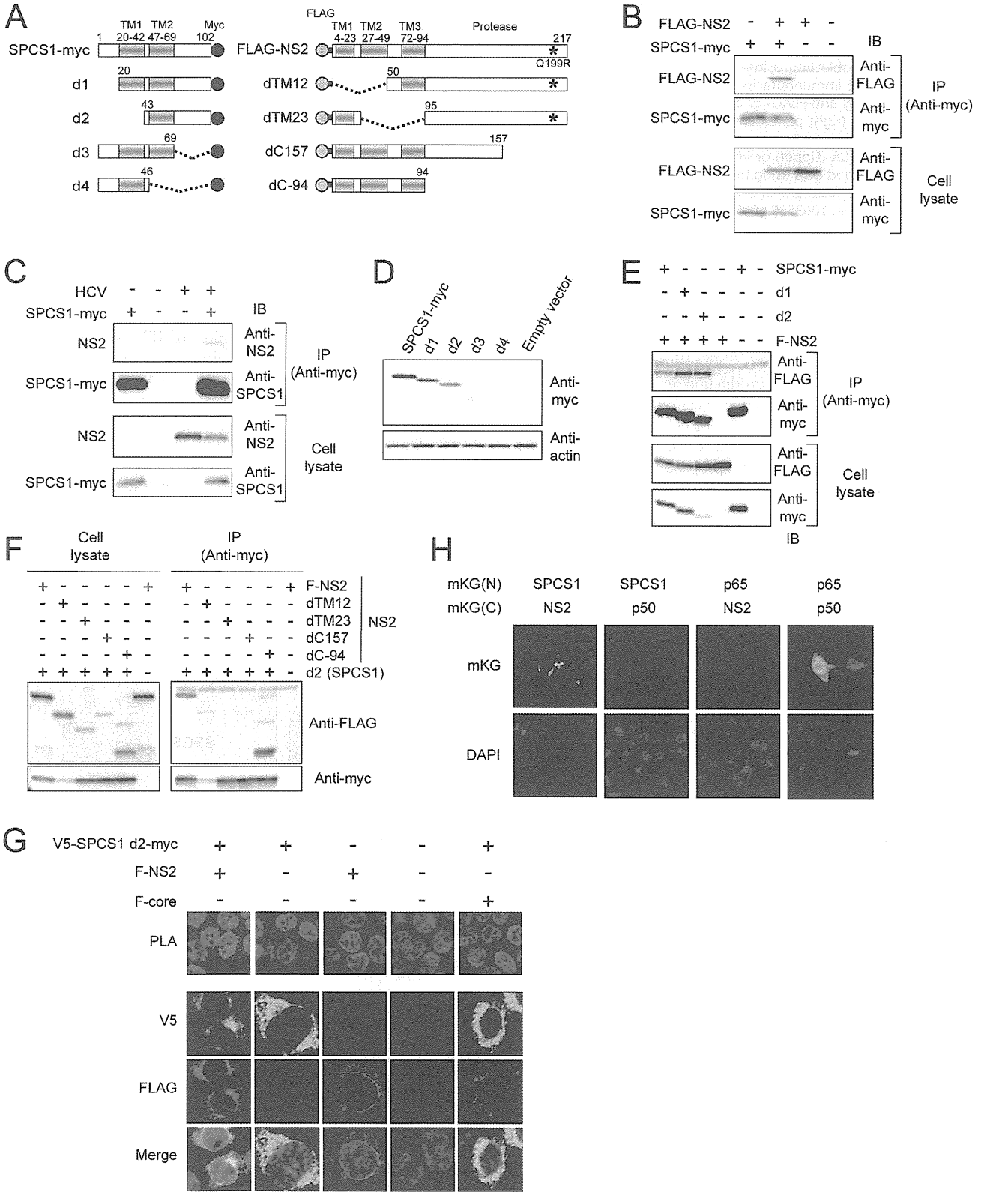

Figure 1. Interaction of HCV NS2 protein with SPCS1 in mammalian cells. (A) Expression constructs of SPCS1-myc and FLAG-NS2 used in this study. TM regions are represented as gray. Myc-tag regions are depicted by the black circles. Gray circles and bold lines indicated FLAG-tag and spacer (GGGGS) sequences, 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.
doi:10.1371/journal.ppat.1003589.g001

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

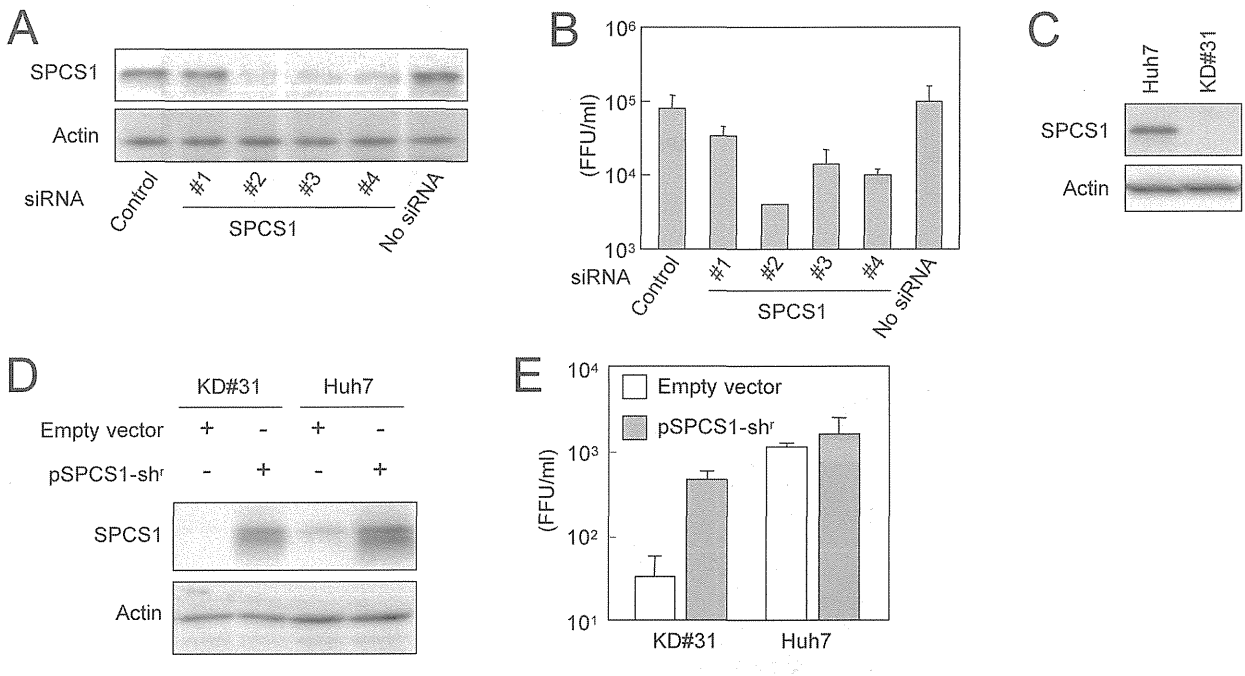

Figure 2. Effect of SPCS1 knockdown on the production of HCV. (A) Huh7.5.1 cells were transfected with four different siRNAs targeted for SPCS1 or control siRNA at a final concentration of 15 nM, and infected with HCVcc at a multiplicity of infection (MOI) of 0.05 at 24 h post-transfection. Expression 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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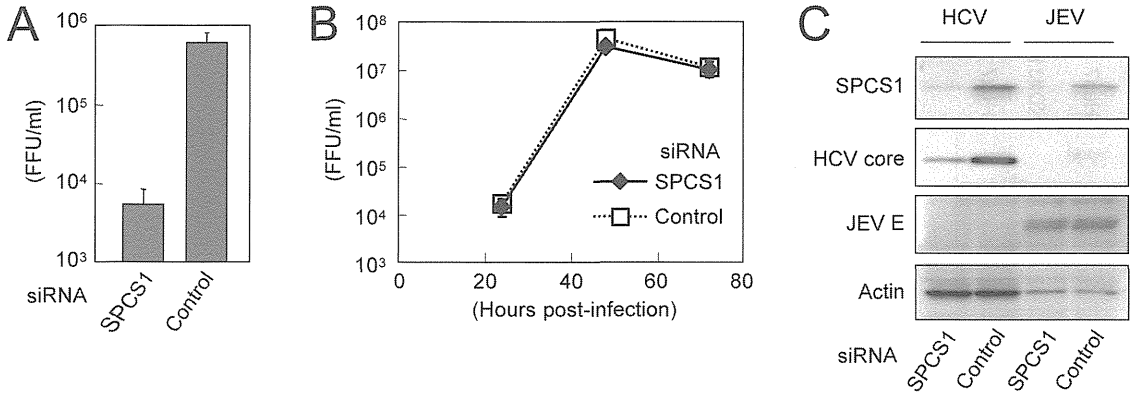

Figure 3. Effect of SPCS1 knockdown on the propagation of JEV. Huh7.5.1 cells were transfected with SPCS1 siRNA or control siRNA at a final concentration of 10 nM, and infected with JEV or HCVcc at an MOI of 0.05 at 24 h post-transfection. (A) Infectious titers of HCVcc in the supernatant at 3 days post-infection 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.
doi:10.1371/journal.ppat.1003589.g003

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

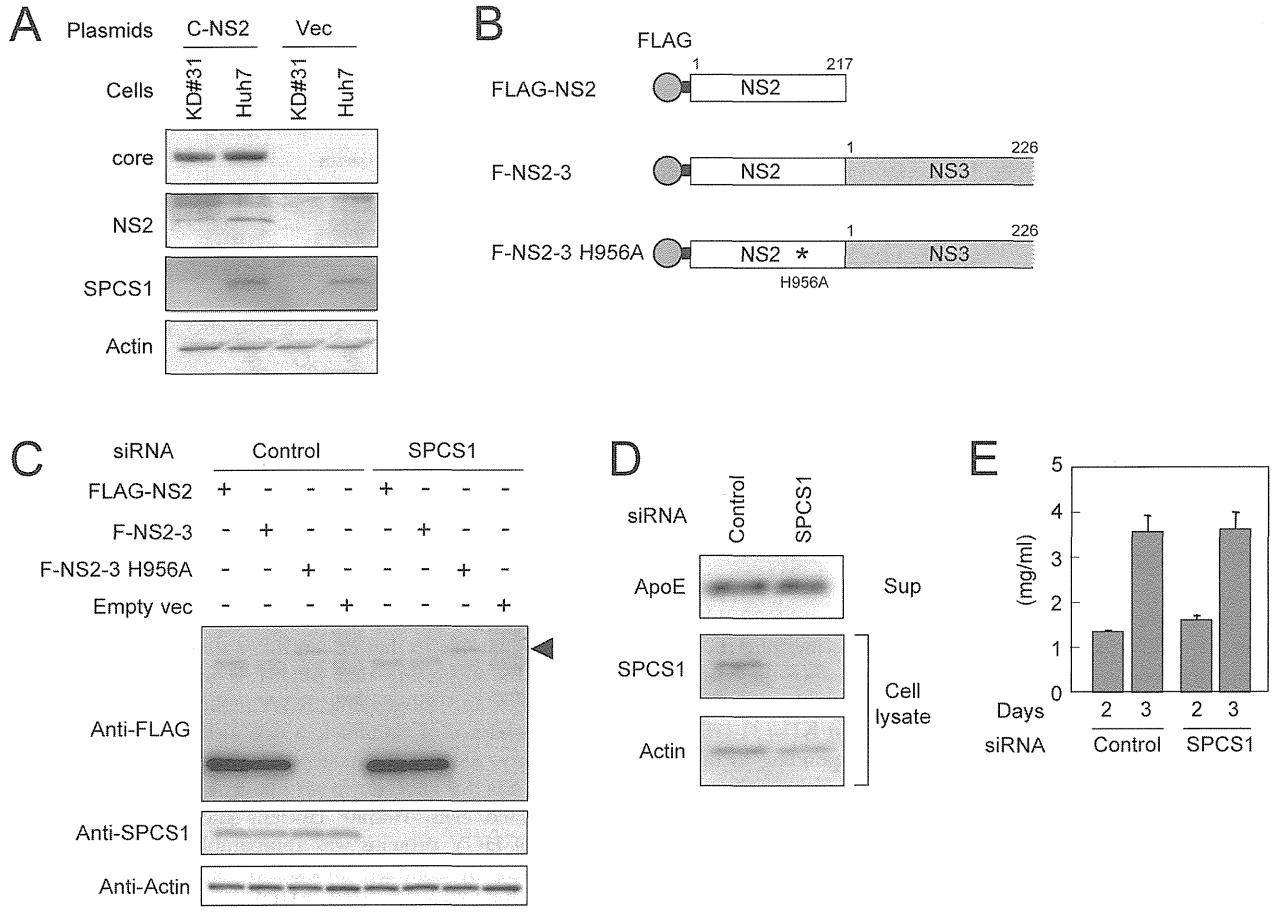

Figure 4. Effect of SPCS1 knockdown on the processing of HCV structural proteins and secretion of host proteins. (A) Core-NS2 polyprotein was expressed in KD#31 cells or parental Huh-7 cells. Core, NS2, SPCS1, and actin were detected by immunoblotting 2 days post-transfection. (B) Expression constructs 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.
doi:10.1371/journal.ppat.1003589.g004

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.

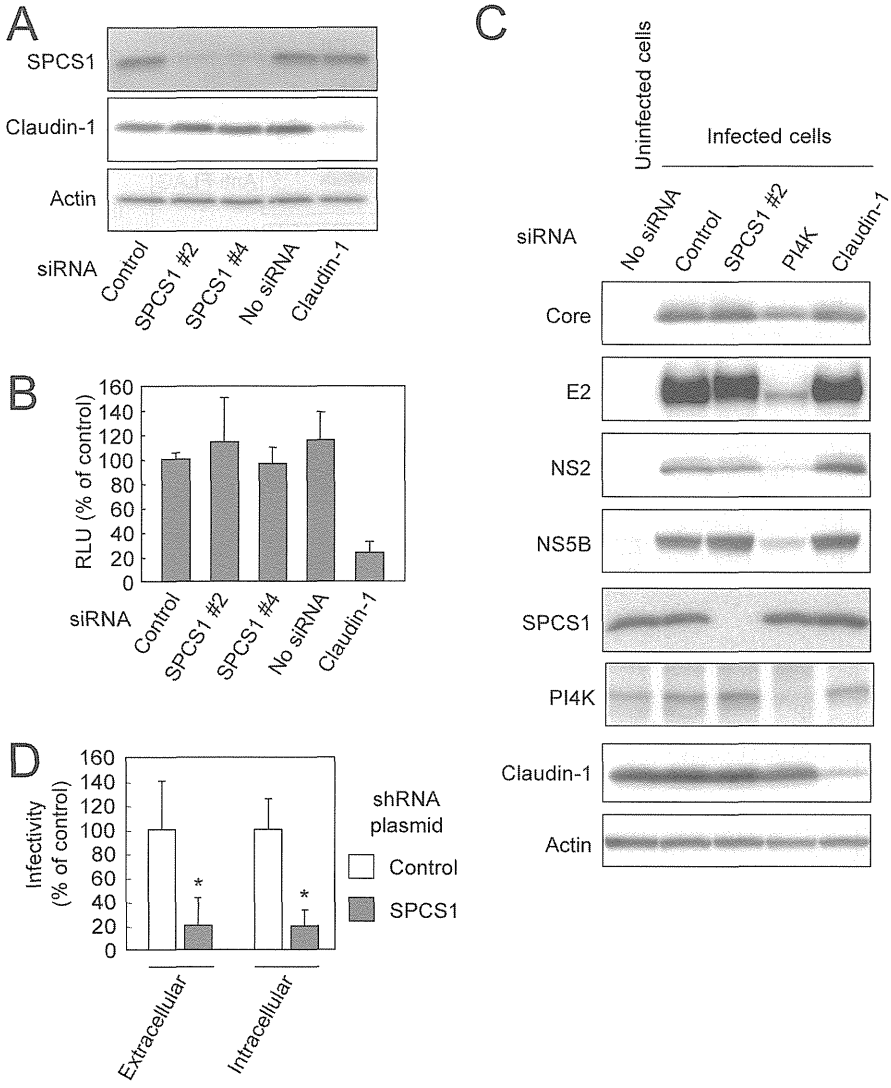

Figure 5. Effect of SPCS1 knockdown on entry into cells, genome replication, and assembly or release of infectious virus. (A) Huh7.5.1 cells were transfected with siRNA for SPCS1 or claudin1, or control siRNA at a final concentration of 30 nM. Expression levels of endogenous SPCS1, claudin-1, and actin 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.
doi:10.1371/journal.ppat.1003589.g005

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

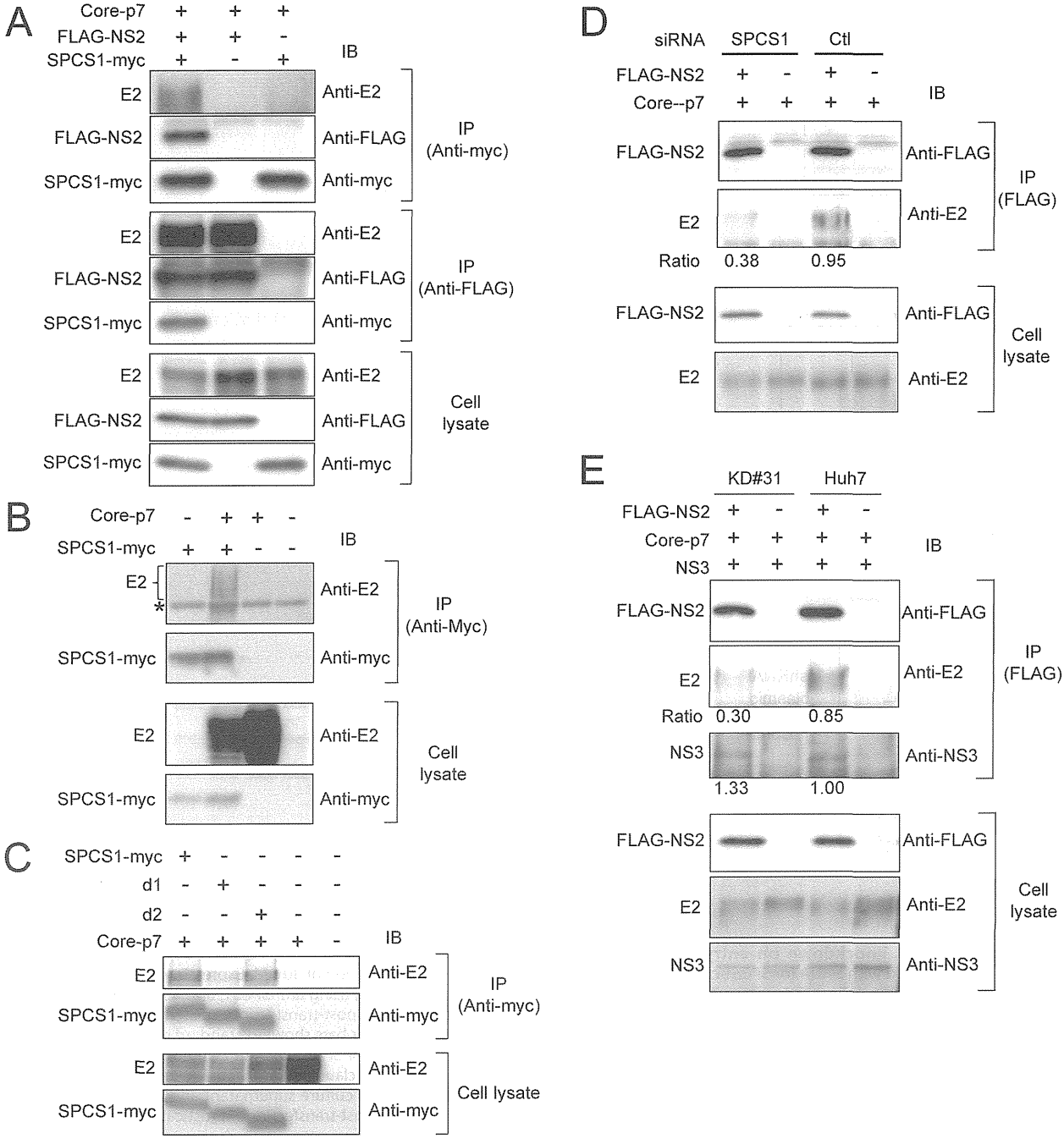

Figure 6. SPCS1 forms a complex with NS2 and E2. (A) Lysates of cells, which were co-transfected with Core-p7, FLAG-NS2, and SPCS1-myc expression plasmids, were immunoprecipitated with anti-myc or anti-FLAG antibody. The resulting precipitates and whole cell lysates used in IP were examined by immunoblotting 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.

doi:10.1371/journal.ppat.1003589.g006

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

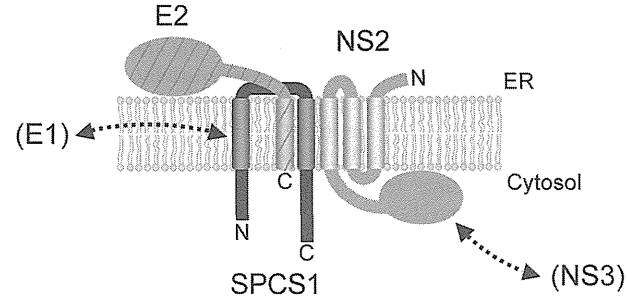

Figure 7. A proposed model for a complex consisting of NS2, SPCS1 and E2 associated with ER membranes.
doi:10.1371/journal.ppat.1003589.g007

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)

Acknowledgments

We are grateful to Francis V. Chisari (The Scripps Research Institute) for providing Huh7.5.1 cells, and Drs. C.K. Lim and T. Takasaki (National Institute of Infectious Diseases) for providing rabbit polyclonal anti-JEV antibodies. We thank M. Sasaki and T. Date for their technical assistance, and T. Mizoguchi for secretarial work. We also thank H. Hasegawa, T. Kato, T. Masaki, N. Watanabe, and A. Murayama for their helpful discussions.

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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Zinc-finger antiviral protein mediates retinoic acid inducible gene I–like receptor-independent antiviral response to murine leukemia virus

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Contributed by Shizuo Akira, June 5, 2013 (sent for review May 14, 2013)

When host cells are infected by an RNA virus, pattern-recognition receptors (PRRs) recognize the viral RNA and induce the antiviral innate immunity. Toll-like receptor 7 (TLR7) detects the genomic RNA of incoming murine leukemia virus (MLV) in endosomes and mediates the antiviral response. However, the RNA-sensing PRR that recognizes the MLV in the cytosol is not fully understood. Here, we definitively demonstrate that zinc-finger antiviral protein (ZAP) acts as a cytosolic RNA sensor, inducing the degradation of the MLV transcripts by the exosome, an RNA degradation system, on RNA granules. Although the retinoic acid inducible gene I (RIG-I)–like receptors (RLRs) RIG-I and melanoma differentiation-associated protein 5 detect various RNA viruses in the cytosol and induce the type I IFN-dependent antiviral response, RLR loss does not alter the replication efficiency of MLV. In sharp contrast, the loss of ZAP greatly enhances the replication efficiency of MLV. ZAP localizes to RNA granules, where the processing-body and stress-granule proteins assemble. ZAP induces the recruitment of the MLV transcripts and exosome components to the RNA granules. The CCCH-type zinc-finger domains of ZAP, which are RNA-binding motifs, mediate its localization to RNA granules and MLV transcripts degradation by the exosome. Although ZAP was known as a regulator of RIG-I signaling in a human cell line, ZAP deficiency does not affect the RIG-I–dependent production of type I IFN in mouse cells. Thus, ZAP is a unique member of the cytosolic RNA-sensing PRR family that targets and eliminates intracellular RNA viruses independently of TLR and RLR family members.

host defense | retrovirus | ZC3HAV1

Innate immunity is induced after the recognition of viral RNAs by pattern-recognition receptors (PRRs) and is the first line of the host defenses against a variety of RNA viruses (1, 2). Among the PRRs, the Toll-like receptor (TLR) and retinoic acid-inducible gene I (RIG-I)-like receptor (RLR) families play major roles in the recognition of viral RNAs. The RLR's RIG-I [also called DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (DDX58)] and melanoma differentiation-associated protein 5 [MDA5, also called interferon induced with helicase C domain 1 (IFIH1)] are RNA helicases that sense the ds form of viral RNAs in the cytosol (3, 4). After sensing dsRNA, the RLRs trigger a signaling pathway that activates interferon (IFN) regulatory factor 3 (IRF3) and IRF7, transcription factors that induce IFN stimulation-responsive, element-dependent transcription (5, 6). This results in the production of type I IFN and the expression of IFN-inducible antiviral proteins. The sensing of viral RNAs by TLR family members also induces the IRF3- and IRF7-dependent type I IFN response (1, 2). In epithelial cells, TLR3, a sensor of dsRNA, detects the incoming RNA virus genomes in endosomes and induces the activation of IRF3, leading to the production of type I IFN (7, 8). In plasmacytoid dendritic cells, TLR7, a sensor of single-stranded (ss) RNA, detects incoming RNA virus genomes in endo-lysosomes and triggers the activation of IRF7, leading to the robust production of type I IFN (9–13). Thus, TLRs and RLRs play major roles in the establishment of an antiviral state by mediating the production of type I IFN.

Murine leukemia virus (MLV), a retrovirus belonging to the gammaretroviral genus of the family *Retroviridae*, is a causative agent of cancer in murine hosts (14, 15). Although type I IFN is essential for the protection of hosts from lethal infection with a variety of RNA viruses, such as influenza A virus (IAV) and vesicular stomatitis virus (VSV), type I IFN is not essential for induction of the antiviral state against MLV (16–18). Therefore, a different type of innate immune system has been proposed to protect hosts from MLV infection. Although TLR7 has been shown to induce virus-neutralizing immunity after MLV genomic RNA is detected in endosomes (16), the RNA sensor responsible for the elimination of MLV in the cytosol has not been fully understood. RLRs are candidate RNA sensors of intracellular MLV. RLRs might mediate the antiviral response to MLV after the viral RNA is detected, independently of type I IFN because RLRs stimulate not only IRF3/IRF7, but also other transcription factors, such as NF-κB and activator protein 1, which are responsible for the production of inflammatory cytokines and chemokines (19). Another candidate sensor is zinc-finger antiviral protein [ZAP, also called zinc finger CCCH-type, antiviral 1 (ZC3HAV1)]. ZAP was originally identified with an expression cloning method as one of the antiviral proteins directed against MLV (20). ZAP reduces the level of MLV transcripts in the cytosol to suppress MLV infection at the posttranscriptional stage, whereas ZAP does not inhibit the early stage of the MLV infection. ZAP recognizes the MLV transcripts via its CCCH-type zinc-finger domains and binds with RNA helicases and the components of the exosome (an RNA degradation system) to induce the degradation of the MLV transcripts (21–25). However, it is unclear whether endogenous ZAP is involved in the antiviral response to replication-competent MLV in primary cells. In the present study, we examined the roles of these two types of cytosolic RNA sensors and demonstrated the spatial regulation of the innate immune response directed against intracellular MLV.

Author contributions: T. Saitoh and S.A. designed research; H.L., J.K., Y.S., S.Y., T.K., T.M., M.T., T. Satoh, O.T., N.Y., and Y.M. performed research; and T. Saitoh wrote the paper.

The authors declare no conflict of interest.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1310604110/-/DCSupplemental.

Results

RLRs Do Not Regulate the Antiviral Response to MLV in Primary Mouse Embryonic Fibroblasts. We first examined the involvement of RLRs in the antiviral response to MLV in mouse embryonic fibroblasts (MEFs). The replication efficiency of MLV in *Ddx58*$^{-/-}$/*Ifih1*$^{-/-}$ MEFs was similar to that in *Ddx58*$^{+/+}$/*Ifih1*$^{+/+}$ MEFs (Fig. 1*A*). Furthermore, the replication efficiency of MLV in *Irf3*$^{-/-}$/*Irf7*$^{-/-}$ MEFs was similar to that in *Irf3*$^{+/-}$/*Irf7*$^{+/-}$ MEFs (Fig. 1*B*). Consistent with this, the levels of *Ifnb1* and *chemokine (C-X-C motif) ligand 10* (*Cxcl10*) mRNAs did not change during MLV infection (Fig. 1 *C–F*). The RLR–IRF3/7 signaling axis is essential for the up-regulation of *Ifnb1* and *Cxcl10* mRNAs during VSV infection. R848, a ligand of TLR7, failed to stimulate MEFs isolated from C57BL/6 mice (Fig. S1), indicating that no RNA-sensing TLR family member recognizes MLV in the extracellular space of MEFs. Therefore, MLV evades the RLR and TLR systems and does not induce the type I IFN response in MEFs.

Endogenous ZAP Limits the Replication of MLV in Primary MEFs. We next investigated the role of ZAP, another cytosolic sensor of viral RNA, in the antiviral response to MLV. Previous studies have demonstrated that the ectopic expression of ZAP potently inhibits replication-incompetent MLV in the cytoplasm of various types of cell lines (20). Therefore, we generated *Zc3hav1*$^{-/-}$ mice to examine whether endogenous ZAP controls the replication of MLV in primary cells (Fig. S2). Detectable levels of ZAP protein were expressed in *Zc3hav1*$^{+/+}$ MEFs before and after MLV infection (Fig. S2*D*). Whereas ZAP deficiency did not alter the replication efficiency of VSV in MEFs (Fig. S3), ZAP deficiency greatly enhanced the replication efficiency of MLV (Fig. 2 *A* and *B*). These findings indicate that endogenous ZAP is responsible for the antiviral response to replication-competent MLV in primary mouse cells.

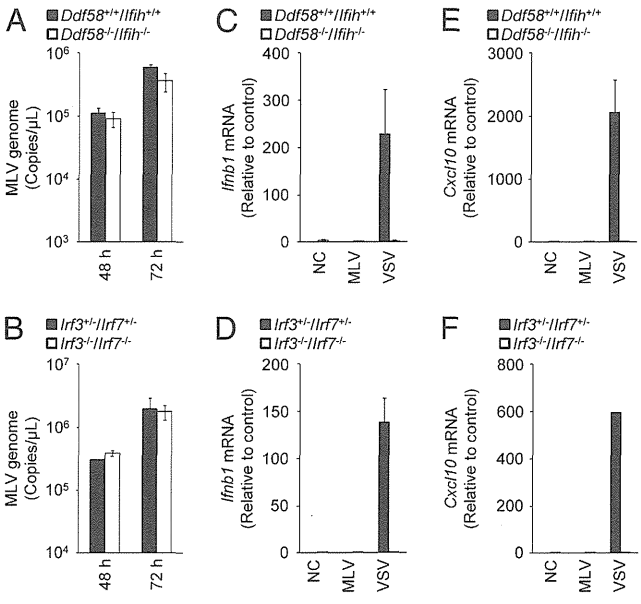

Fig. 1. RIG-I–like receptors are not essential for the antiviral response to MLV in primary MEFs. (*A* and *B*) *Ddx58*$^{+/+}$/*Ifih1*$^{+/+}$ and *Ddx5*$^{-/-}$/*Ifih1*$^{-/-}$ MEFs (*A*) or *Irf3*$^{+/-}$/*Irf7*$^{+/-}$ and *Irf*$^{-/-}$/*Irf7*$^{-/-}$ MEFs (*B*) were infected with MLV (2 × 10^{10} copies per μL) for 48 or 72 h. The copy numbers of the MLV genome in the culture supernatants were measured by quantitative RT-PCR. (*C–F*) *Ddx58*$^{+/+}$/*Ifih1*$^{+/+}$ and *Ddx58*$^{-/-}$/*Ifih1*$^{-/-}$ MEFs (*C* and *E*) or *Irf3*$^{+/-}$/*Irf7*$^{+/-}$ and *Irf3*$^{-/-}$/*Irf7*$^{-/-}$ MEFs (*D* and *F*) were infected with MLV (2 × 10^{10} copies per μL) or VSV [multiplicity of infection (MOI) = 1] for 12 h. The levels of *Ifnb1* (*C* and *D*) and *Cxcl10* (*E* and *F*) mRNAs were measured by quantitative RT-PCR. The results shown are means ± SD (n = 3).

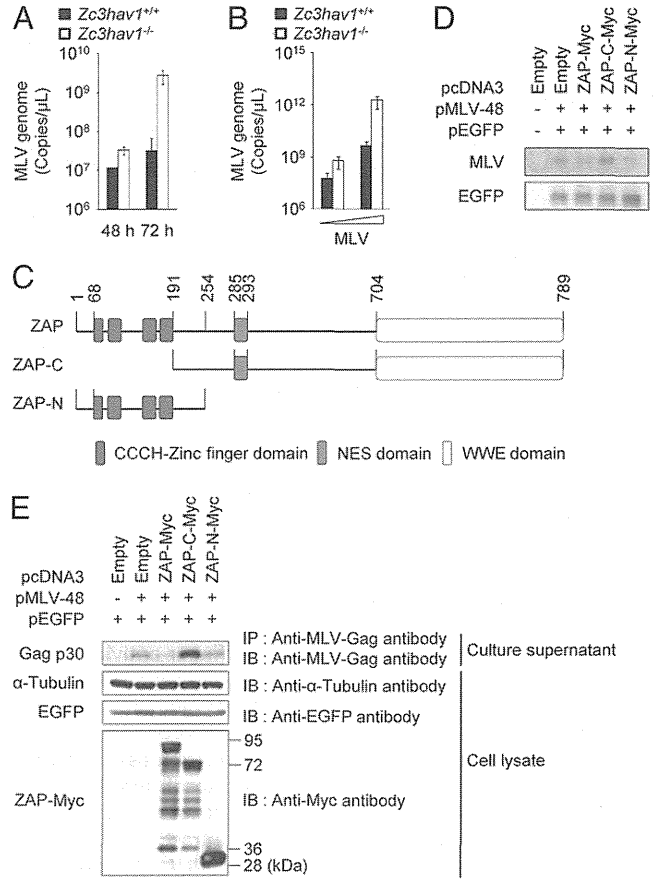

Fig. 2. ZAP inhibits MLV replication in primary MEFs. (*A*) *Zc3hav1*$^{+/+}$ and *Zc3hav1*$^{-/-}$ MEFs were infected with MLV (2 × 10^{10} copies per μL). Viral RNA was isolated at the indicated time points. The copy numbers of the MLV genome in the culture supernatants were measured by quantitative RT-PCR. (*B*) *Zc3hav1*$^{+/+}$ and *Zc3hav1*$^{-/-}$ MEFs were infected with increasing doses of MLV (2 × 10^{8} and 2 × 10^{9} copies per μL) for 96 h. The copy numbers of the MLV genome in the culture supernatants were measured by quantitative RT-PCR. (*C*) Domain architecture of ZAP. (*D* and *E*) 293T cells were transfected with pMLV-48 and pEGFP-N1 together with the indicated ZAP expression plasmids for 48 h. Cytoplasmic RNA was subjected to Northern blotting analysis of the indicated RNAs (*D*). The culture supernatants were subjected to immunoprecipitation coupled to immunoblotting to detect the indicated proteins (*E*). The results shown are means ± SD (n = 3). NES, nuclear export signal.

The CCCH-type zinc-finger domains of ZAP are known to recognize the MLV transcripts and to induce its degradation (21, 25). Consistent with this, the ectopic expression of the N-terminal portion of ZAP, which contains the CCCH-type zinc-finger domains, but not the ectopic expression of the C-terminal portion of ZAP, which lacks CCCH-type zinc-finger domains, reduced the level of MLV transcripts in the cytosol (Fig. 2 *C* and *D*). The ectopic expression of the CCCH-type zinc-finger domains of ZAP also suppressed the expression of the Gag protein of MLV (Fig. 2*E*). Therefore, the CCCH-type zinc-finger domains of ZAP are essential for its antiviral action against MLV.

CCCH-Type Zinc-Finger Domains of ZAP Mediate Its Localization to the RNA Granules. The involvement of ZAP in the antiviral response to MLV prompted us to determine the mechanism underlying the ZAP-dependent degradation of the MLV transcripts. Although a previous study showed that ZAP acts in the cytosol (20), it was still unclear where in the cytosol ZAP eliminates the MLV transcripts. Therefore, we examined whether ZAP localizes to a cytosolic compartment, such as in the processing bodies

(P-bodies) (26). When it was ectopically expressed, ZAP localized to cytoplasmic dot-like structures in a manner that was dependent on its CCCH-type zinc-finger domains (Fig. 3*A*). The ZAP-positive dot-like structures colocalized with marker proteins for P-bodies, such as DCP1 decapping enzyme homolog A (*Saccharomyces cerevisiae*; DCP1A) and DDX6 (Fig. 3*B*). ZAP induced the enlargement of the DCP1A- and DDX6-positive dot-like structures, suggesting that the ZAP-positive dot-like structures are not conventional P-bodies. ZAP also colocalized with marker proteins for stress granules, such as GTPase-activating protein (SH3 domain) binding protein 1 (G3BP1) and cytotoxic granule-associated RNA binding protein (TIA-1) (Fig. S4). Furthermore, the RNA helicase DEAH (Asp-Glu-Ala-His) box polypeptide 30 (DHX30), which binds to ZAP to facilitate its antiviral action against MLV (24), colocalized with ZAP to the DCP1A-positive dot-like structures (Fig. S5). By contrast, ZAP did not colocalize with mitochondrial preprotein translocases of the outer membrane 20 (TOM20), 70-kDa peroxisomal membrane protein (PMP70), early endosome antigen 1 (EEA1), or lysosomal-associated membrane protein 1 (LAMP1), marker proteins for the mitochondria, peroxisomes, endosomes, and lysosomes, respectively (Fig. 3*C*). These findings indicate that ZAP localizes to the RNA granules, where the marker proteins for P-bodies and stress granules assemble.

ZAP Recruits the MLV Transcripts and Exosome Components to RNA Granules. The localization of the MLV transcripts has been poorly understood. We used an improved RNA FISH method to visualize the subcellular localization of viral RNA and identified the cytosolic compartments in which ZAP acts on the MLV transcripts. The MLV transcripts mainly localize in the cytosol and colocalize with DCP1A-positive RNA granules at low frequency (Fig. 4). However, the ectopic expression of ZAP reduced the level of MLV transcripts in the cytosol and dramatically altered its localization from the cytosol to ZAP- and DCP1A-positive RNA granules (Fig. 4 and Fig. S6). Therefore, ZAP tethers the MLV transcripts and transfers it to the RNA granules.

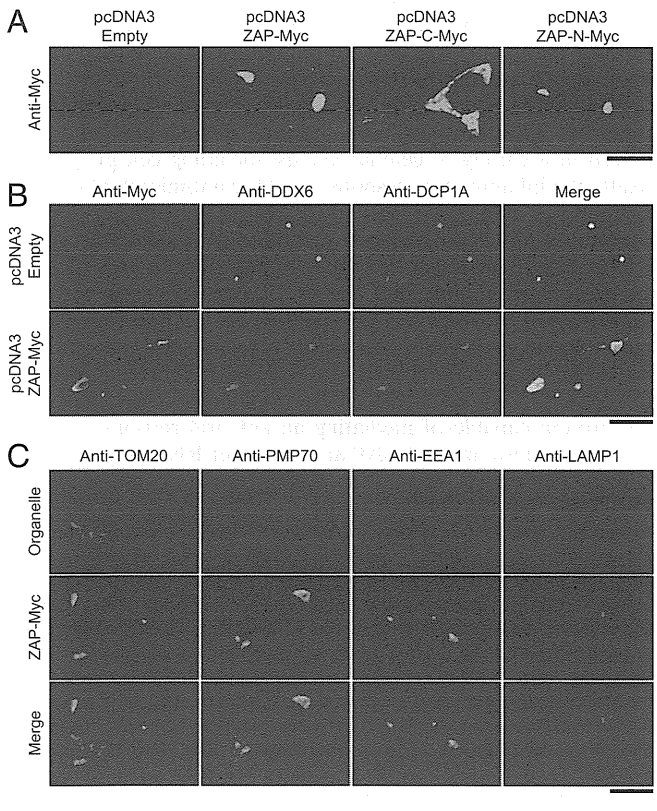

Fig. 3. ZAP localizes to DCP1A- and DDX6-positive RNA granules. (*A*–*C*) 293T cells were transfected with the indicated vectors for 48 h and then fixed. The samples were immunostained with the indicated antibodies and then observed by confocal laser scanning microscopy. The data are representative of three independent experiments. (Scale bars, 10 μm.)

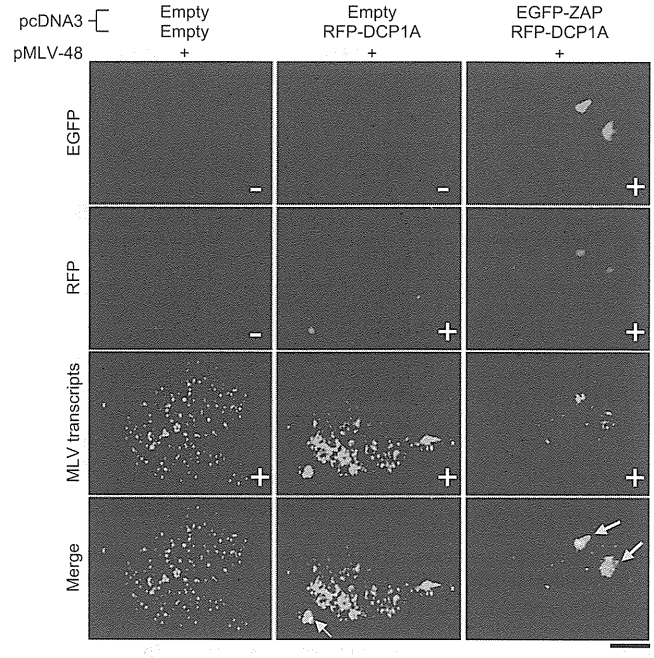

Fig. 4. ZAP recruits the MLV transcripts to RNA granules. 293T cells were transfected with the indicated plasmids for 48 h and then fixed. The samples were subjected to in situ hybridization analysis with a fluorescent probe for MLV transcripts and then observed by confocal laser scanning microscopy. (Scale bar, 10 μm.)

Because ZAP is not a ribonuclease, it requires the support of an RNA degradation system to destabilize the MLV transcripts. Consistent with this, previous studies have shown that exosome components and RNA helicases interact with ZAP to mediate the antiviral response to MLV (22–24). Therefore, we focused on the localization of exosome component 5 (EXOSC5, also known as RRP46) (27). The ectopic expression of EXOSC5 reduced the level of MLV transcripts in the cytosol (Fig. 5*A*). Under normal conditions, EXOSC5 localized in the cytosol and nuclei, and colocalized with the DCP1A-positive RNA granules at low frequency (Fig. 5*B*). However, when ZAP was ectopically expressed, EXOSC5 moved from the cytosol to the ZAP- and DCP1A-positive RNA granules (Fig. 5*B*). These findings indicate that ZAP recruits the exosome component to the RNA granules to induce the degradation of MLV transcripts.

ZAP Does Not Regulate the RIG-I–Dependent Type I IFN Response in Primary Mouse Cells. A recent study showed that ZAP positively regulated RIG-I signaling during RNA virus infection in a human cell line (28). Therefore, we examined the involvement of ZAP in the RIG-I–dependent type I IFN response in primary mouse cells. In *Zc3hav1*$^{-/-}$ primary MEFs, the IFN-β and Cxcl10 proteins were produced normally in response to VSV, an RNA virus recognized by RIG-I (Fig. 6 *A* and *B*). Although ZAP deficiency greatly enhanced the replication of MLV (Fig. 2 *A* and *B*), no IFN-β or Cxcl10 protein was produced in *Zc3hav1*$^{-/-}$ MEFs infected with MLV. In *Zc3hav1*$^{-/-}$ mouse primary dendritic cells, IFN-β and Cxcl10 were also normally produced in response to

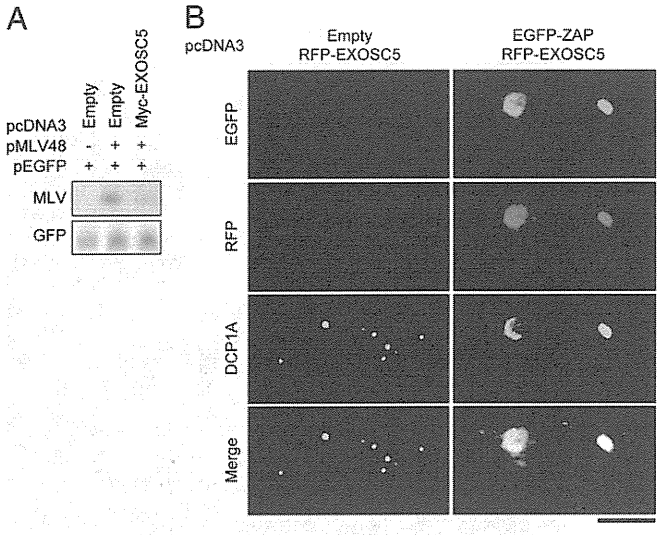

Fig. 5. EXOSC5 colocalizes with ZAP on RNA granules. (*A*) 293T cells were transfected with pMLV-48 and pEGFP-N1 together with the indicated ZAP expression plasmids for 48 h. Cytoplasmic RNA was subjected to Northern blotting analysis to detect the indicated RNAs. (*B*) 293T cells were transfected with the indicated plasmids and then fixed. The samples were immunostained with anti-DCP1A antibody and then observed by confocal laser scanning microscopy. The data are representative of three independent experiments. (Scale bar, 10 μm.)

Newcastle disease virus (NDV) and IAV, RNA viruses recognized by RIG-I (Fig. 6 *C* and *D*). Furthermore, ZAP deficiency did not affect the production of IFN-β in MEFs stimulated with the RIG-I ligand, 5′ triphosphate dsRNA (3pRNA) (Fig. S7 *A* and *B*), the MDA5 ligand poly(rI–rC), and a synthetic dsDNA poly(dA–dT) (Fig. S7*C*). These findings indicate that ZAP is not a regulator of the RIG-I–dependent type I IFN response in primary mouse cells and strengthen our conclusion that ZAP eliminates MLV independently of the RLR–IRF3/7 signaling axis.

Discussion

In this study, we showed that endogenous ZAP suppresses the replication of MLV in MEFs. This raises the issue of whether endogenous ZAP suppresses the replication of other types of RNA viruses, including human retroviruses. The RNAi-mediated knockdown of *ZC3HAV1* mRNA enhanced the replication of xenotropic MLV-related virus, an artificial retrovirus belonging to the gammaretroviral genus of the family *Retroviridae* (29), in 293T cells (Fig. S8 *A* and *B*), whereas the knockdown of *ZC3HAV1* mRNA did not enhance the replication of human T-cell leukemia virus type I, a retrovirus belonging to the deltaretroviral genus of the family *Retroviridae* (30), in MT-2 cells (Fig. S8 *C* and *D*). In a previous study, the knockdown of *ZC3HAV1* mRNA enhanced the replication of HIV-1, a retrovirus belonging to the lentiviral genus of the family *Retroviridae* (31), in HOS-CD4 cells expressing chemokine (C-C motif) receptor 5 (32). Therefore, ZAP functions in human cells to target not all but certain types of retroviruses. ZAP is also known to suppress the replication of RNA viruses belonging to the families *Filoviridae* and *Togaviridae* (33, 34). Although ZAP has been shown to recognize the viral RNA of RNA viruses belonging to the families *Filoviridae*, *Togaviridae*, and *Retroviridae via*, its CCCH-type zinc-finger domains, the common features that are recognized by these domains, such as specific sequences or structural characteristics, have not been determined. Further studies are required to identify the RNA ligand of ZAP that induces the destabilization of the viral RNA by the RNA degradation machinery.

Although accumulating evidence indicates that ZAP counters a variety of RNA viruses under in vitro experimental conditions (20, 33, 34), it is still unclear whether ZAP protects hosts from RNA viral infections in vivo. RNA-sensing TLRs and the ssDNA cytosine deaminase apolipoprotein B mRNA-editing, enzyme-catalytic, polypeptide-like 3 are other antiviral systems that affect mouse retroviruses, and also control the replication of endogenous retroviruses (ERVs) (16, 35–37). Therefore, ZAP might also contribute to the antiviral response to ERVs and prevent the ERV-induced generation of tumors in vivo. To assess this, we are now establishing a colony of *Zc3hav1*$^{-/-}$ mice in the C57BL/6 genetic background. In a future study, we will attempt to determine the in vivo role of ZAP in the host defense responses to endogenous and exogenous microbes.

The CCCH-type zinc-finger–domain-containing protein family regulates RNA synthesis, splicing, and degradation, and is involved in a variety of cellular events, including cell growth, cell death, the inflammatory response, and the antimicrobial response (38, 39). To date, more than 50 CCCH-type zinc-finger-domain–containing proteins have been identified (40). Although various CCCH-type zinc-finger-domain-containing proteins, including tristetraprolin, roquin, and regnase-1, have been shown to be regulators of cytokine mRNA stability, ZAP is the only CCCH-type zinc-finger–domain-containing protein known to promote the destabilization of viral RNA (20, 41–43). Therefore, it will be interesting to identify a CCCH-type zinc-finger–domain-containing protein capable of mediating an antiviral response to RNA viruses that have evaded ZAP and the other RNA-sensing PRRs.

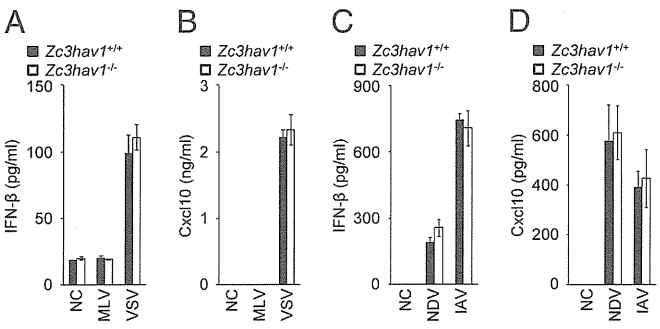

Fig. 6. ZAP is not essential for the RIG-I–mediated type I IFN response. (*A* and *B*) *Zc3hav1*$^{+/+}$ and *Zc3hav1*$^{-/-}$ MEFs were infected with MLV (2×10^{10} copies per μL) or VSV (MOI = 1) for 12 h. The levels of IFN-β (*A*) and Cxcl10 (*B*) proteins in the culture supernatants were measured with ELISAs. (*C* and *D*) *Zc3hav1*$^{+/+}$ and *Zc3hav1*$^{-/-}$ bone marrow-derived dendritic cells were infected with NDV (2.5×10^5 pfu/mL) or IAV (PR8, 100 Hematoglutinin) for 24 h. The levels of IFN-β (*C*) and Cxcl10 (*D*) proteins in the culture supernatants were measured with ELISAs. The results shown are means ± SD ($n = 3$).

Materials and Methods

Reagents. Anti-MLV-Gag antibody (ABIN457547) was purchased from Antibodies-online. Anti–α-tubulin antibody (T6199) was purchased from Sigma. Anti-GFP antibody (598) was purchased from MBL. Chicken anti–avian myelocytomatosis viral oncogene homolog (Myc) antibody (A190-103A) for the immunostaining assay was purchased from Bethyl Laboratories. Mouse anti–Myc-tag antibody (2276S) for immunoblotting was purchased from Cell Signaling. Anti-DDX6 (ab40684), anti-PMP70 (ab3421), and anti-LAMP1 (ab24170) antibodies were purchased from Abcam. Anti-DCP1A antibody (H00055802-M06) was purchased from Abnova. Anti-TOM20 antibody (SC-11415) was purchased from Santa Cruz Biotechnology. Anti-EEA1 antibody (610456) was purchased from BD Biosciences. The ELISA kit for mouse IFN-β was purchased from Pestka Biomedical Laboratories Interferon Source. The ELISA kit for mouse Cxcl10 was purchased from R&D Systems.

Plasmids. pMLV-48 (GenBank accession no. J02255.1) was previously described (44) and kindly donated by H. Fan (University of California, Irvine, CA). pcDNA3.1(+) was purchased from Invitrogen. To generate the ZAP

expression constructs, NheI/NotI cDNA fragments encoding full-length mouse ZAP (GenBank accession no. NM_028864.2) and the C-terminal portion of ZAP and a BamHI/NotI cDNA fragment encoding the N-terminal portion of ZAP were amplified from pCMV–SPORT6–Zc3hav1 (MMM1013-7511214, Open Biosystems) by PCR and cloned into the corresponding restriction sites of pcDNA3 to produce pcDNA3–ZAP, pcDNA3–ZAP–C, and pcDNA3–ZAP–N, respectively. To generate the expression construct for the EGFP–ZAP fusion protein, an NheI/SpeI cDNA fragment encoding EGFP was amplified from pEGFP-N1 (Clontech) by PCR and cloned into the NheI site of pcDNA3–ZAP to produce pcDNA3–EGFP–ZAP. To generate the red fluorescent protein (RFP) expression construct, a BamHI/EcoRI cDNA fragment of RFP was amplified from pTagRFP-N1 (Evrogen) by PCR and cloned into the BamHI/EcoRI sites of pcDNA3 to produce pcDNA3–RFP. To generate the expression constructs for the RFP–DCP1A and RFP–EXOSC5 fusion proteins, EcoRI/NotI cDNA fragments of human DCP1A and human EXOSC5 were amplified from a 293T cDNA library by PCR, and cloned into the EcoRI/NotI sites of pcDNA3–RFP to produce pcDNA3–RFP–DCP1A and pCDNA3–RFP–EXOSC5.

Mice, Cells, and Viruses. C57BL/6 mice were purchased from CLEA Japan, Inc. *Irf3*$^{-/-}$*/Irf7*$^{-/-}$ mice were kindly donated by T. Taniguchi (The University of Tokyo, Tokyo, Japan). The *Ddx58*$^{-/-}$*/Ifih1*$^{-/-}$ mice have been described previously (45). The mice were maintained in our animal facility and treated in accordance with the guidelines of Osaka University. Primary MEFs were prepared from pregnant female mice on embryonic day 13.5, as described previously (4). To prepare bone marrow-derived dendritic cells, mouse bone marrow cells were cultured in the presence of 10 ng/mL GM-CSF (PeproTech) for 6 d, during which time the culture medium was replaced with medium containing GM-CSF every 2 d. The 293T cells have been described previously (46). Replication-competent MLV was produced by 293T cells transfected with pMLV-48. To induce infection, MLV was incubated with MEFs for 2 h in the presence of 10 μg/mL Polybrene (Millipore). VSV, IAV (A/Puerto Rico/8/34, H1N1 strain), and NDV have been described elsewhere (3, 4).

Quantitative RT-PCR. Total RNA was isolated using the ZR RNA MicroPrep kit (Zymo Research), according the manufacturer's instructions. Viral RNA was isolated from the culture supernatants using the ZR Viral RNA kit (Zymo Research), according the manufacturer's instructions. RT was performed using random primers and Verso reverse transcriptase (Thermo Scientific) according to the manufacturer's instructions. For quantitative PCR, the cDNA fragments were amplified from the RT products with Real-Time PCR Master Mix (Toyobo) according to the manufacturer's instructions. The fluorescence from the TaqMan probe for each cytokine was detected with a 7500 Real-Time PCR System (Applied Biosystems). To determine the relative induction of cytokine mRNAs, the level of mRNA expressed from each gene was normalized to the expression of 18S RNA. The copy number of the MLV genomic RNA was determined with the dsDNA copy number calculator program. The experiments were repeated at least three times, with reproducible results.

ELISAs. The levels of IFN-β and Cxcl10 in the culture supernatants were measured with ELISAs in accordance with the manufacturer's instructions. The experiments were repeated at least three times, with reproducible results.

Northern Blotting. Cytoplasmic RNA was extracted using the Cytoplasmic and Nuclear RNA Purification Kit (Norgen) according the manufacturer's instructions. The RNA obtained was separated electrophoretically, transferred to nylon membranes, and hybridized with the indicated probes. An RNA probe was designed to hybridize specifically to the Gag region from nucleotide 1291 to nucleotide 1472 of the MLV transcripts. The experiments were repeated at least three times, with reproducible results.

Immunoblotting. Immunoblotting was performed as described previously (47). The experiments were repeated at least three times, with reproducible results.

Immunostaining Assay. Cells cultured in microscopy chambers (ibidi) were fixed with 3% (wt/vol) paraformaldehyde and then processed for immunostaining as described previously (47). The samples were examined under an LSM 780 confocal laser scanning microscope (Carl Zeiss). The experiments were repeated at least three times, with reproducible results.

Detection of the MLV Transcripts with FISH. The cells were fixed with 4% paraformaldehyde. FISH was performed using the QuantiGene ViewRNA ISH Cell Assay kit (Veritas) according to the manufacturer's instructions. A Cy5-labeled FISH probe was designed to hybridize specifically to the Gag region from nucleotide 607 to nucleotide 1833 of the MLV transcripts. The samples were examined under an LSM780 confocal laser scanning microscope. The experiments were repeated at least three times, with reproducible results.

ACKNOWLEDGMENTS. We thank Drs. H. Fan, D. Trono, H. Miyoshi, and T. Taniguchi for providing invaluable materials and the members of the Laboratory of Host Defenses for their assistance. This work was supported by a Japan Society for the Promotion of Science Grant-in-Aid for Challenging Exploratory Research (to T. Saitoh); the Cabinet Office, Government of Japan, and the Japan Society for the Promotion of Science Funding Program for World-Leading Innovative Research and Development on Science and Technology "FIRST Program" (to S.A.); and National Institutes of Health Grant P01-AI070167 (to S.A.).

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