1991; Wang and Heitman, 2005). CypB participates in various biological functions, such as chaperone activities, immunosuppression, transcriptional regulation, apoptosis, and viral propagation (Allain et al., 1996; Kim et al., 2008; Rycyzyn and Clevenger, 2002; Watanabe et al., 2010; Watashi et al., 2005; Zhang and Herscovitz, 2003). Cyclosporin A (CsA), an inhibitor for Cyps, significantly impaired the propagation of JEV. Knockdown of CypB reduced the RNA replication in the JEV replicon cells, whereas it exhibited no effect on the infection of a pseudotype virus bearing JEV envelope proteins. Furthermore, CypB was colocalized and immunoprecipitated with the JEV NS4A protein. Collectively, these results suggest that CypB plays a crucial role in the propagation of JEV through its interaction with NS4A.

Results

CsA suppresses the production of JEV by inhibiting Cyps

CsA is an immunosuppressive agent widely used in the management of organ transplantation. In addition to this activity, it has been reported that CsA has potent antiviral effects against HCV (Chatterji et al., 2009; Kaul et al., 2009; Watashi et al., 2005; Yang et al., 2008), HIV (Franke et al., 1994; Thali et al., 1994), measles virus (MV) (Watanabe et al., 2010), influenza A virus (Liu et al., 2009), vesicular stomatitis virus (VSV) (Bose et al., 2003), and vaccinia virus (VV) (Castro et al., 2003; Damaso and Moussatche, 1998). To examine the possibility that CsA has an antiviral effect on JEV, mammalian cell lines including Huh7, BHK, and N18 cells were treated with various concentrations of CsA followed by infection with JEV. At 48 h post-infection, cells were subjected to immunoblotting. The level of expression of JEV NS1 was significantly decreased by treatment with CsA in a dose-dependent manner in all the cell lines examined (Fig. 1A). Furthermore, infectious particle production in the culture supernatant was also reduced by the treatment with CsA under the conditions employed without exhibiting any serious cytotoxic effect (Fig. 1B).

CsA exhibits three distinct inhibitory activities on, respectively, the calcineurin NF-AT signaling pathway, the peptidylprolyl *cis-trans* isomerase (PPIase) activity of Cyps, and the transport activity of p-glycoprotein (Silverman et al., 1997). To determine the antiviral activity of CsA, we used CsA derivatives and FK506, an immunosuppressant structurally different from CsA. cyclosporin D (CsD) has almost no effect on the calcineurin pathway (Sadeg et al., 1993) and cyclosporin H (CsH) has a specific inhibitory activity on the p-glycoprotein (Silverman et al., 1997). FK506 also inhibits the calcineurin NF-AT signaling pathway (Almawi and Melemedjian, 2000). Huh7 cells were infected with JEV and treated with various concentrations of the compounds at 1 h post-infection. The cells and culture supernatants were harvested at 48 h after treatment and the expression of JEV NS1 and infectivity were determined, respectively (Fig. 2). Treatment with CsA and CsD reduced the expression of the NS1 and the production of JEV in a dose-dependent manner, whereas CsH and FK506 exhibited almost no effect on the propagation of JEV (Fig. 2). These results suggest that CsA inhibits JEV propagation through the inhibition of Cyps, but not through the inhibition of calcineurin and p-glycoprotein.

CypB participates in the propagation of JEV

Cyps possessing the PPIase activity are highly conserved and ubiquitously expressed in both prokaryotic and eukaryotic cells (Wang and Heitman, 2005). Next, to determine whether the particular Cyp isoform participates in the propagation of JEV, short interference RNAs (siRNAs) targeted to CypA, CypB, or CypC were transfected into Huh7 cells and the expression of each Cyp was determined by immunoblotting or real-time PCR at 24 h post-transfection. CypA and CypB were specifically decreased by the transfection of the siRNAs (Fig. 3A). Although CypC could not be detected by immunoblotting due to the lack of a specific antibody in our laboratory, CypC mRNA was decreased by approximately 90% upon transfection with siRNA targeted

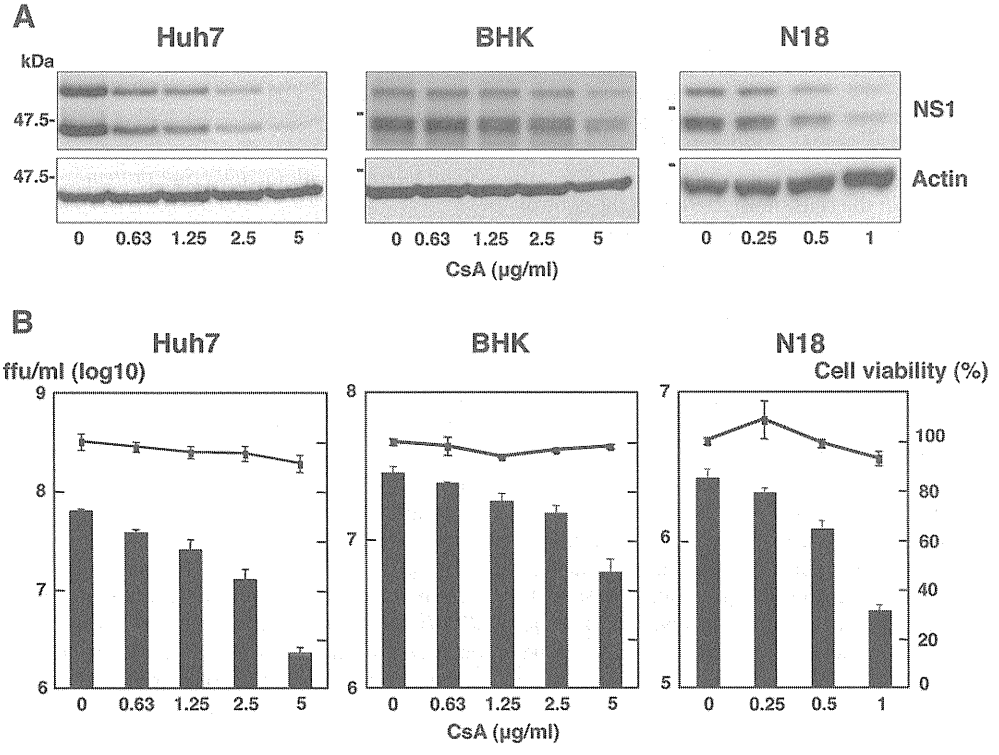


Fig. 1. Effect of CsA on the propagation of JEV in mammalian cells. (A) JEV was inoculated at an MOI of 0.1 (Huh7 and BHK cells) or 10 (N18 cells) and incubated for 1 h. Cells were washed with 10% FBS DMEM and treated with the indicated concentrations of CsA in 10% FBS DMEM for 48 h. The propagation of JEV was assessed by the expression of NS1. NS1 and actin were detected by immunoblotting. (B) The production of infectious JEV in the culture supernatant at 48 h post-infection was determined in Vero cells by a focus-forming assay. Cell viability was determined at 48 h post-incubation of CsA. The results are representative of three independent assays, with the error bars indicating the standard deviations.

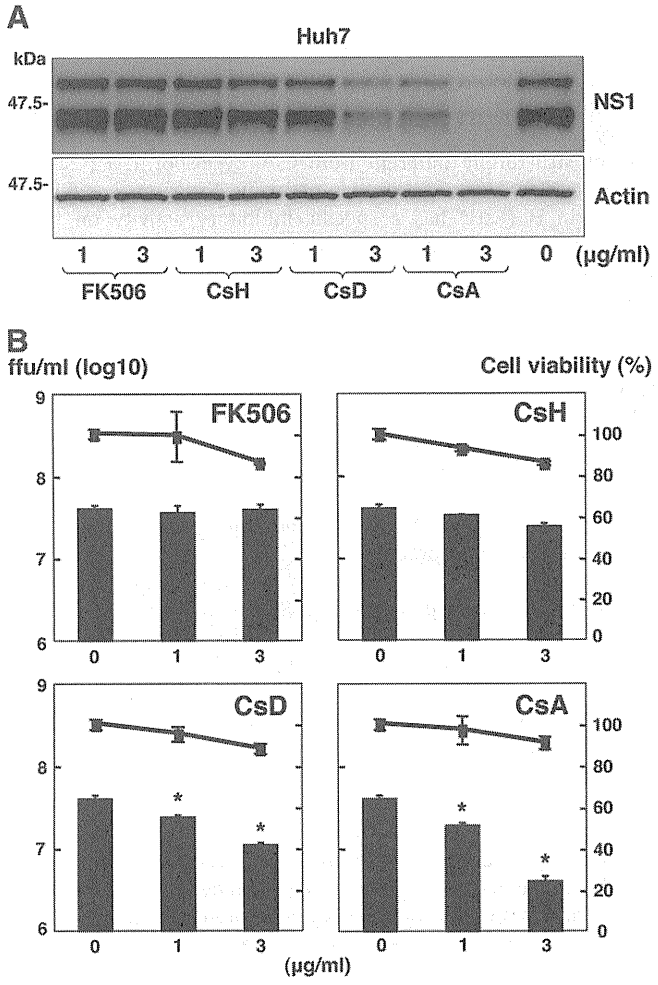


Fig. 2. CsA inhibits JEV propagation through the inhibition of Cyps. Huh7 cells were infected with JEV at an MOI of 0.1 for 1 h and then treated with 10% FBS DMEM containing the indicated concentrations of CsA, CsD, CsH, or FK506 for 48 h. The propagation of JEV was evaluated by immunoblotting (A) and focus-forming assay (B). The results are representative of three independent assays, with the error bars indicating the standard deviations. Asterisks indicate significant differences (*$P<0.01$).

to CypC compared to the level in the cells transfected with the control siRNA (Fig. 3B). JEV was inoculated into cells transfected with the siRNA at 48 h post-transfection and the cells and culture supernatants were harvested at 48 h post-infection. Expression of JEV NS1 was most effectively decreased by the knockdown of CypB, followed by CypC, and knockdown of CypA resulted in a marginal reduction of NS1 expression compared to the control siRNA (Fig. 3C). Furthermore, the production of JEV was also effectively suppressed in cells with knockdown of CypB, followed by those with knockdown of CypC and CypA (Fig. 3D). These results suggest that CypB plays an important role in the propagation of JEV. To further confirm the effect CypB on the propagation of JEV, we established stable knockdown cell lines expressing a short hairpin RNA (shRNA) targeted to CypB. Consistent with the data from transient knockdown experiments, both expression of NS1 and virus production were significantly reduced in the CypB-knockdown cell lines (Bose et al., 2003; Castro et al., 2003) in accordance with the reduction of CypB (Fig. 4A and B). There was no significant difference in cell growth among the cell lines (Fig. 4C).

PPIase activity of CypB is crucial for the propagation of JEV

The PPIase activity of Cyps is suggested to catalyze the proper folding of certain proteins (Andreotti, 2003; Wang and Heitman, 2005). It has been demonstrated that PPIase activity of Cyps is required for HCV replication (Chatterji et al., 2009; Kaul et al., 2009; Watashi et al., 2005). To examine the effect of the PPIase activity of CypB on the propagation of JEV, we constructed an expression plasmid encoding a PPIase-defective CypB in which the Arg^{62} was replaced with Ala, because the Arg^{62} in CypB has been shown to be critical for PPIase catalytic activity (Carpentier et al., 1999). Each of the expression plasmids encoding the FLAG-tagged wild- or Ala^{62}-CypB carrying the silent mutations resistant to the siRNA was introduced into the stable CypB-knockdown cell line (Bose et al., 2003) and cultured for a week in the presence of neomycin. Although expression of both endogenous and exogenous CypB was detected at a similar level (Fig. 4D), JEV production was partially rescued by introducing the wild-CypB but not the Ala^{62}-CypB (Fig. 4E). These results indicate that the PPIase activity of CypB is crucial for the propagation of JEV.

CypB participates in the replication but not in the entry of JEV

To further examine the effect of CsA on the JEV life cycle, we generated a subgenomic replicon of JEV to assess the effect of CsA on the JEV RNA replication (Fig. 5A). The replicon cells treated with CsA for 6 days exhibited a significant reduction of NS1 expression compared to the non-treated cells (Fig. 5B). The replicon RNA transcribed from the pJErepIRESpuro was transfected into the stable CypB-knockdown (#4) or control cell lines and incubated for 3 weeks in the presence of puromycin. A few colony formation was detected in the CypB-knockdown cell line, in contrast to the abundant colony formation in the control cell line (Fig. 5C). These results suggest that CypB is required for the efficient replication of JEV.

Next, to examine the impact of CypB on the entry of JEV, we generated pseudotype VSVs bearing envelope proteins of JEV (JEVpv) or VSV (VSVpv). Because these viruses possess the luciferase gene, the infectivity can be assessed by the luciferase activity (Tani et al., 2010). Huh7 cells pretreated with various concentrations of CsA were infected with JEVpv or VSVpv, and the infectivity was assessed by the expression of luciferase. There was no significant effect of CsA on the infection of either pseudotype virus (Fig. 5D). Similarly, no effect was observed on the infection of the pseudotype viruses in the CypB-knockdown cell lines (Fig. 5E). Collectively, these results clearly indicate that CypB participates in the replication but not in the entry of JEV.

CypB interacts with the JEV NS4A protein

Many viruses have been shown to utilize Cyps through the interaction with their viral proteins. For example, HCV recruits CypA and CypB to enhance viral RNA replication through the interaction with NS5A and NS5B, respectively (Chatterji et al., 2009; Kaul et al., 2009; Watashi et al., 2005; Yang et al., 2008). To determine whether the JEV proteins interact with CypB, we prepared expression plasmids encoding each of the JEV nonstructural proteins involved in the viral RNA replication. FLAG-tagged CypB was co-expressed with each of the HA-tagged JEV nonstructural proteins in 293T cells and immunoprecipitated with anti-HA antibody. The precipitates were subjected to immunoblotting by using either anti-FLAG or anti-HA antibodies. CypB was co-precipitated with the JEV NS4A protein but not with other proteins (Fig. 6A). Furthermore, interaction of CypB with NS4A was reduced in the immunoprecipitation analysis in the presence of CsA (Fig. 6B). To gain more insight into the interaction between CypB and NS4A, the intracellular localization of these proteins was examined by confocal microscopy. Huh7 cells were transfected with an expression plasmid encoding HA-tagged NS4A or an empty vector and fixed at 48 h post-transfection. Endogenous CypB was detected in the perinuclear region together with NS4A protein. In addition, NS4A colocalized with ER marker protein, calnexin (Fig. 6C). These results suggest that NS4A protein interacts with CypB at the replication complex localized in the ER.

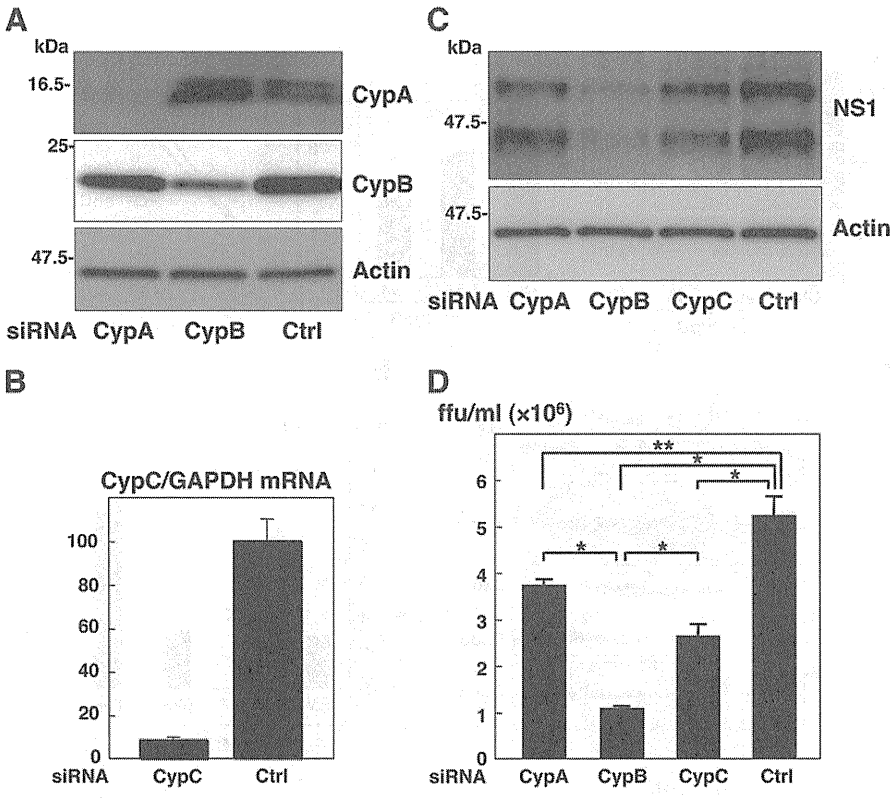


Fig. 3. CypB plays an important role in the propagation of JEV. (A) Knockdown of endogenous CypA and CypB by siRNA. Huh7 cells were transfected with 35 nM of siRNA targeted to CypA, CypB, or a non-specific control. Cell lysates after 96 h post-transfection were analyzed for expression of CypA, CypB, or actin by immunoblotting. (B) Huh7 cells transfected with 35 nM of siRNA targeted to CypC or a non-specific control were harvested at 24 h post-transfection. CypC mRNA levels were determined by quantitative real-time PCR. The level of CypC mRNA was normalized to the amount of GAPDH mRNA and expressed as a percentage of the control value. (C, D) Huh7 cells were transfected with siRNA targeted to CypA, CypB, or CypC and infected with JEV at an MOI of 0.1 at 48 h post-transfection. The propagation of JEV was determined by immunoblotting (C) and focus-forming assay (D). The results are representative of three independent assays, with the error bars indicating the standard deviations. Asterisks indicate significant differences (*$P<0.01$; **$P<0.05$).

Discussion

In this study, we have shown that CsA inhibits the replication of JEV through the inhibition of the PPIase activity of Cyps. A previous study showed that CsA does not induce interferon in Huh7 cells (Nakagawa et al., 2005), suggesting that the antiviral activity of CsA on the propagation of JEV relies on the inhibition of Cyps. Cyps are highly conserved PPIases that catalyze the *cis-trans* isomerization of peptide bonds to facilitate certain protein foldings (Andreotti, 2003; Wang and Heitman, 2005) and are involved in the correct folding of host and viral proteins. Among the Cyp isoforms, CypA and CypB are the most abundantly expressed in cells and play key roles in the propagation of various viruses. CypA is incorporated into HIV, influenza A virus, VSV, and VV to regulate their replication (Bose et al., 2003; Castro et al., 2003; Damaso and Moussatche, 1998; Franke et al., 1994; Liu et al., 2009; Thali et al., 1994). CypB is incorporated into MV particles to facilitate an efficient infection (Watanabe et al., 2010). Both CypA and CypB have been shown to serve as host factors involved in the replication of HCV through the interaction with NS5A and NS5B (Chatterji et al., 2009; Kaul et al., 2009; Watashi et al., 2005; Yang et al., 2008).

Recently, Qing et al. reported that CypA plays an important role in the replication of flaviviruses such as WNV, YFV, and DENV. The PPIase activity of CypA was shown to be crucial for the efficient replication of the viruses, indicating that CypA acts as a molecular chaperone for the viral and host proteins required for an effective RNA replication (Qing et al., 2009). Indeed, knockdown of CypA suppressed the JEV propagation in this study, but that of CypB exhibited more potent impairment of the JEV propagation, suggesting that CypB plays a crucial role in the propagation of JEV. However, we could not exclude the possibility of the involvement of other Cyps in the replication of JEV. Multiple Cyps have been shown to involved in the life cycle of HCV (Gaither et al., 2010; Nakagawa et al., 2005) and the knockdown experiment of Cyps in this study suggests that not only CypB, but also CypC and CypA are involved in the propagation of JEV. At least 16 Cyps have been shown to participate in various cellular functions in humans (Wang and Heitman, 2005), and therefore, further studies to clarify the precise function of these Cyps in the life cycle of the flaviviruses are needed.

In addition to Cyps, flavivirus recruits several host chaperones for an efficient propagation. HSP70 and HSP90 have been identified as comprising the DENV receptor complex in human cell lines. These chaperones presumably facilitate the viral envelope dimer–trimer transition after the binding of the envelope protein to the cellular receptor (Reyes-Del Valle et al., 2005). Moreover, inhibition of the interaction between the ER chaperone calnexin and JEV glycoproteins has been suggested to affect the folding of viral proteins, leading to a reduction in the mortality rate in a mouse model of lethal infection (Wu et al., 2002). It has been reported that ER chaperones including BiP, calnexin, and calreticulin interact with the DENV envelope protein, and that knockdown of these chaperones decreased viral production (Limjindaporn et al., 2009). In addition, BiP was shown to be upregulated in cells infected with DENV to facilitate viral production (Wati et al., 2009), and BiP and calreticulin have been associated with CypB (Zhang and Herscovitz, 2003). Therefore, these ER resident chaperones are considered to play important roles in the flavivirus replication through the proper folding of the viral and host proteins making up the viral RNA replication complex.

Lack of recovery of JEV propagation in the CypB-knockdown cell lines by the expression of the PPIase-deficient CypB mutant suggests that PPIase activity is crucial for the JEV production. Although the PPIase activity of CypA has been shown to be required for flavivirus replication

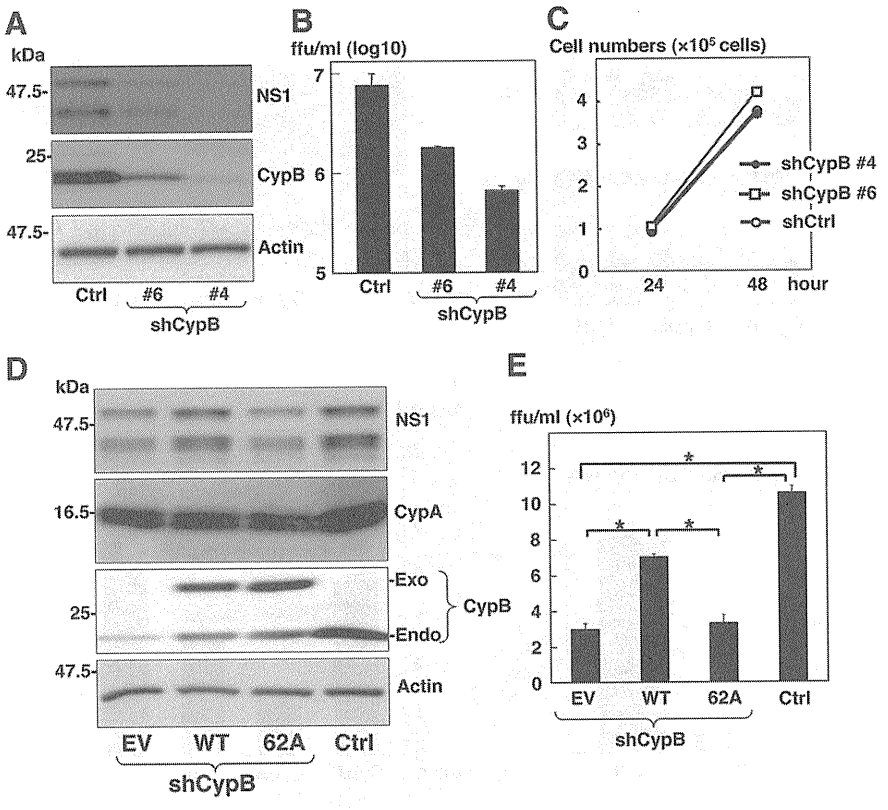


Fig. 4. PPIase activity of CypB is crucial for the propagation of JEV. Huh7 cell lines expressing shRNA targeted to CypB or the control were infected with JEV at an MOI of 0.1 for 1 h and cultured in 10% FBS DMEM for 48 h. The expressions of NS1, CypB, and actin were detected by immunoblotting (A). The propagation of JEV was determined by focus-forming assay (B). Growth kinetics of the stable CypB-knockdown cell lines were determined by the method of trypan blue dye exclusion (C). The stably knocked-down cell lines were transfected with the siRNA-resistant FLAG-tagged wild- or Ala^{62}-CypB, or empty vector and cultured for 1 week in the presence of 1 μg/ml puromycin. The remaining cells were infected with JEV at an MOI of 1. The expressions of NS1, CypA, endogenous and exogenous CypBs, and actin were detected by immunoblotting (D). Virus production in the culture supernatant at 36 h post-infection was determined by a focus-forming assay (E). The results are representative of three independent assays, with the error bars indicating the standard deviations. Asterisks indicate significant differences (*$P<0.01$).

through the interaction with the NS5 polymerase (Qing et al., 2009), CypB was colocalized and specifically co-immunoprecipitated with JEV NS4A. CypA is abundantly expressed in the cytoplasm of mammalian cells (Galigniana et al., 2004) and NS5 is predominantly detected on the cytoplasmic side of the ER (Zhang et al., 1992). Thus, it is conceivable that an interaction between CypA and NS5 occurs on the cytoplasmic side of the ER. On the other hand, CypB is localized in the ER lumen and targeted to the secretory pathway via its ER signal sequence (Price et al., 1994, 1991). NS4A is predicted to be a three-transmembrane protein with its C-terminal end localized in the ER lumen (Miller et al., 2007). Therefore, it is plausible that CypB interacts with NS4A within the ER lumen and confers proper folding to form the RNA replication complex of JEV. Expression of DENV NS4A alone has been shown to induce rearrangement of the cytoplasmic membrane to form the convoluted membrane required for viral replication (Roosendaal et al., 2006). It might be feasible to speculate that JEV NS4A undergoes conformational change through the interaction with CypB and induces formation of the convoluted membrane in the ER essential for genome replication of JEV. It was reported that HCV NS5A from CsA resistant mutant exhibits an enhanced interaction with CypB and NS5B facilitates a stronger binding of the mutant NS5A to endogenous CypB than wild-type in cell culture (Fernandes et al., 2010). Study of the molecular mechanism underlying the CsA resistant of JEV may shed light on the complex interaction among Cyps and viral proteins.

In conclusion, we have demonstrated that CsA suppresses the propagation of JEV by inhibiting the interaction between CypB and NS4A, which is required for viral RNA replication. Further studies are needed to elucidate the precise molecular mechanism underlying the involvement of cellular Cyps in the efficient propagation of JEV. Three inhibitors of the PPIase activity of Cyps, DEBIO-025, SCY635, and NIM811, are currently under clinical trial for the treatment of hepatitis C patients (Puyang et al., 2010). The PPIase inhibitor may be an attractive therapeutic target for the treatment of patients infected with not only HCV but also other flaviviruses.

Materials and methods

Plasmids

The human CypB gene was amplified from the total cDNA of Huh7 by PCR using *LA taq* (Takara Bio Inc., Shiga, Japan) and cloned into pcDNA3.1 and pCAGPM (Mori et al., 2007). The plasmids encoding the NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 of the JEV AT31 strain were generated by PCR and cloned into pCAGPM. The pSilencer-CypB, carrying an shRNA targeted to CypB under the control of the U6 promoter, was constructed by cloning of the oligonucleotide pair 5′-GATCCGGTGGAGAGCACCAAGACATTCAAGAGATGTCTTGGTGCTCTC-CACCTTTTTTGGAAA-3′-5′-AGCTTTTCCAAAAAAGGTGGAGAGCACCAA-GACATCTCTTGAATGTCTTGGTGCTCTCCACCG-3′ between the *Bam*HI and *Hin*dIII sites of pSilencer 2.1-U6 hygro (Ambion, Austin, TX). A plasmid coding a mutant CypB resistant to shRNA was prepared by insertion of four silent mutations (the nucleotides at positions 543, 549, 555, and 561 were changed from G to A, G to A, C to G, and A to C, respectively) into CypB cDNA by the method of splicing by overlap extension (Ho et al., 1989). The pSilencer negative-control plasmid (Ambion) has no homology to any human gene. The pJErep plasmid was kindly provided by Dr. Konishi (Kobe University, Kobe, Japan). A puromycin-resistant gene under the internal ribosomal entry site (IRES) of encephalomyocarditis virus was inserted into pJErep and designated as pJErepIRESpuro.

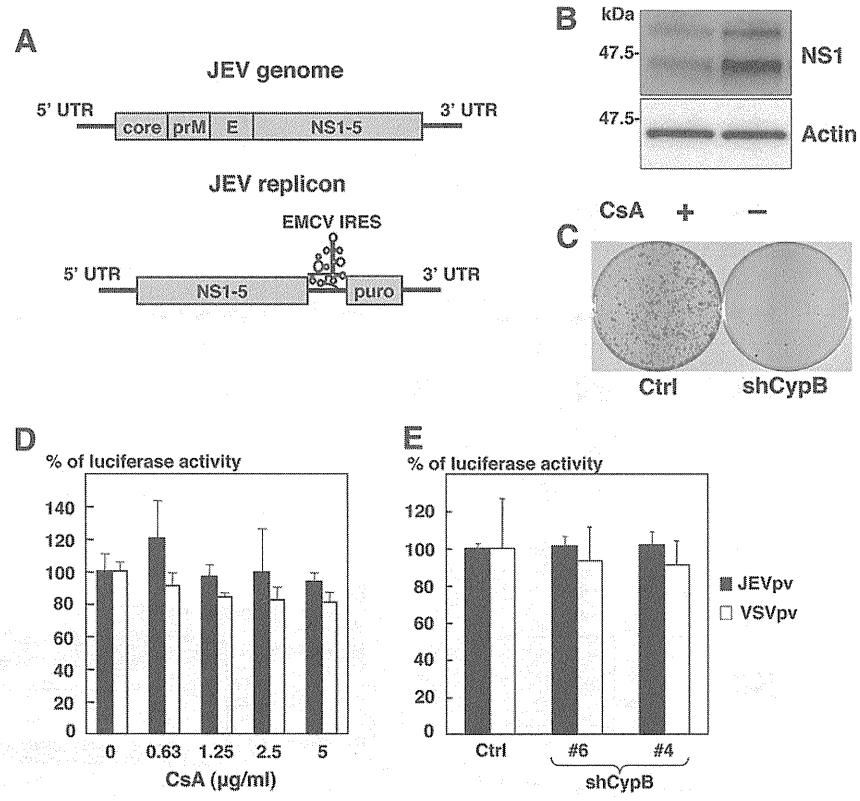


Fig. 5. CypB participates in the replication but not in the entry of JEV. (A) Schematic representations of the JEV genome and its subgenomic replicon. (B) JEV replicon cells were treated with CsA (1 μg/ml) for 6 days, and the expressions of NS1 and actin were detected by immunoblotting. (C) The stable CypB-knockdown and control cell lines were electroporated with the JEV replicon RNA and cultured for 3 weeks in the presence of 1 μg/ml of puromycin. The remaining cells were fixed with 4% paraformaldehyde and stained with crystal violet. (D) Huh7 cells treated with the indicated concentrations of CsA for 1 h were infected with the pseudotype viruses, JEVpv and VSVpv, and luciferase activities were determined at 24 h post-infection. (E) The stable CypB-knockdown and control cell lines were incubated with the pseudotype viruses, and the luciferase activities were determined. The results shown are representative of three independent assays, with error bars indicating standard deviations.

Cells and viruses

All cell lines were cultured at 37 °C under the condition of a humidified atmosphere and 5% CO_2. The human embryonic kidney cell line, 293T, African green monkey kidney cell line, Vero, hepatocellular carcinoma cell line, Huh7, mouse neural cell line, N18, and baby hamster kidney cell line, BHK, were maintained in Dulbecco's modified Eagle's medium (DMEM) (Sigma, St. Louis, MO) supplemented with 100 U/ml penicillin, 100 μg/ml streptomycin, non-essential amino acid (Sigma), and 10% fetal bovine serum (FBS). The mosquito C6/36 cell line (*Aedes albopictus*) was cultured at 27 °C and maintained in modified Eagle's medium (MEM) (Sigma). Huh7 cells were transfected with pSilencer-CypB or control plasmid and drug-resistant clones were selected by treatment with hygromycin B (Wako, Tokyo, Japan) at a final concentration of 50 μg/ml. Huh7 cells were electroporated with *in vitro*-transcribed RNA from pJErepIRESpuro and drug-resistant clones were selected by treatment with puromycin (InvivoGen, San Diego, CA) at a final concentration of 1 μg/ml. Wild-type JEV strain AT31 was used as described previously (Tani et al., 2010). The wild-type JEV was amplified on C6/36 cells and stored at −80 °C. Pseudotype VSVs bearing JEV PrM and E proteins (JEVpv) and VSVG (VSVpv) were produced in 293T cells transfected with pCAG105E and pCAGVSVG, respectively, as described previously (Tani et al., 2010). The infectivities of JEV and the pseudotype VSVs were assessed by both a focus-forming assay and luciferase activity as described previously (Tani et al., 2010). Cell viability was determined by using CellTiter-Glo (Promega Corporation, Madison, WI) according to the manufacturer's protocol.

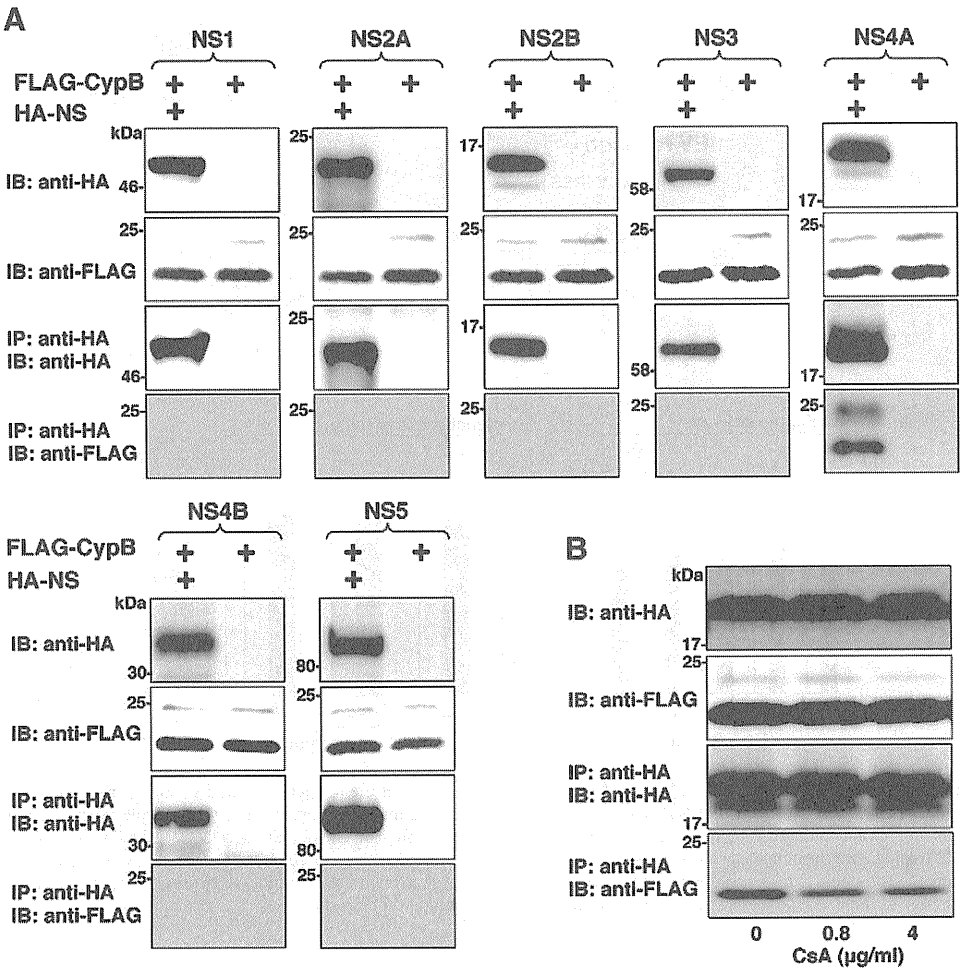
Reagents and antibodies

CsA and FK506 were purchased from Sigma, and CsD and CsH from Eton Bioscience Inc. (San Diego, CA). Mouse monoclonal antibodies to tags of HA and FLAG and β-actin were previously described (Taguwa et al., 2009). Rabbit polyclonal antibodies to CypA and CypB were purchased from Upstate Cell Signaling (Lake Placid, NY) and Affinity BioReagents (Golden, CO), respectively. Rabbit polyclonal antibody to calnexin was purchased from Santa Cruz Biotechnology (Santa Cruz, CA). Mouse monoclonal antibody to JEV NS1 protein (34A1) was kindly provided by Dr. Yasui.

Transfection, immunoblotting, and immunoprecipitation

Transfection and immunoprecipitation were carried out as described previously (Taguwa et al., 2009). Immunoprecipitates boiled in loading buffer were subjected to 12.5% sodium dodecyl sulfate-polyacrylamide gel electrophoresis. The proteins were transferred to polyvinylidene

Fig. 6. NS4A protein recruits CypB to the replication complex in the JEV-infected cells. (A) FLAG-tagged CypB was co-expressed with HA-tagged NS1, NS2A, NS2B, NS3, NS4A, NS4B, or NS5 in 293T cells and immunoprecipitated with anti-HA antibody. The immunoprecipitates were subjected to immunoblotting by using either anti-FLAG or anti-HA antibody. (B) FLAG-tagged CypB was co-expressed with HA-tagged NS4A in 293T cells. The cell lysates obtained after lysis with the buffer containing CsA were immunoprecipitated with anti-FLAG antibody. The immunoprecipitates were subjected to immunoblotting by using either anti-FLAG or anti-HA antibody. (C) Huh7 cells transfected with an expression plasmid encoding HA-tagged NS4A or empty vector were fixed at 48 h post-transfection, permeabilized, and stained with the appropriate antibodies to HA (green), calnexin (red), and CypB (red). Cell nuclei were stained with DAPI (blue). Intracellular localization of CypB and NS4A was examined by confocal microscopy.


A
NS1
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FLAG-CypB
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IP: anti-HA
IB: anti-FLAG
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NS5
B
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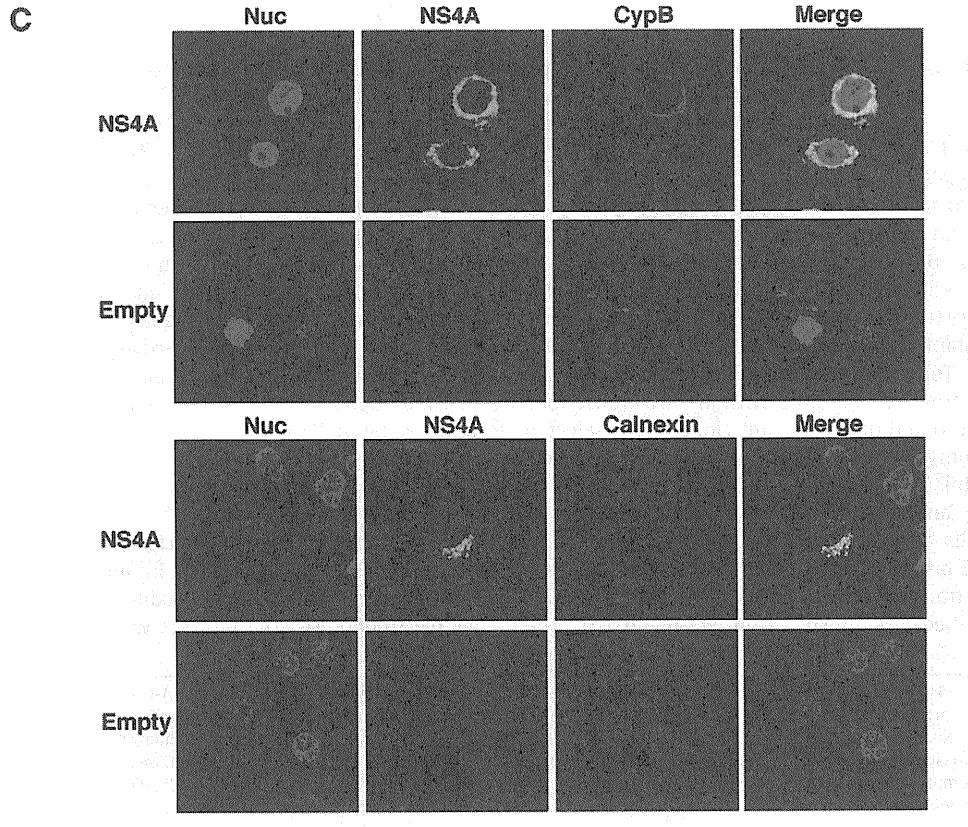
CsA (μg/ml)


C
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difluoride membranes (Millipore, Bedford, MA) and were reacted with the appropriate antibodies. The immune complexes were visualized with Super Signal West Femto substrate (Pierce, Rockford, IL) and detected by an LAS-3000 image analyzer system (Fujifilm, Tokyo, Japan).

Gene silencing by siRNA

The siRNAs against CypA and CypB were 5′-AAGCATACGGGTCCTGGCATC-3′ and 5′-AAGGTGGAGAGCACCAAGACA-3′, respectively (QIAGEN, Tokyo, Japan). FlexTube siRNAs against CypC and the negative control were purchased from QIAGEN. The cells were grown on 6-well plates and transfected with 35 nM siRNA by using Dharmafect (Dharmacon, Buckinghamshire, UK) according to the manufacturer's protocol. The transfected cells were incubated in DMEM supplemented with 10% FBS.

Quantitative RT-PCR

RNA was determined by the method described previously (Taguwa et al., 2009). The total RNA was prepared from cells by using an RNeasy mini kit (QIAGEN). First-strand cDNA was synthesized using an RNA LA PCR™ *in vitro* cloning kit (Takara Bio Inc.) and random primers. Each cDNA was determined by Platinum SYBR Green qPCR SuperMix UDG (Invitrogen, San Diego, CA) according to the manufacturer's protocol. Fluorescent signals were analyzed by an ABI PRISM 7000 (Applied Biosystems, Tokyo, Japan).

In vitro transcription and RNA transfection

Plasmid pJErepIRESpuro linearized at the *Swa* I site was transcribed *in vitro* using an mMESSAGE mMACHINE (Ambion) according to the manufacturer's protocol. The *in vitro*-transcribed RNA was introduced into Huh7 cells at 5 million cells/0.5 ml by electroporation at 270 V and 960 μF using Gene Pulser™ (Bio-rad, Hercules, CA).

Colony formation assay

Colony formation was determined as previously described (Taguwa et al., 2009). Briefly, *in vitro*-transcribed RNA was electroporated into Huh7 cells and plated on DMEM containing 10% FBS and non-essential amino acids. The medium was replaced with fresh DMEM containing 10% FBS, non-essential amino acids, and 1 μg/ml puromycin at 24 h post-transfection. The remaining colonies were fixed with 4% paraformaldehyde (PFA) and stained with crystal violet at 3 weeks after electroporation.

Indirect immunofluorescence assay

Cells cultured on glass slides were fixed with 4% PFA in phosphate buffered saline (PBS) at room temperature for 30 min. After washing three times with PBS, the cells were permeabilized for 20 min at room temperature with PBS containing 0.25% saponin and blocked with phosphate buffer containing 2% BSA for 1 h at room temperature. The cells were incubated with blocking buffer containing mouse anti-HA or rabbit anti-CypB at room temperature for 1 h, then washed three times with PBS and incubated with blocking buffer containing AF488-conjugated anti-mouse IgG and AF594-conjugated anti-rabbit IgG at room temperature for 1 h. Cell nuclei were stained blue with DAPI. Finally, the cells were washed three times with PBS and observed a FluoView FV1000 laser scanning confocal microscope (Olympus, Tokyo, Japan).

Statistical analysis

Results are expressed as the means ± standard deviation. The significance of differences between the means was determined by Student's *t*-test.

Acknowledgments

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Elimination of Hepatitis C Virus from Hepatocytes by a Selective Activation of Therapeutic Molecules

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Abstract

To eliminate hepatitis C virus (HCV) from infected hepatocytes, we generated two therapeutic molecules specifically activated in cells infected with HCV. A dominant active mutant of interferon (IFN) regulatory factor 7 (IRF7) and a negative regulator of HCV replication, VAP-C (Vesicle-associated membrane protein-associated protein subtype C), were fused with the C-terminal region of IPS-1 (IFNβ promoter stimulator-1), which includes an HCV protease cleavage site that was modified to be localized on the ER membrane, and designated cIRF7 and cVAP-C, respectively. In cells expressing the HCV protease, cIRF7 was cleaved and the processed fragment was migrated into the nucleus, where it activated various IFN promoters, including promoters of IFNα6, IFNβ, and IFN stimulated response element. Activation of the IFN promoters and suppression of viral RNA replication were observed in the HCV replicon cells and in cells infected with the JFH1 strain of HCV (HCVcc) by expression of cIRF7. Suppression of viral RNA replication was observed even in the IFN-resistant replicon cells by the expression of cIRF7. Expression of the cVAP-C also resulted in suppression of HCV replication in both the replicon and HCVcc infected cells. These results suggest that delivery of the therapeutic molecules into the liver of hepatitis C patients, followed by selective activation of the molecules in HCV-infected hepatocytes, is a feasible method for eliminating HCV.

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Introduction

Hepatitis C virus (HCV) is a major cause of chronic liver diseases. A high risk of chronicity is the major concern of HCV infection, since chronic HCV infection often leads to liver cirrhosis and hepatocellular carcinoma [1,2]. Although the proportion of patients achieving a sustained virological response (SVR) has been increased by the recent used of combination therapy with pegylated-interferon-α (PEG-IFNα) and ribavirin (RBV), half of patients still exhibit no response to this therapy, suggesting that the IFN signaling pathway is modulated by HCV infection. In addition, various side effects have been reported in more than 20% of patients treated with this combination therapy [3].

HCV belongs to the family *Flaviviridae* and possesses a single positive-stranded RNA genome that encodes a single polyprotein composed of about 3,000 amino acids. The HCV polyprotein is processed into 10 viral proteins by host and viral proteases. Viral structural proteins, including the capsid protein and two envelope proteins, are located in the N-terminal one third of the polyprotein, followed by nonstructural proteins. The NS2 protease cleaves its own carboxyl terminus and NS3 cleaves the downstream positions to produce NS4A, NS4B, NS5A and NS5B. Although laboratory strains of HCV propagating in cell culture (HCVcc) have been established based on the full-length genome of the genotype 2a JFH1 strain [4], establishment of a robust cell culture system capable of propagating serum-derived HCV from hepatitis C patients has not yet been achieved.

Type I IFN exhibits potent antiviral effects through the regulation of hundreds of IFN-stimulated genes (ISGs) which encode proteins involved in the establishment of antiviral state in cells [5]. IFNs induce transcription of ISGs through activation of the Jak-STAT pathway [6]. Binding of type I IFN to the IFN receptor induces phosphorylation of the receptor-associated tyrosine kinases, Jak1 and Tyk2, and then these kinases activate STAT1 and STAT2. The phosphorylated STATs migrate into the nucleus and activate ISG promoters through binding to the specific responsible elements. HCV infection has been suggested to impair the IFN production through multiple pathways. The IFN-induced Jak-STAT signaling is inhibited in cells and transgenic mice expressing HCV proteins and in the liver biopsy samples of chronic hepatitis C patients [7–9].

Induction of type I IFN upon infection with pathogens is crucial for innate immunity, and it is mediated by the activation of pattern-recognition receptors, including Toll-like receptors (TLRs) and cytosolic receptors, such as RIG-I and MDA5 [10–12]. The induction of type I IFN is primarily controlled at the gene transcriptional level, wherein a family of transcription factors known as IFN regulatory factors (IRFs) play a pivotal role. IRF3

and IRF7 are known to be essential for the RIG-I-, MDA5-, and TLR-mediated type I IFN production pathways. IRF3 is induced primarily by a response to initiate IFNβ production, whereas IRF7 is induced by IFNβ and participates in the late phase for IFNβ induction [13]. All TLRs, except for TLR3, activate the MyD88-dependent pathway, whereas TLR3 and TLR4 activate the TRIF-dependent pathway. HCV NS3/4A protease has been shown to impair the production of IFNβ as well as the subsequent IFN-inducible genes through the inactivation of the adaptor molecules involved in the TLR-dependent and -independent signaling pathways [14–18]. On the other hand, Vilasco *et al.* suggested that impairment of IKKi - which, along with TBK1, is one of the important factors participating in IRF3 phosphorylation and activation - in the HCV replicon cells plays at least a partial role in the restoration of type I IFN signaling pathways [19]. In addition, IRF7 was shown to participate in the positive feedback of type I IFN signaling through the IFN receptor [13]. Therefore, we tried to examine the effect of exogenous expression of IRF7 under the assumption that IRF7 is a potent type I IFN inducer and capable of modulating the viral propagation in hepatocytes infected with HCV.

In this study, we generated two therapeutic molecules consisting of a dominant active mutant of IRF7 or VAP-C, a negative regulator of HCV replication [20], followed by the C-terminal region of IFN promoter stimulator 1 (IPS-1), including the cleavage site of the HCV NS3/4A protease, which was modified so that the cleavage site localized on the ER membrane [21]. The expression of the plasmids encoding these molecules in the HCV replicon and HCVcc-infected cells resulted in a substantial suppression of HCV propagation, suggesting the possibility that these or other similar molecules could be used therapeutically to eliminate HCV from hepatocytes infected with HCV.

Results

IRF7m, a dominant active mutant of IRF7, activates the IFN promoters in cells replicating HCV

Previous studies have shown that an IRF7 mutant, IRF7m, lacking the amino acid residues from 284 to 454, a region that includes the auto-inhibitory domain (from amino acid residue 305 to 467), and an IRF3 mutant, IRF3m, carrying the substitution of Ser^{396} to Asp in the carboxyl terminal region (Fig. 1A), induced a potent activation of type I IFN promoter in non-hepatic cell lines irrespective of viral infection [22–25]. We first examined the effect of the expression of the IRF dominant active mutants on the inhibition of HCV RNA replication through the production of type I IFN. HCV replicon cells and Huh7OK1 cells infected with HCVcc were transfected with the plasmids encoding either wild-type or dominant active mutant of IRF3 or IRF7 together with the reporter plasmids encoding a luciferase gene under the control of the promoters of IFNα6, IFNβ and ISRE, respectively. Among these examined constructs, we observed significant activation of the promoters of IFNα6 and ISRE in the replicon and HCVcc-infected cells compared with naïve and mock-infected cells upon expression of IRF7m, while we observed no activation of the IFNα6 promoter in cells expressing IRF3m (Figs. 1 B and 1C). Potent stimulation of the IFNβ promoter was observed in the replicon cells expressing IRF7m but not in cells infected with HCVcc. Next we examined the antiviral activity of the IRF constructs in both replicon (Fig. 1D) and HCVcc-infected cells (Fig. 1E). The expression of the plasmid encoding IRF7m resulted in potent suppression of viral protein and viral RNA syntheses in both cell types. Although expression of IRF3m induced a slight suppression of viral propagation in cells infected with HCVcc, expression of the IRF constructs except for IRF7m did not induce the significant suppression of viral replication and propagation. These results suggest the possibility of elimination of HCV through a specific induction of type I IFN by the expression of IRF7m in HCV-infected cells.

cIRF7, a chimeric construct of IRF7m, specifically activates the IFN promoters in cells replicating HCV

To induce IFNs in cells infected with HCV but not in uninfected cells through a selective activation of IRF7m, we constructed a chimeric IRF7 (cIRF7) consisting of the IRF7m fused with FLAG-tag and the C-terminal amino acid residues from 503 to 540 of IPS-1 modified to be localized on ER (Fig. 2A upper) [21]. HCV NS3/4A protease cleaves the carboxyl site of Cys^{508} in the C-terminal domain of IPS-1. Although cIRF7 is anchored in the ER and exhibits no activation in uninfected cells, cIRF7 would be cleaved by the NS3/4A protease in cells infected with HCV and the released N-terminal fragment would migrate into the nucleus and activate various IFN promoters (Fig. 3). Immunoblot analyses revealed that cIRF7 was cleaved in 293T cells expressing HCV NS3/4A protease of a wild type but not in those expressing the mutant protease NS3/4A(S139A), and a mutant cIRF7(C508A) which has a substitution of Cys^{508} to Ala, exhibited resistance to the cleavage by the HCV protease (Fig. 2A bottom). To assess a specific activation of the IFN promoters after cleavage of the cIRF7 by HCV NS3/4A, 293T cells expressing FLAG-tagged HCV proteases were transfected with the plasmids encoding the luciferase gene under the control of the promoter of IFNα6, IFNβ or ISRE together with the plasmid encoding either cIRF7 or cIRF7(C508A). Expression of cIRF7 but not of cIRF7(C508A) induced the activation of the IFNα6, IFNβ and ISRE promoters in cells expressing HCV NS3/4A protease but not in those expressing the mutant protease NS3/4A(S139A) (Fig. 2B). Next we examined the activation of the IFN promoters associated with the expression of the plasmid encoding cIRF7 in the replicon and HCVcc-infected cells. Expression of cIRF7 but not of cIRF7(C508A) induced the activation of the IFN promoters in both cell types (Figs. 2C and 2D). On the other hand, these promoters were not activated by the expression of cIRF7 in the replicon cells harboring subgenomic RNA of Japanese encephalitis virus (JEV) and Huh7 cells infected with JEV (Fig. 2E). These results suggest that the cIRF7 expression is a feasible method for specifically activating the IFN promoters in cells infected with HCV.

Specificity of activation of the IFN promoters by the expression of cIRF7

To further examine the specificity of the activation of the IFN promoters by the expression of cIRF7 in cells replicating HCV, a plasmid encoding either cIRF7 or IRF7m was co-transfected with that encoding the luciferase gene under the ISRE promoter into the HCV replicon or HCVcc-infected cells and cultured in the presence or absence of inhibitors for HCV replication. Treatment with an HCV protease inhibitor (BILN2061) or cyclosporine A (CsA) inhibited the activation of the ISRE promoter by the expression of cIRF7 in the HCV replicon and HCVcc-infected cells in a dose-dependent manner, in contrast to the resistance to the treatments in cells expressing the IRF7m (Fig. 4A and Fig. 4B). Recently, it was shown that an NS3/4A protease of GB virus B (GBV-B), which is the virus genetically related most closely to HCV, also impairs the dsRNA-induced IFN production through a cleavage of IPS-1[26]. Therefore, to assess the possibility of activation of cIRF7 by other flaviviral proteases, cleavage of cIRF7

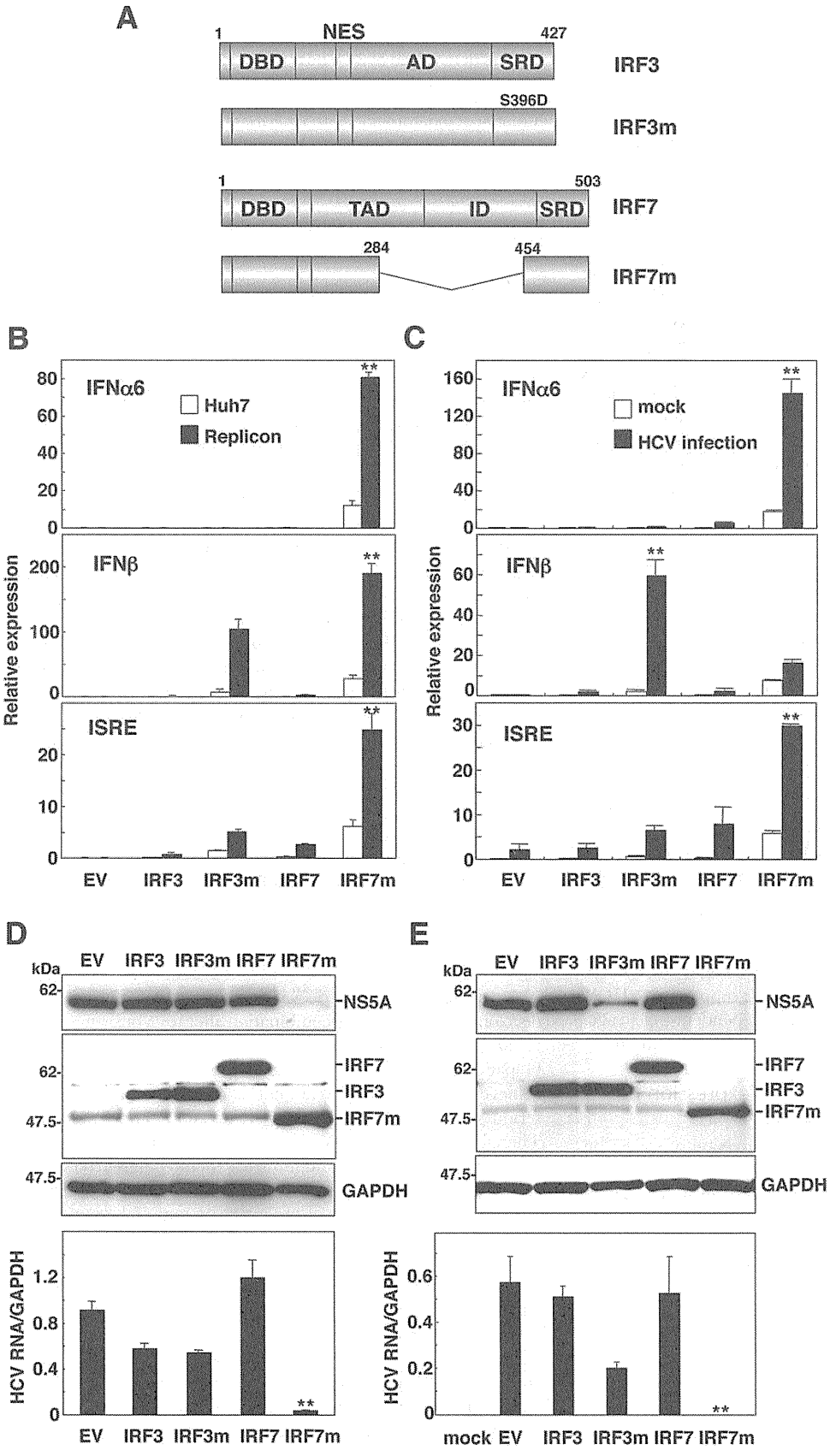

Figure 1. Dominant active mutant of IRF7 activates IFN promoters in cells replicating HCV. (A) Structures of IRF3, IRF7 and the dominant active mutants, IRF3m and IRF7m. The DNA-binding domain, nuclear export sequence, transactivation domain, association domain, inhibitory domain, and signal response domain are indicated as DBD, NES, TAD, AD, ID, and SRD, respectively. Huh7 cells and HCV replicon cells (1×10^5 cells/

well) (B), and Huh7OK1 cells (7.5×10^4 cells/well) infected with HCVcc at an moi of 1 and incubated for 72 h (C) were transfected with 100 ng of plasmid encoding the luciferase gene under the control of the IFNα6, IFNβ, or ISRE promoter together with an empty vector (EV) or a plasmid encoding each of the IRF constructs. The relative luciferase activity of cell lysates was determined at 24 h post-transfection. HCV replicon cells (3×10^5 cells/well) (D) and Huh7OK1 cells (1.5×10^5 cells/well) infected with HCVcc at an moi of 1 and incubated for 72 h (E) were transfected with EV or a plasmid encoding each of the IRF constructs and the expressions of NS5A, IRFs, and GAPDH (upper panel) and synthesis of viral RNA (lower panel) at 72 h post-transfection were determined by immunoblotting and real-time PCR after standardization with GAPDH, respectively. The data shown in this figure are representative of three independent experiments. The error bars represent the standard deviations. Asterisks indicate significant differences (**$P<0.01$) versus the control cells or mock-infected cells.
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and activation of the IFN promoters were evaluated in 293T cells expressing the viral proteases of HCV, GBV and JEV. Immunoblot analyses revealed that cIRF7 was processed by the viral proteases of HCV and GBV but not by that of JEV and the activation of the IFN promoters was well correlated with the cleavability of the cIRF7 (Fig. 4C). Although the GBV protease exhibited an efficient activation of cIRF7 comparable to HCV protease, processing of cIRF7 and activation of the IFN promoters by the GBV protease was not inhibited by the pretreatment with the HCV protease inhibitor (Figs. 4D and 4E). These results indicate that cIRF7 is capable of activating the IFN promoters through a specific cleavage by the protease in cells infected with HCV.

Nuclear localization of cIRF7 in cells expressing HCV protease

From these results, it was suggested that cIRF7 is cleaved by the HCV protease and the processed fragment migrates into the nucleus and activates IFN promoters (Fig. 3). To confirm the nuclear localization of the cleaved cIRF7, we constructed an EGFP-cIRF7 and determined its subcellular localization in cells expressing the HCV protease and in the HCV replicon cells by confocal microscopy. Nuclear accumulation of the cIRF7 was observed in cells expressing EGFP-cIRF7 together with NS3/4A, but not in those with NS3/4A(S139A) or NS5A and also not in cells co-expressing EGFP-cIRF7(C508A) and NS3/4A (Fig. 5A). Furthermore, expression of EGFP-cIRF7 but not of EGFP-cIRF7(C508A) induced a nuclear accumulation of cIRF7 in the HCV replicon cells, and nuclear localization of the cIRF7 abrogated the expression of viral antigen (NS3), in contrast to the co-localization of EGFP-cIRF7(C508A) and the ER marker PDI, which had no discernible antiviral effect (Fig. 5B). These results suggest that cIRF7 is capable of suppressing HCV replication through an HCV protease-dependent cleavage, migration into the nucleus and activation of the IFN promoters.

Suppression of HCV replication by the expression of cIRF7

To examine the inhibitory effect of the expression of cIRF7 on HCV replication, a plasmid encoding either cIRF7 or cIRF7(C508A) was transfected into the HCV replicon and HCVcc-infected cells, and HCV replication was evaluated by immunoblotting and real-time PCR. The expression of cIRF7 but not of cIRF7(C508A) resulted in cleavage by the HCV protease, and a clear reduction of viral protein and RNA syntheses in both replicon and HCVcc-infected cells (Figs. 6A and 6B). In addition, we examined the effect of cIRF7 on the replication of HCV in the 4βR replicon cells [27,28], which have been shown to exhibit more resistant to the IFNα treatment than Con1 replicon cells (Fig. 6C upper left). Expression of the cIRF7 in the 4βR replicon cells but not in those cured HCV RNA (4βRc cells) induced an activation of the ISRE promoter (Fig. 6C lower left). Expression of cIRF7 but not of cIRF7(C508A) also resulted in processing by the HCV protease and suppression of viral protein and RNA syntheses in the 4βR replicon cells (Fig. 6C right panels).

Suppression of HCV replication by the expression of cVAP-C

Human vesicle-associated membrane protein-associated protein subtype A (VAP-A) and B (VAP-B) are known to be involved in the regulation of membrane trafficking, lipid transport and metabolism, and the unfolded protein response [29]. VAP-A and VAP-B have been shown to be involved in the replication of HCV, and we have shown recently that human VAP-C, a splicing variant of VAP-B, negatively regulates HCV replication by interfering with the interaction of VAP-A and VAP-B with HCV NS5B [20]. We next examined the possibility of using a selective activation of VAP-C to suppress HCV replication in cells infected with HCVcc. We generated expression plasmids encoding a chimeric VAP-C fused with the IPS-1 sequence (cVAP-C), a cVAP-C(C508A) which is made resistant to the HCV protease by a substitution in the cleavage site similar to the substitutions made in cIRF7(C508A), or VAP-C (Fig. 7A). The cVAP-C was cleaved in cells infected with HCVcc, and expression of cVAP-C and VAP-C suppressed expression of NS5A, in contrast to the weak reduction of NS5A in the infected cells expressing cVAP-C(C508A), probably due to a slight cleavage of cVAP-C(C508A) (Fig. 7B, top). Furthermore, the production of viral RNA and infectious particles in the culture supernatants of cells infected with HCVcc was also impaired by the expression of cVAP-C and VAP-C, but not of cVAP-C(C508A) in a dose-dependent manner (Fig. 7B, middle and bottom). Collectively, these results suggest that delivery of the therapeutic molecules into liver of hepatitis C patients, followed by selective activation of the molecules in HCV-infected hepatocytes, is a feasible method for eliminating HCV.

Discussion

An effective prophylactic vaccine against HCV has not been developed yet. Although combination therapy consisting of PEG-IFNα and RBV has been introduced for the treatment of hepatitis C patients, and 50% of individuals infected with genotype 1 achieved a SVR, this treatment is sometimes associated with serious side effects, including depression and anemia [3]. Therefore, new anti-HCV drugs targeted to HCV protease and polymerase and capable of optimizing therapy are currently in the early stages of the development [30,31]. However, it is difficult to achieve a complete removal of viruses by antiviral drugs targeted to the viral enzymes from patients persistently infected with RNA viruses that exhibit a quasispecies nature, such as human immunodeficiency virus (HIV) and HCV. Viral quasispecies are not a simple collection of diverse mutants but a group of interactive variants capable of adapting to new environments [32]. Furthermore, introduction of antiviral drugs may induce an emergence of drug-resistant breakthrough viruses as seen in the case of HIV infection. Therefore, a novel therapeutic approach for hepatitis C patients in addition to the current chemotherapies is required to overcome serious adverse effects and improve the ratio of patients achieving SVR.

In this study, we have generated two therapeutic molecules, cIRF7 and cVAP-C, which are selectively activated in cells

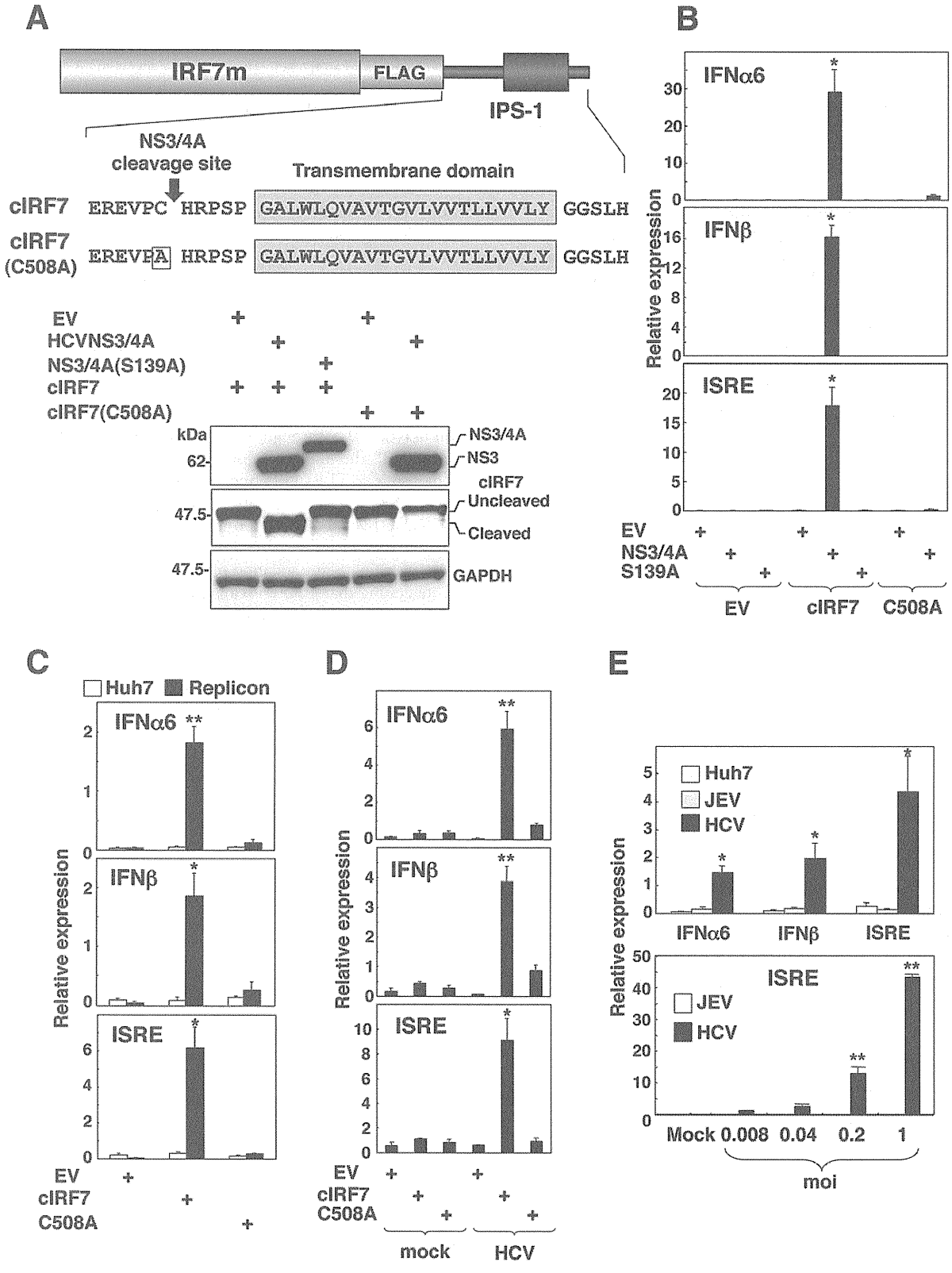

Figure 2. Construction of cIRF7 capable of activating the IFN promoters in cells replicating HCV. (A top) Schematic representation of the cIRF7 constructs. cIRF7 consists of IRF7m, FLAG-tag, and IPS-1 (503 to 540 amino acid residues) sequences containing a cleavage site by HCV NS3/4A protease, a transmembrane domain and a cytoplasmic region modified to localize on the ER. cIRF7(C508A) has a substitution of Cys508 to Ala which renders it resistant to the cleavage by the HCV protease. (A bottom) Immunoblot analyses of 293T cells transfected with a plasmid encoding either cIRF7 or cIRF7(C508A) together with either an empty vector (EV) or a plasmid encoding either FLAG-tagged HCVNS3/4A or FLAG-tagged HCVNS3/4A (S139A). (B) 293T cells (2×10^5 cells/well) were transfected with a plasmid of EV, FLAG-tagged HCVNS3/4A or FLAG-tagged HCVNS3/4A(S139A) in combination with a plasmid of EV, cIRF7 or cIRF7 (C508A) together with 100 ng of the reporter plasmid encoding the luciferase gene under the

control of the IFNα6, IFNβ or ISRE promoter, and luciferase activity was determined at 24 h post-transfection. (C) HCV replicon cells (1.5×10^5 cells/well) and (D) Huh7OK1 cells (7.5×10^4 cells/well) infected with HCVcc at an moi of 1 and incubated for 72 h were transfected with 100 ng of each of the reporter plasmids together with plasmid of EV, cIRF7 or cIRF7(C508A) and luciferase activity was determined at 24 h post-transfection. (E) Huh7 cells, HCV subgenomic replicon cells, and JEV subgenomic replicon cells (1×10^5 cells/well) (top) and Huh7OK1 cells (7.5×10^4 cells/well) infected with JEV and HCV (bottom) at an moi of 0.008, 0.04, 0.2, and 1 and incubated for 24 h and 72 h, respectively, were transfected with 100 ng of each of the reporter plasmids together with cIRF7 and the luciferase activity was determined at 24 h post-transfection. The data shown in this figure are representative of three independent experiments. The error bars represent the standard deviations. Asterisks indicate significant differences (*$P<0.05$, **$P<0.01$) versus the control cells or mock-infected cells.
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replicating HCV. To tightly regulate activation of the molecules in HCV- infected cells, we employed the C-terminal amino acid sequence of human IPS-1, which has been identified as an adaptor molecule involved in the RIG-like receptor (RLR) signaling pathways. It has been demonstrated that HCV NS3/4A protease efficiently cleaves the upstream position of the transmembrane region of IPS-1 on the mitochondrial outer membrane and disrupts the IFN signaling pathway [15–18]. Furthermore, to avoid induction of mitochondrial dysfunction and cell death due to the expression of the therapeutic molecules on the mitochondria, we replaced three arginine residues among the C-terminal five residues of IPS-1 with non-charged amino acid glycine residues (RRRLH to GGGLH) so that these three residues would be localized on the ER membrane [21]. HCV is suggested to replicate on the ER membrane, and therefore subcellular localization and distance of the cleavage site of the substrates from the membrane could be crucial for an efficient processing. The tightly regulated activation of the therapeutic molecules in cells replicating HCV observed in this study might be largely attributable to the ER localization of the therapeutic molecules.

Irrespective of IFN sensitivity, the expression of cIRF7 in the HCV replicon cells induced the activation of type I IFN promoter and inhibited the viral RNA replication, suggesting the possibility that cIRF7 could be used for the treatment of hepatitis C patients who are infected with HCV resistant to IFNα therapy. The expression of IRF3m in cells infected with HCVcc induced a higher antiviral response than that in the Con1 replicon cells in spite of the comparable transcription of IFNβ mRNA between the two cell types Fig. 1), suggesting that differences among HCV genotypes might be caused to the difference to the sensitivity of IFNβ. To assess the real efficacy of cIRF7 for suppression of HCV replication, we must await the establishment of robust cell culture systems capable of propagating various genotypes of HCV derived from the sera of hepatitis C patients.

It has been shown previously that HCV interferes with the induction of type I IFN through the cleavage of IPS-1 by NS3/4A protease [15–18], the interaction of NS5A with MyD88, a major adaptor molecule of TLRs [33], and the intervention of the IFNα-activated Jak-STAT signaling pathway by HCV proteins [7–9]. After cleavage by the HCV protease, the processed cIRF7 migrates into the nucleus and activates various IFN promoters, and it may participate in regulation of the expression of hundreds of ISGs, suggesting that cIRF7 is capable of inducing an antiviral response through the Jak-STAT-independent pathway. Although it has been reported previously that the basal expression of IRF7 and the IRF7-induced activation of the IFNα promoter are impaired in the HCV replicon cells [34], in this study we have shown that cIRF7 is activated in cells infected with HCVcc and capable of inducing type I IFN. Collectively, these results suggest that cIRF7 is capable of eliminating HCV that persistently infects

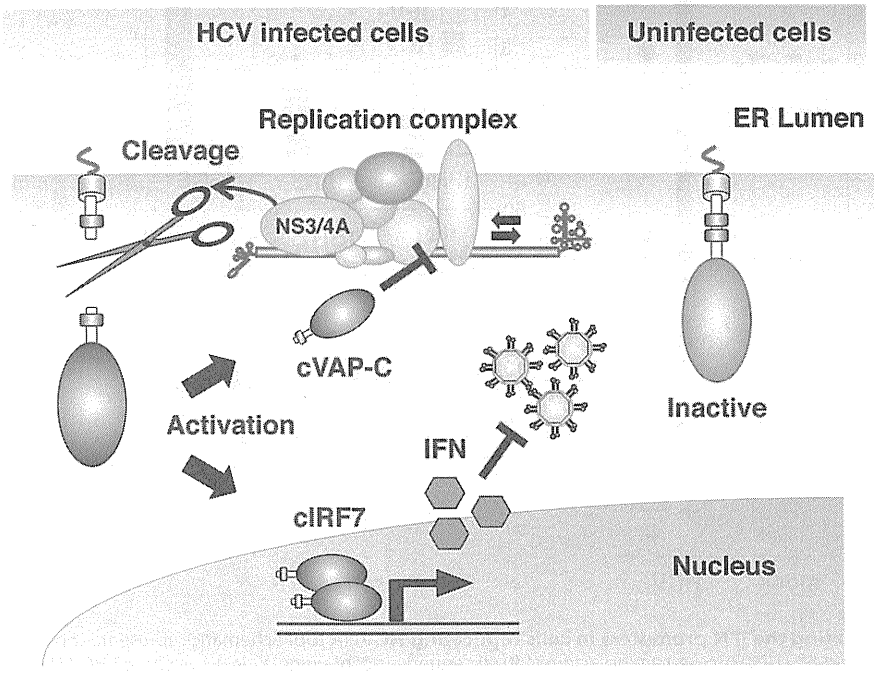

Figure 3. Scheme of activation of the therapeutic molecule in cells infected with HCV. The chimeric molecules are cleaved by HCV NS3/4A protease and the released fragments inhibit propagation of HCV through induction of IFN after translocation into the nucleus (cIRF7) or disruption of the replication complex (cVAP-C), whereas the molecule is stably anchored in the ER within uninfected cells.
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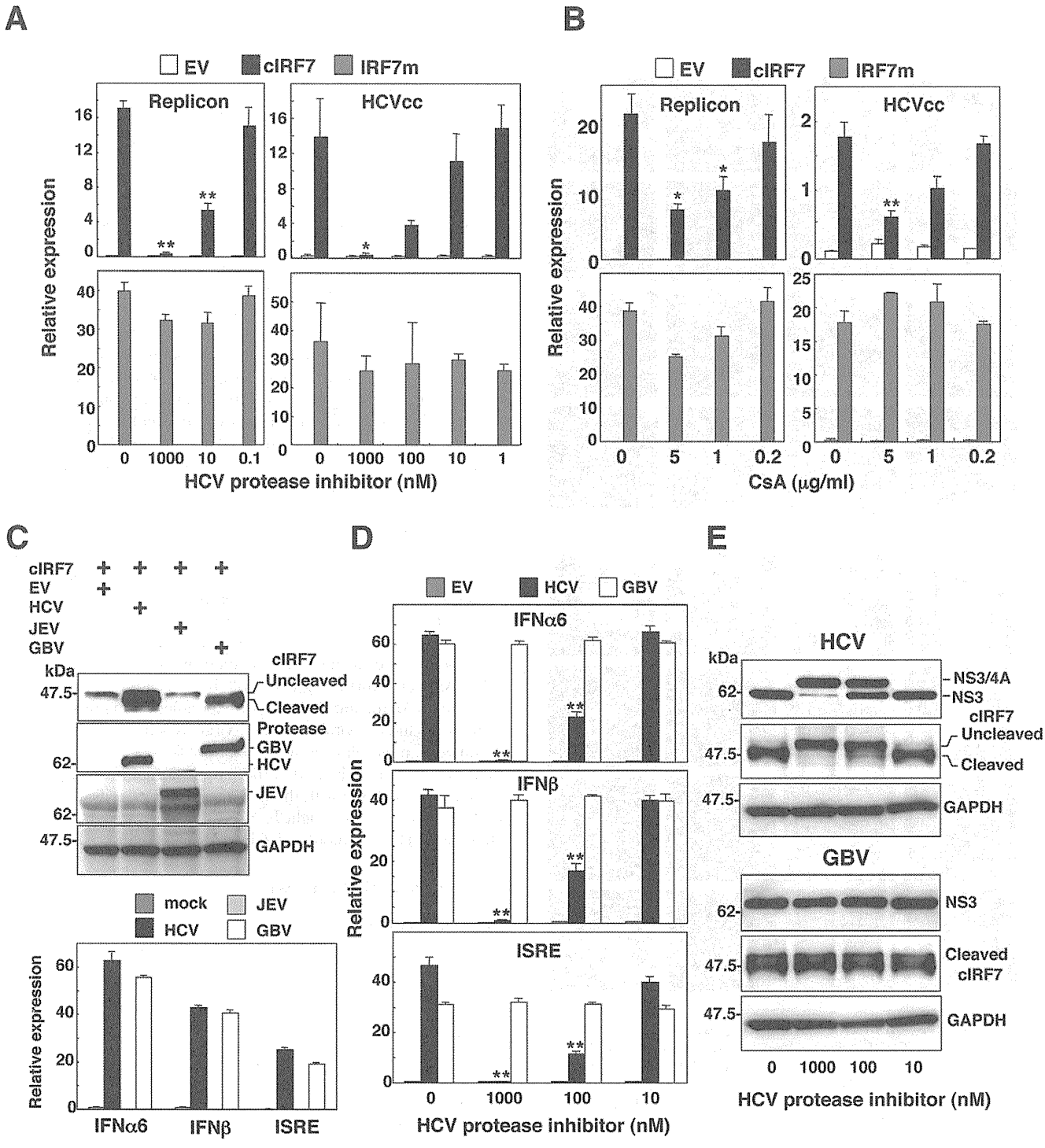

Figure 4. Specificity of activation of the IFN promoters by the expression of cIRF7. (A) HCV replicon cells (1.5×10^5 cells/well) or Huh7OK1 cells (7.5×10^4 cells/well) infected with HCVcc at an moi of 1 and incubated for 72 h were treated with various concentrations of HCV protease inhibitor (A) or cyclosporine A (CsA) (B), transfected with an empty vector (EV) (white bars) or plasmids encoding cIRF7 (black bars) or IRF7m (gray bars) together with 100 ng of a reporter plasmid encoding the luciferase gene under the control of the ISRE promoter, and luciferase activity was determined at 24 h post-transfection. (C top) A plasmid encoding cIRF7 was co-transfected with a plasmid encoding either FLAG-tagged HCVNS3/4A, FLAG-tagged GBVNS3/4A, or HA-tagged JEVNS2b/3 into 293T cells, and the expressions of cIRF7, viral proteases and GAPDH were determined by immunoblotting. (C bottom) 293T cells (2×10^5 cells/well) transfected with a plasmid encoding either EV (dark gray bars), FLAG-tagged HCVNS3/4A (black bars), FLAG-tagged GBVNS3/4A (white bars), or HA-tagged JEVNS2b/3 (gray bars) together with 100 ng of the plasmid encoding the luciferase gene under the control of the promoter of either IFNα6, IFNβ or ISRE, and luciferase activity was determined at 24 h post-transfection. (D) 293T cells (2×10^5 cells/well) were transfected with 100 ng of the reporter plasmids together with plasmids encoding EV (gray bars), FLAG-tagged HCVNS3/4A (black bars) or FLAG-tagged GBVNS3/4A (white bars) in the presence or absence of the HCV protease inhibitor, and luciferase activity was determined at 24 h post-transfection. (E) cIRF7 was co-expressed with FLAG-tagged HCVNS3/4A or FLAG-tagged GBVNS3/4A in 293T cells in the presence or absence of the HCV protease inhibitor, and the expressions of cIRF7, viral proteases and GAPDH were determined by immunoblotting. The data shown in this figure are representative of three independent experiments. The error bars represent the standard deviations. Asterisks indicate significant differences (*$P<0.05$, **$P<0.01$) versus the control cells or mock-infected cells.
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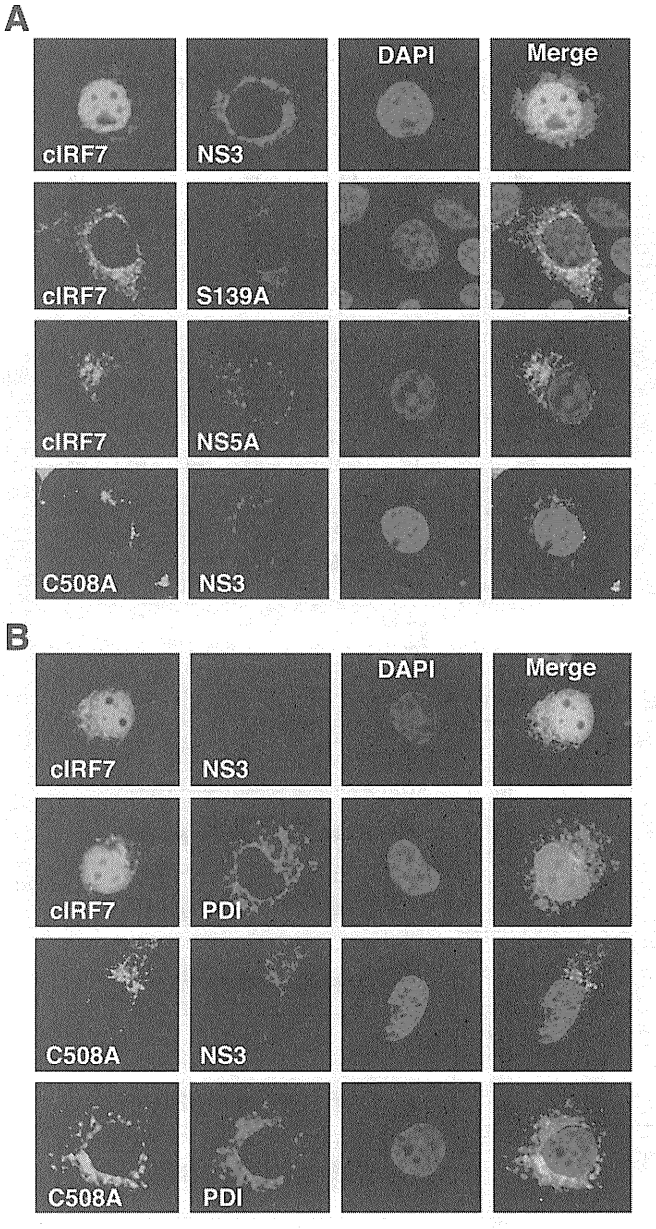

Figure 5. Activation of cIRF7 in cells expressing HCV protease. (A) Huh7OK1 cells (5×10^4 cells/well) were co-transfected with plasmids encoding either EGFP-cIRF7 or EGFP-cIRF7(C508A) and plasmids encoding either HCVNS3/4A, HCVNS3/4A(S139A) or NS5A, harvested at 24 h post-transfection, fixed with 4% paraformaldehyde in PBS, and permeabilized with 0.25% saponin. HCV NS3 and NS5A were stained with the appropriate antibodies, followed by staining with AF594-conjugated second antibodies. (B) HCV replicon cells (5×10^4 cells/well) were transfected with plasmids encoding either EGFP-cIRF7 or EGFP-cIRF7(C508A), and endogenous expression of HCV NS3 and an ER marker, PDI, was detected in cells treated and stained with the appropriate antibodies as described above. Subcellular localization of cIRF7s, HCV proteins and PDI was determined by confocal microscopy after staining of nuclei by DAPI. The data shown in this figure are representative of three independent experiments.
doi:10.1371/journal.pone.0015967.g005

human hepatocytes through an induction of sufficient amounts of type I IFN.

It is well known that patients achieving a rapid viral clearance by the treatment with PEG-IFNα showed a significant up-regulation of ISG, whereas a high level expression of ISG is observed in nonresponsive patients before IFN therapy, probably due to a rapid induction of negative regulators for the IFN signaling pathway, such as the suppressor of cytokine signaling proteins [35,36]. These results suggest that chronic hepatitis C patients with a pre-activated IFN signaling pathway respond poorly to IFN therapy. In this study we also demonstrated that activation of various IFN promoters by the expression of the dominant active mutants of IRFs was more accentuated in cells replicating HCV rather than naïve cells, probably due to an undetectable expression of ISG in cells replicating HCV RNA as described previously [37]. However, the precise mechanisms underlying the enhancement of IFN activity by the expression of a dominant active mutant of IRFs in cells replicating HCV remain unknown. Fillipowicz *et al.* suggested the possibility of recovery of the sensitivity to IFN therapy by the restoration of the endogenous IFN system to a "naïve" state through a blockage of the IFN response in nonresponders before treatment [36]. However, modulation of ISG expression before IFN therapy may induce a flare of HCV propagation in the liver of chronic hepatitis C patients. Therefore, it might be interesting to examine whether an effectiveness of cIRF7 are sustained in a state of occurring a negative regulator for IFN signaling pathway and preactivated IFN signaling pathway in cells replicating HCV.

VAP-A and VAP-B are suggested to be involved in the construction of the HCV replication complex consisting of viral proteins and host cellular lipid components, and that VAP-C interrupts the VAP-A and VAP-B functions and negatively regulates the HCV propagation and not expressed in human hepatocytes probably involves in the determination of tissue tropism of HCV [20]. Although further studies will be needed to elucidate the effectiveness of the molecules *in vivo* experiment using drug delivery systems including viral and non-viral vectors in more detail, therapeutic molecules consisting of host factors involved in IFN induction such as IRF7 and in the suppression of HCV replication such as VAP-C fused with the IPS-1 sequences specifically cleaved by the HCV protease might be a promising approach capable of eliminating HCV without induction of severe cellular toxicity.

Materials and Methods

Cells and viruses

Vero and 293T cell lines were purchased from American Type Culture Collection (Manassas, VA). Huh7 cell line was kindly provided by Ralf Bartenschlager. Huh7OK1 cell line was previously established from interferone-treated Huh7 cells including HCV replicon and exhibited high susceptibility to HCVcc propagation [38]. These cell lines were maintained in Dulbecco's modified Eagle's medium (DMEM) (Sigma, St. Louis, MO) supplemented with 10% fetal calf serum (FCS). Huh-9–13 cells harboring an HCV subgenomic RNA replicon of genotype 1b [39] were cultured in DMEM supplemented with 10% FCS, 1 mg/ml G418 and nonessential amino acids. The infectious RNA of the JFH1 strain was introduced into Huh7OK1 cells and the infectious titers were expressed as focus-forming units (FFU) [4]. Huh7 cells harboring a JEV subgenomic RNA replicon (Nakayama strain) were cultured in DMEM supplemented with 10% FCS and 1 μg/ml puromycin. Preparation of the HCV subgenomic replicon cells 4βR exhibiting an IFN-resistant phenotype and their cured cells 4βRc were described previously [27,28]. All cells were cultured at 37°C in a humidified atmosphere with 5% CO_2.

Plasmids and reagents

The cDNA fragments encoding IRF3 and IRF7 were amplified by PCR from a total RNA from THP-1 cells and cloned into

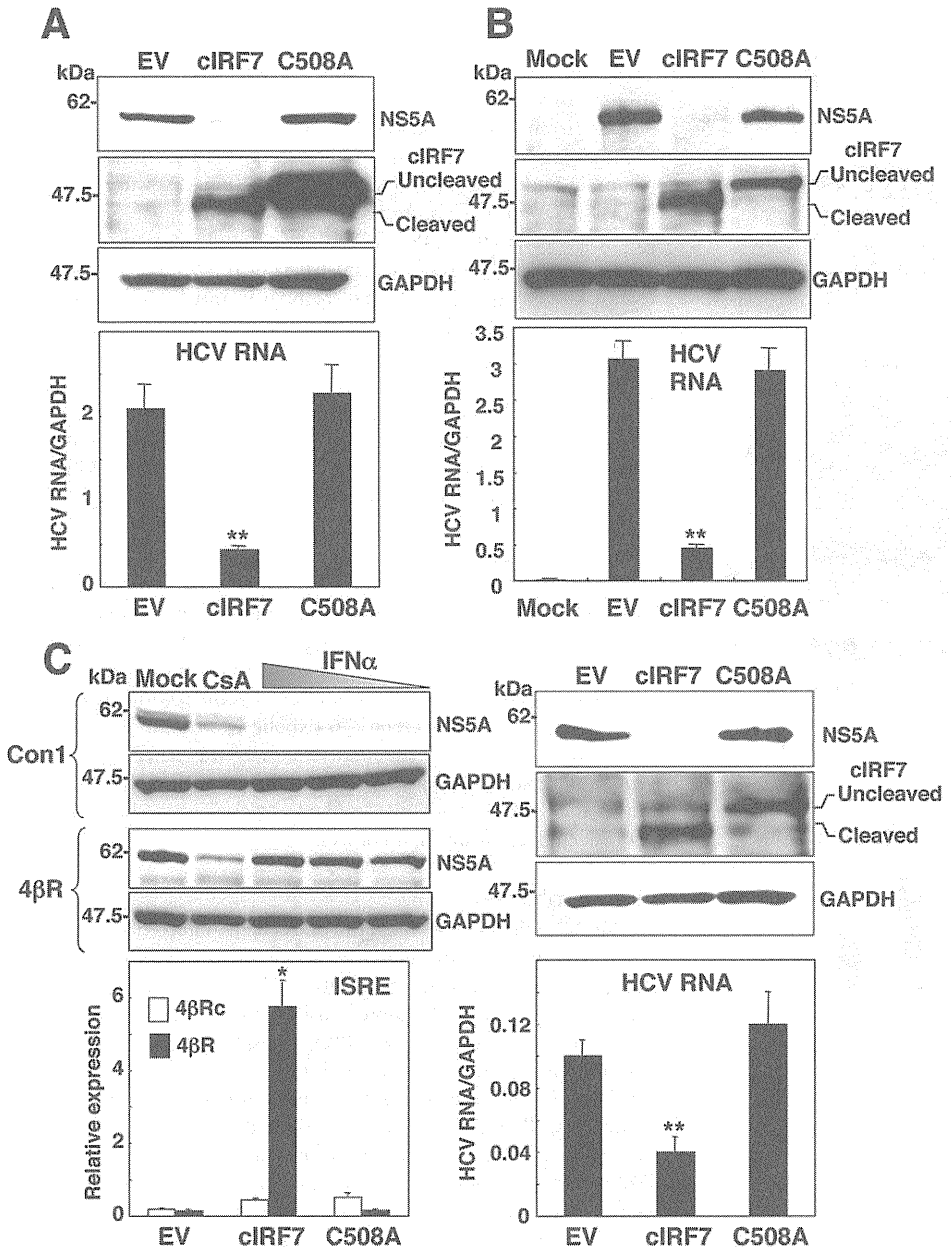

Figure 6. Suppression of HCV replication by the expression of cIRF7. (A) HCV replicon cells (3×10^5 cells/well) and (B) Huh7OK1 cells (1.5×10^5 cells/well) infected with HCVcc at an moi of 1 and incubated for 72 h were transfected with a plasmid encoding either empty vector (EV), cIRF7 or cIRF7(C508A), and the expression of NS5A, cIRF7s and GAPDH (upper panels) and synthesis of viral RNA (lower panels) were determined at 72 h post-transfection by immunoblotting and real-time PCR, respectively. (C upper left) HCV Con1 replicon cells and 4βR replicon cells exhibiting an IFN-resistant phenotype (1.5×10^5 cells/well) were treated with the CsA (5 μg/ml) or 10^4, 10^3, and 10^2 units/ml of recombinant human IFNα and the expressions of NS5A and GAPDH were determined by immunoblotting. The 4βR replicon cells (3×10^5 cells/well) were transfected with EV or plasmid encoding either cIRF7 or cIRF7(C508A), and the expressions of NS5A, cIRF7s and GAPDH (C upper right) and synthesis of viral RNA (C lower right) were determined at 72 h post-transfection by immunoblotting and real-time PCR, respectively. The 4βR cells and their cured cells (4βRc) with the HCV genome eliminated (1×10^5 cells/well) were transfected with EV or plasmid encoding either cIRF7 or cIRF7(C508A) together with 100 ng of plasmid encoding the luciferase gene under the control of the ISRE promoter, and luciferase activity was determined at 24 h post-transfection (C lower left). The data shown in this figure are representative of three independent experiments. The error bars represent the standard deviations. Asterisks indicate significant differences (*$P<0.05$, **$P<0.01$) versus the control cells or mock-infected cells.
doi:10.1371/journal.pone.0015967.g006

pcDNA3.1-C-myc-His (Invitrogen, Carlsbad, CA). The mutants carrying a deletion in the auto-inhibitory domain (from amino acid residue 284 to 454) of IRF7 and the substitution of Ser^{396} with phosphomimetic Asp located in the carboxyl terminus of IRF3 were generated by the method of splicing by overlap extension and cloning into pcDNA3.1myc-His and designated as IRF7m and IRF3m, respectively. N-terminally FLAG-tagged wild-type NS3/4A protease and its mutant substituted with Ser^{139} to replaced with Ala (S139A) were prepared as described previously [33]. The cDNA fragment encoding a JEV protease was amplified from a total RNA of Vero cells infected with JEV (AT31 strain) and cloned into pcDNA3.1Flag/HA [40], The cDNA fragment

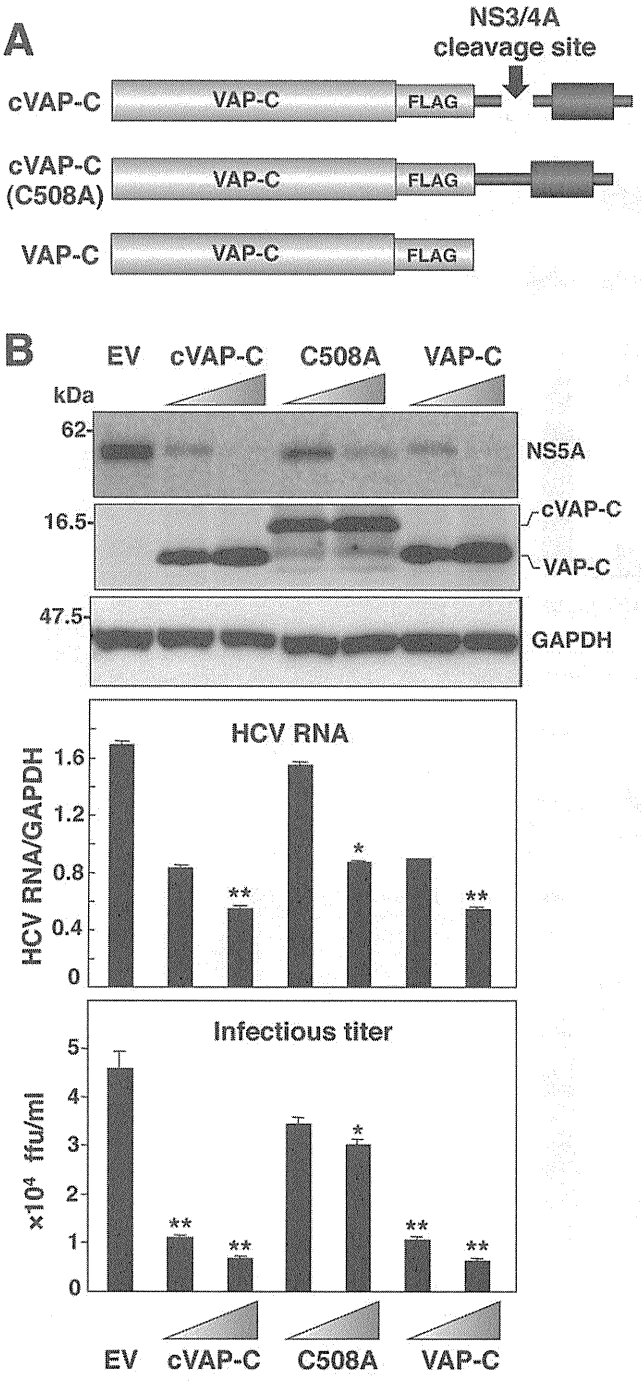

Figure 7. Suppression of HCV replication by the expression of cVAP-C. (A) Schematic representation of cVAP-C, cVAP-C(C508A) and VAP-C. Like cIRF7, cVAP-C is composed of the sequences of VAP-C, FLAG-tag, and the C-terminus domain of IPS-1. (B) Huh7OK1 cells (1.5×10^5 cells/well) infected with HCVcc at an moi of 1 and incubated for 72 h were transfected with EV, or plasmid encoding either cIRF7 or cIRF7(C508A), and the expressions of NS5A, VAP-Cs and GAPDH (top panel), synthesis of viral RNA (middle panel) and infectious titers in the culture supernatants were determined at 72 h post-transfection by immunoblotting, real-time PCR, and focus forming assay, respectively. The data shown in this figure are representative of three independent experiments. The error bars represent the standard deviations. Asterisks indicate significant differences (*$P<0.05$, **$P<0.01$) versus the control cells or mock-infected cells.
doi:10.1371/journal.pone.0015967.g007

encoding a GBV-B protease was amplified from pGBB (kindly provided by Dr. H. Akari) [41] by PCR and cloned into pcDNA3.1Flag/HA. The chimeric IRF7 (cIRF7) composed of the IRF7m fused with FLAG-tag and the C-terminus of human IPS-1 (from amino acid residues 503 to 540 amino acid residues) containing a cleavage site of HCV NS3/4A, transmembrane domain and the ER retention signal [21] (Fig. 2A) was cloned into pcDNA3.1-c-myc-His. A cIRF7 mutant, C508A, was generated to be resistant to HCV NS3/4A protease by substitution of Cys^{508} of cIRF7 to Ala. The reporter constructs of IFNα6, IFNβ, and ISRE were kindly provided by Drs. T. Kawai and S. Akira. All PCR products were confirmed by sequencing by an ABI PRISM 310 genetic analyzer (Applied Biosystems, Tokyo, Japan). The HCV NS3/4A protease inhibitor, BILN2061 was purchased from Acme Bioscience (Belmont, CA). Human recombinant IFNα and cyclosporine A (CsA) were purchased from PBL Biomedical Laboratories (New Brunswick, NJ) and Wako Pure Chemical Industries (Osaka, Japan), respectively.

Reporter assay

Huh7 cells, HCV replicon cells, and Huh7OK1 cells infected with HCVcc were seeded onto 12-well plates at the concentration of 1.5×10^5 cells/well and transfected with 100 ng of each of the plasmids encoding the luciferase gene under the control of the IFNα6, IFNβ and ISRE promoter together with the various constructs by using FuGene^{TM}6 (Roche Molecular Biochemicals, Mannheim, Germany). Luciferase activity was determined by the Dual-luciferase reporter assay system (Promega Inc., Madison, WI) and the *Renilla* luciferase reporter gene was simultaneously transfected as an internal control.

Immunoblotting

HCV replicon cells and Huh7OK1 cells infected with HCVcc were transfected with the plasmids encoding each of the wild-type and the dominant active mutants of IRFs and harvested at 72 h post-transfection. Cells were washed three times with ice-cold phosphate-buffered saline (PBS), suspended in lysis buffer containing 20 mM Tris-HCl (pH 7.4), 135 mM NaCl, 1% Triton X-100, 10% glycerol and protease inhibitor cocktail tablets (Roche Molecular Biochemicals) and centrifuged at 14,000×g for 15 min at 4°C after incubation for 30 min at 4°C. Cell lysates were subjected to sodium dodecyl sulfate-12.5% polyacrylamide gel electrophoresis (SDS-PAGE) after boiling in sample buffer and transferred to polyvinylidene difluoride membranes (Millipore, Tokyo, Japan). The membranes were blocked with PBS containing 0.05% Tween 20 and 5% skim milk at room temperature for 1 h, incubated with mouse monoclonal anti-FLAG M2 (Sigma), anti-hemagglutinin (HA) 16B12 (HA.11; BabCO, Richmond, CA), anti-NS5A mouse monoclonal antibody (Austral Biologicals, San Ramon, CA), anti-GAPDH (Santa Cruz Biotechnology, Santa Cruz, CA), or anti-hexahistidine monoclonal antibody (Santa Cruz) at room temperature for 1 h, and then with horseradish peroxidase-conjugated anti-mouse IgG or anti-rabbit IgG antibody at room temperature for 1 h. The immune complexes were visualized with Super Signal West Femto substrate (Pierce, Rockford, IL) and detected by an LAS-3000 image analyzer system (Fujifilm, Tokyo, Japan).

Quantitative reverse-transcription polymerase chain reaction (qRT-PCR)

A total RNA was prepared from HCV replicon cells and Huh7OK1 cells infected with HCVcc transfected with the plasmids encoding each of the IRF constructs using an RNeasy

mini kit (QIAGEN, Valencia, CA) and first-strand cDNA was synthesized by using ReverTra Ace (TOYOBO, Osaka, Japan) and oligo $(dT)_{20}$ primer. The expression of each cDNA was estimated by Platinum SYBR Green qPCR SuperMix UDG (Invitrogen) according to the manufacturer's protocol. Fluorescent signals were analyzed by an ABI PRISM 7000 (Applied Biosystems). The HCV and GAPDH genes were amplified using the primer pairs of 5′-GAGTGTCGTGCAGCCTCCA-3′ and 5′-CACTCGCAAGCACCCTATCA-3′, and 5′-ACCACAGTC-CATGCCATCAC-3′ and 5′-TCCACCACCCTGTTGCTGTA-3′, respectively. The expression of each of mRNA was normalized with that of GAPDH.

Subcellular localization of cIRF7 in HCV- replicating cells

Cells transfected with the plasmids were harvested at 24 h post transfection, washed twice with PBS, fixed with PBS containing 4% paraformaldehyde, and permeabilized by incubation with PBS containing 0.25% saponin for 10 min. Cells were incubated for 1 h at 4°C with 1μg/ml of anti-NS3 (251) mouse monoclonal antibody (Santa Cruz), anti-NS5A mouse monoclonal antibody (Austral Biologicals), or mouse monoclonal antibody to protein disulfide isomerase (PDI) (Affinity Bioreagents, Golden, CO) in PBS containing 10% FCS (PBSF), and then incubated at room temperature for 1 h with 0.5 μg/ml of Alexa Flour 594-conjugated anti-mouse IgG (Molecular Probes, Eugene, OR) after three time washes with PBSF. Cell nuclei were stained with 4′, 6-diamidino-2-phenylindole (DAPI). After an extensive wash with PBSF, the samples were examined with a Fluoview FV1000 laser scanning confocal microscope (OLYMPUS, Tokyo, Japan).

Statistical analysis. Results were expressed as the mean ± standard deviation. The significance of differences in the means was determined by Student's *t* test.

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Author Contributions

Conceived and designed the experiments: TA Y. Matsuura. Performed the experiments: XW TA HK ST Y. Mori HT KM. Analyzed the data: NK TS MT. Contributed reagents/materials/analysis tools: NK MT. Wrote the paper: TA Y. Matsuura.

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