(4EBP1). p70 S6 kinase phosphorylates ribosomal S6 protein, resulting in an increase of the protein synthesis complex. Phosphorylated 4EBP1 results in its dissociation from the eukaryotic translation initiation factor 4E (eIF4E), which consequently enables eIF4E to regulate the translation initiation. Thus, together, p70 S6 kinase and 4EBP1 are responsible for the mTOR-dependent regulation of cellular translation. Moreover, both have been demonstrated to be involved in the regulation of HCV replication [6].

The finding that BCAA, per se, can activate signaling pathways suggests that they may affect HCV replication, presumably via the activation of the mTOR pathway. However, to date, no detailed investigation has been reported. Therefore, we attempt to clarify whether BCAA have a role in regulating HCV replication by using the HCV replicon system and cell culture of infectious-HCV (HCVcc). The present study reveals that although BCAA, especially valine, suppresses HCV genome replication, they eventually promote total HCV production by accelerating viral formation.

2. Methods

2.1. Cells

The hepatoma-derived cell line Huh7 and its derivatives, Huh7.5 and Huh7-25 [11], were maintained in DMEM supplemented with 10% FCS. The HCV subgenomic replicon cell line Huh-RepSI [10], and the HCV genome-length replicon cell line 2–3 [12], both harboring the HCV-N strain (genotype 1b), were previously described. The molar ratio of the BCAA mixture was adjusted to Leu:Ile:Val = 2.0:1.0:1.2 according to data from previous studies [13]. For assays to examine the role of BCAA, cells were cultured in BCAA-deficient DMEM with 10% FCS supplemented with BCAA mixtures of various concentrations (0–2 mM).

2.2. Cell culture-infectious HCV

JFH-1 is a cell culture-infectious virus of genotype 2a as previously described [14]. HJ3-5(YH/QL) is a chimeric cell culture-infectious virus with a genome consisting of the core to NS2 sequence of genotype 1a (H77) virus placed within the background of the genotype 2a JFH-1 virus. This virus contained compensatory mutations in E1 (Y361H) and NS3 (Q1251L) [15]. These two mutations rendered the chimeric RNA highly infectious.

2.3. In Vitro transcription and transfection of synthetic RNA

Plasmid DNAs encoding HJ3-5(wild) and HJ3-5(YH/QL), a wild-type chimeric virus and a chimeric virus carrying two mutations, respectively, were linearized by *Xba*I prior to transcription. RNA was synthesized with the T7 RiboMAX Express Large Scale RNA Production System (Promega, Madison, WI, USA) following the

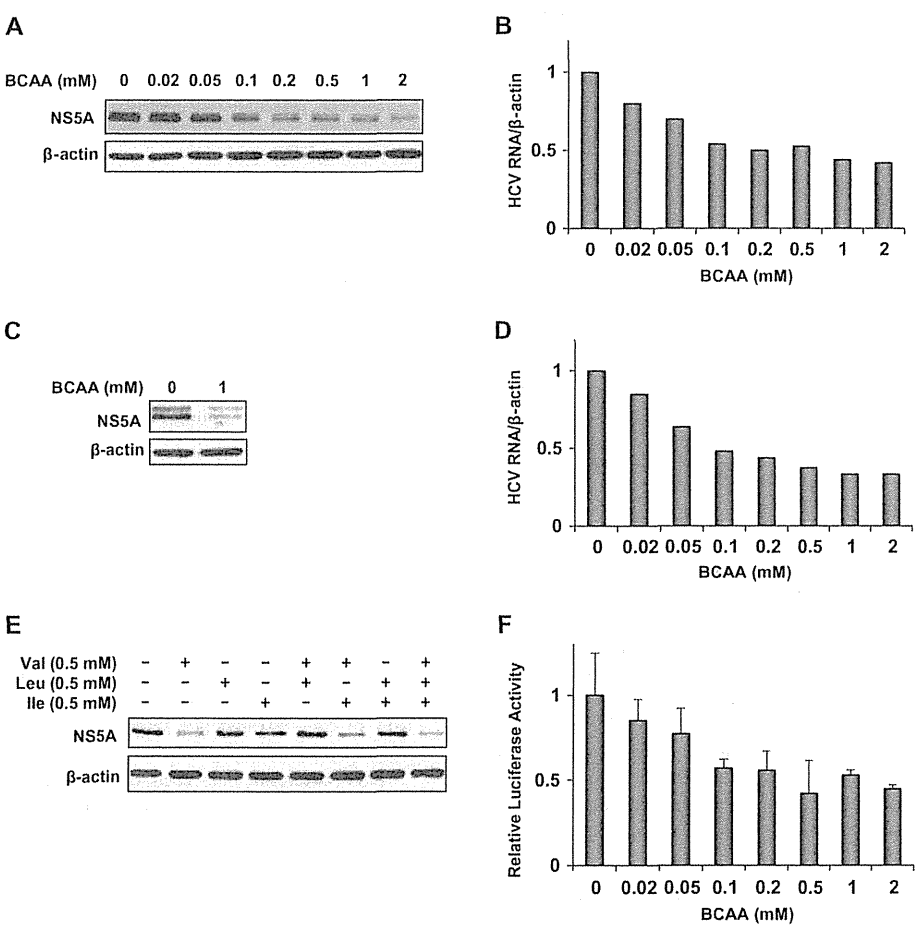

Fig. 1. BCAA limits the abundance of HCV replicon in HCV replicon cells. (A–D). Huh-RepSI (A and B) and 2–3 (C and D) cells were cultured in media for 2 days, with BCAA supplemented at concentrations of 0–2 mM. Total protein or total RNA was recovered and assayed for immunoblot (A and C) or real-time RT-PCR (B and D), respectively. (E) Three BCAAs (0.5 mM each) were added to BCAA-free culture medium of Huh-RepSI. After incubation for 2 days, immunoblot analysis of NS5A and beta-actin were performed. (F) Huh-RepSI cells were transfected with pRLHL, cultured in media with various BCAA concentrations between 0 and 2 mM. After incubation for 2 days, a dual luciferase assay was performed. The ratio of firefly luciferase activity to renilla luciferase activity was then calculated.

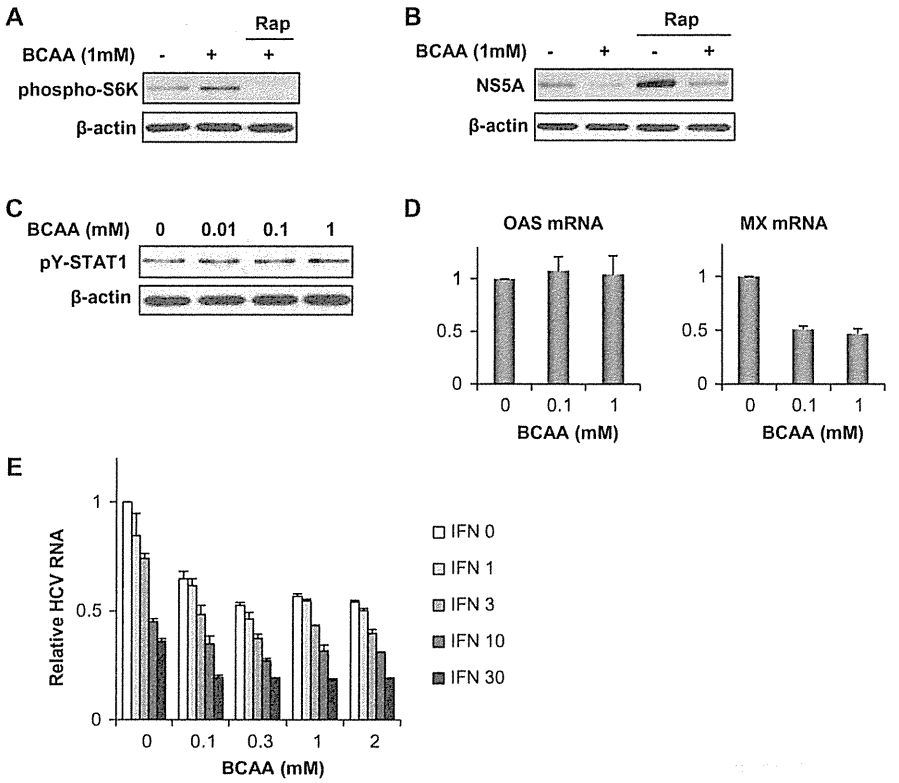

Fig. 2. BCAA-induced suppression of HCV replicon is independent of mTOR or JAK/STAT signaling. (A) Immunoblot of phosphorylated p70 S6 kinase and beta-actin in Huh-RepSI cells cultured in a medium with or without BCAA (1 mM). Rapamycin was added at 100 nM to the BCAA-containing medium. (B) Immunoblot analysis of NS5A and beta-actin in Huh-RepSI cells cultured in a medium with 1 mM BCAA or rapamycin (100 nM). (C) Huh-RepSI cells were incubated in media with various BCAA concentrations (0, 0.01, 0.1, 1 mM), and then, immunoblot analyses of phosphorylated STAT1 (Tyr701) and beta-actin were performed. (D) Huh-RepSI cells were incubated in media with various BCAA concentrations (0, 0.1, 1 mM), and then, a real-time RT-PCR analysis, for expression of OAS and MX, was performed. (E) Huh-RepSI cells were incubated in culture media with various BCAA concentrations (0–2 mM) and IFN-α (0–30 U/ml). HCV RNA abundance was normalized with beta-actin allowing the relative HCV RNA levels to be calculated, setting the HCV RNA level of 0 U/ml IFN-α and 0 mM BCAA as 1. Rap: rapamycin.

manufacturer's suggested protocol. For electroporation, Huh7 cells were washed twice with ice cold phosphate-buffered saline (PBS) and resuspended at a concentration of 10^7 cells/ml in PBS. Subsequently, 10 μg of RNA was mixed with 500 μl of the cell suspension in a cuvette, with a gap width of 0.2 cm (GenePulser II System; Bio-Rad, Hercules, CA, USA). The mixture was immediately subjected to two pulses of current with the intensities of 1.2 kV, 25 μF, and maximum resistance. Following a 10-min incubation at room temperature, the cells were transferred into growth medium.

2.4. Titration of HCV infectivity

Huh-7.5.1 cells were seeded in 96-well plates at a density of 1×10^4 cells per well 24 h prior to culture media inoculation of the HCV infected cells. Three days after infection, HCV-positive cells were detected with mouse monoclonal antibody that recognized core proteins stained with an Alexa Fluor 488 anti-mouse secondary antibody (Invitrogen, Carlsbad, CA, USA). The infectivity titer was expressed as focus-forming units per mL of supernatant (ffu/mL), expressing the mean number of HCV core-positive foci. The intracellular infectivity and specific intracellular infectivity titer were determined as described previously [16].

3. Results

3.1. BCAA suppresses the amount of HCV replicon

To investigate the role of BCAA in HCV replication, we first examined the effect of BCAA on the HCV replicon. An HCV subgenomic replicon cell line, Huh-RepSI, was incubated in culture medium that contained various concentrations of BCAA (0–2 mM) for 2 days. HCV replicon RNA, as well as the amount of protein, was suppressed by adding BCAA in a dose-dependent manner (Fig. 1A and B). To confirm the effect of BCAA, another replicon cell line, 2–3, carrying a genome-length HCV replicon, was used. In this experiment, suppression of the replicon by BCAA was observed, which is in agreement with the Huh-RepSI assay (Fig. 1C and D). This activity suggested that BCAA possessed the ability to suppress HCV replication.

Three BCAAs exist: valine, leucine, and isoleucine. As previously demonstrated, leucine contains the biological activity to activate mTOR. In addition, we showed that mTOR, which is activated by PI3 kinase/Akt, was able to suppress HCV replication [6]. Therefore, it is possible that the BCAA-mediated suppression of HCV replication was due to leucine. To test this hypothesis, the three amino acids were added independently to BCAA-deficient medium while monitoring the HCV replication level. Unexpectedly, the result refuted the hypothesis (Fig. 1E). Compared to the cells cultured in BCAA-deficient medium, supplementation with only valine efficiently suppressed the HCV replicon, whereas leucine did not; instead, it caused a slight increase. This result showed that BCAA, especially valine, but not leucine, have a suppressive effect on HCV replication.

3.2. BCAA suppresses HCV IRES activity

HCV replication can be controlled by HCV specific translation regulated by IRES, the 5′ UTR region of HCV. Therefore, we next

investigated the effect of BCAA on HCV IRES activity. To do this, we utilized a dicistronic vector, pRLHL, which consists of firefly luciferase driven by HCV IRES and renilla luciferase, translated in a cap-dependent manner (Sup. Fig. 1). Relative HCV IRES activity was evaluated using the ratio of IRES-specific luciferase activity to the cap-dependent luciferase activity. As shown in Fig. 1F, HCV IRES activity was suppressed by BCAA in a dose-dependent manner, which is similar to the result of the replicon abundance (Fig. 1A and B). Thus, the BCAA-mediated suppression of HCV replication is likely due to the inhibition of HCV IRES activity.

3.3. BCAA-mediated suppression of HCV replicon is independent of the mTOR and JAK/STAT pathways

Previous reports have demonstrated that BCAA is capable of activating mTOR [4], and we have reported that mTOR suppresses HCV replication [6]. Therefore, we examined the contribution of mTOR activation on BCAA-mediated suppression of the HCV replicon. Administration of BCAA efficiently phosphorylated p70 S6 kinase, whereas rapamycin completely inhibited its phosphorylation (Fig. 2A). Despite rapamycin enhancing the amount of HCV replicon, BCAA could efficiently suppress it, even in rapamycin-containing medium (Fig. 2B), suggesting that the suppression of the HCV replicon by BCAA is independent of mTOR activation.

The IFN-JAK/STAT signal is known to be an anti-virus pathway, induced under the condition of virus infection. HCV replication is efficiently inhibited by interferon. Therefore, we examined whether BCAA could modify the IFN signal. First, we performed an immunoblot analysis and evaluated the status of STAT1 activation, in the presence or absence of BCAA. However, the phosphorylated STAT1 level was not altered by BCAA in Huh-RepSl cells, and ISG induction was not observed; instead, the expression level of Mx was suppressed by BCAA (Fig. 2C and D). A previous study showed that rapamycin diminished the suppressive effect of IFN-α toward HCV replication via the suppression of ISG induction [17]. Subsequently, we examined the HCV replicon abundance in cells that were cultured in media with various concentrations of BCAA and IFN-α stimuli. Even with the depletion of BCAA, IFN-α efficiently and dose-dependently suppressed HCV replicon abundance. However, IFN-α-induced anti-HCV activity was not augmented by BCAA supplementation (for example, the replicon RNA level decreased to approximately 30% in both BCAA-depleted medium and 2 mM BCAA-supplemented medium) (Fig. 2E). Consequently, BCAA did not influence JAK/STAT activation, and therefore, the suppression of HCV replicon by BCAA may have been independent of the IFN-α-induced signaling pathway.

3.4. BCAA enhances HCVcc production

Next, we examined the impact of BCAA on HCVcc, a system retaining the entire HCV life cycle in a cultured cell. Here, we used HJ3-5(YH/QL), a chimeric HCV of genotype 1a (H77) and 2a (JFH-1). Surprisingly, the results of HJ3-5(YH/QL) were opposite to that of the HCV replicon: HCV abundance was upregulated in a BCAA dose-dependent manner (Fig. 3A). The HCV replicon contains NS3 to NS5B proteins, which are required for HCV RNA genome replication, but not core, E1 and E2 proteins, which are structural proteins required for viral particle formation. The discrepancy in the results between HCV replicon cells and HCVcc-infected cells might be due to differences in virus particle production.

To investigate this discrepancy, we used the wild-type HJ3-5, designated as HJ3-5(wild). As described in the Methods section, HJ3-5(YH/QL) or the HCVcc used in this study, carries two amino acid substitutions at amino acid 361 and amino acid 1251, within E1 and NS3, respectively. These two mutations render the chimeric RNA highly infectious [15]. However, without these mutations, virus particle assembly and consequent virion release from the cells to the medium would not occur. This process is thought to be due to impaired association of the HCV proteins originating from different genotypes, whereas there is no apparent change in the HCV RNA replication level in the cells [15].

We introduced the *in vitro* transcribed genome RNA of HJ3-5(wild) or HJ3-5(YH/QL) into Huh7 cells with electroporation, and then, we examined the effect of BCAA on the cell line. Normally, synthesized HCV RNA introduced into cells executes replication by utilizing HCV proteins encoded in the genome and host factors, resulting in a robust increase that is detectable after 2–3 days. BCAA decreased the abundance of HJ3-5(wild), which was similar to their effect on the HCV replicon (Fig. 3B and C). Thus, HJ3-5(wild), a virus that is defective in virus particle formation, revealed the opposite reaction to BCAA compared to the virus HJ3-5(YH/QL), a virus that is competent in virus particle formation. Together, these findings revealed that although BCAA had the ability to suppress the HCV genome replication, they promoted viral production by enhancing other steps, which included virus assembly, virus particle release and cell re-infection.

3.5. BCAA promotes infectious HCV particle formation, not virus secretion

To further assess the BCAA intracellular mechanisms that influence the HCV life cycle, we adopted a single-cycle virus production assay [18]. We used Huh7-25 cells due to the lack of surface expression of one of the cellular HCV receptors, CD81, thus being non-permissive to HCV infection. Because HCV genome replication or virus production is intact in Huh7-25, we can evaluate viral replication and secretion without the influence of re-infection.

First, we studied the replication levels of the infectious virus, JFH-1, in Huh7-25 cells. The full length of the JFH-1 genome RNA

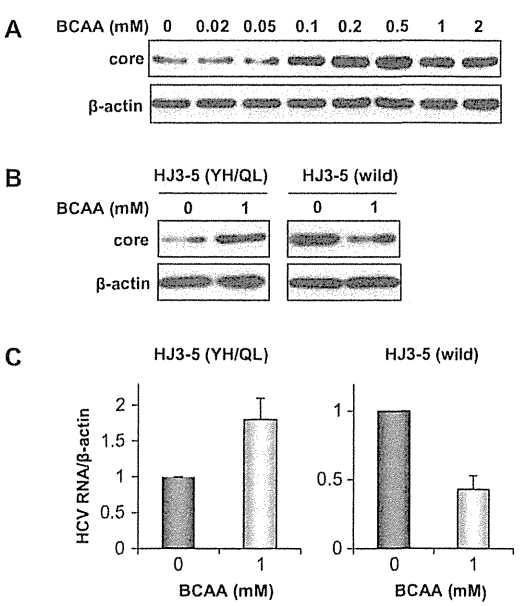

Fig. 3. HCVcc abundance was increased by BCAA. (A) HCVcc-infected Huh7 cells were cultured in media with various BCAA concentrations (0–2 mM). After incubation for 2 days, and an immunoblot analysis of core and beta-actin was performed. (B and C) Synthesized HCV genome RNA of HJ3-5 (YH/QL) or HJ3-5 (wild) was transfected into Huh7 cells via electroporation. After incubation for 24 h, cells were split into 6-well plates and incubated for 2 days in a culture medium with or without 1 mM BCAA. After the cells were harvested, immunoblot analysis of core and beta-actin (B) and real-time RT-PCR analysis (C) were performed.

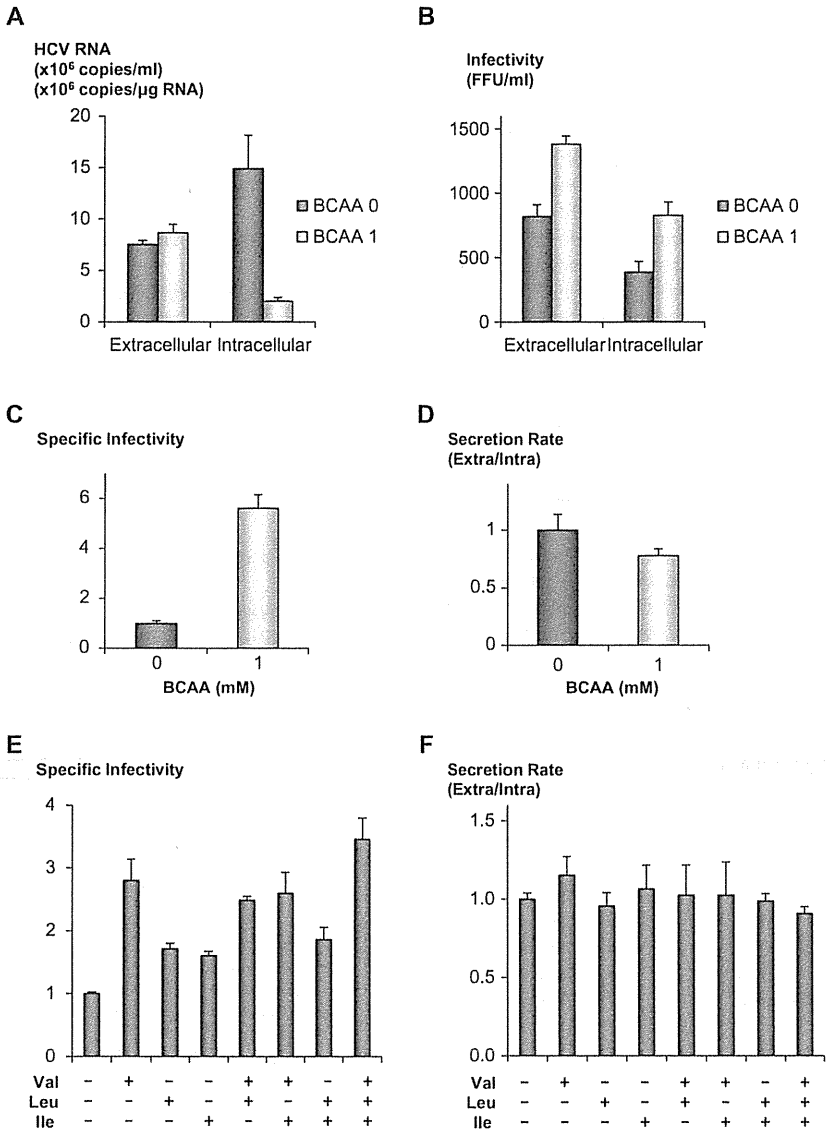

Fig. 4. Single-cycle virus production assay indicates a promoting effect of BCAA on virus formation. (A) Huh7-25 cells were transfected with *in vitro*-transcribed RNA of JFH-1, incubated in media with or without BCAA, followed by the RNA levels in the media or in the cells being calculated using the real-time quantitative RT-PCR method. (B) Infectivities in the media or in the cell lysates were measured. (C) Specific infectivities were calculated by dividing the infectivities by the HCV RNA amounts. (D) Secretion rates were calculated by dividing extracellular infectivities by intracellular infectivities. The data were presented as ratios defining the value of BCAA at 0 mM as 1. (E and F) Specific infectivities and secretion rates in the presence of valine (0.5 mM), leucine (0.5 mM), or isoleucine (0.5 mM). The data were presented as ratios defining the value with no BCAA as 1.

was translated *in vitro* and transfected into the Huh7-25 cells. The cells were cultured in media, with or without 1 mM of BCAA, with the RNA levels being monitored using quantitative RT-PCR. As observed in the experiment of replicon cells or virus particle formation-deficient viruses, the intracellular RNA level of HCV was suppressed by the presence of BCAA (Fig. 4A). However, the levels of extracellular HCV RNA were similar. Despite the suppression of intracellular HCV RNA levels by BCAA-containing medium, the infectivity titer of the intracellular virus in the cells treated with 1 mM BCAA was significantly higher than that of the cells with 0 mM BCAA (Fig. 4B). Extracellular infectivity titers were similar to those of intracellular infectivity. The specific infectivity of intracellular virus was calculated by dividing the infectivity titer by the HCV RNA level and this revealed that cultivation of the cells in a medium of 1 mM BCAA resulted in a 5.6-fold higher specific virus infectivity than that of 0 mM BCAA (Fig. 4C). Next, we measured virus secretion rates by dividing extracellular infectivity titers by intracellular infectivity titers. There was a minimal difference between infectious virus particle secretions (Fig. 4D). Thus, these results indicated that the infectious virion production was promoted in the BCAA-supplemented medium, although the virus RNA replication was suppressed.

In the study using replicon cells, valine was shown amino acid responsible for regulating HCV RNA replication (Fig. 1E). Finally, we assessed the effect of individual BCAA on virus production. HCV infected cells were cultured in media containing each amino acid at 0.5 mM or a combination of them and subsequently specific infectivity and secretion rate were examined (Fig. 4E and F). Among the three BCAAs, valine promoted infectious virus production most effectively, while leucine and isoleucine promoted infectious virus production modestly. Secretion rates did not show a significant difference.

4. Discussion

In the present study, we investigated the role of BCAA in the HCV life cycle and discovered that these amino acids suppress HCV genome replication but promote viral particle formation. Thus far, many reports have indicated that various cellular factors are involved in the regulation of HCV. In particular, intracellular signaling pathways are important modulators for HCV genome replication [5–10]. BCAA, specifically leucine, were demonstrated to have a role in activating the mTOR pathway, leading to protein synthesis such as upregulation of albumin [4] and HGF production [19]. Recently, mTOR was reported to be involved in IFN-α signaling [17]. IFN-α induced phosphorylation of STAT1 was diminished by rapamycin (but not by LY294002, a PI3 kinase inhibitor). Consequently, rapamycin inhibited the IFN-stimulated regulatory element. Although we demonstrated that BCAA can activate mTOR (Fig. 2A), the inhibition of mTOR revealed that it was not the main pathway for the BCAA suppression of HCV replication. BCAA supplementation did not change the STAT1 phosphorylation status, nor did it induce ISG expression, indicating that the JAK/STAT pathway was not relevant for the suppression of HCV replication. Considering that leucine, the factor required for mTOR activation, did not actually take part in regulation of the HCV replicon (Fig. 1E), it was not surprising that mTOR was shown to not be the responsible molecule.

Very recently, Honda et al. demonstrated that STAT1 phosphorylation was increased by BCAA in a dose-dependent manner [20]. They showed that BCAA increased the phosphorylation levels of STAT1, Foxo3a and p70 S6 kinase leading to downregulation of Socs3 expression and HCV replication. The range of BCAA concentration examined in the present study was between 0 and 2 mM. We ranged the concentration of BCAA between 0 and 2 mM because its concentration in blood is approximately 1.6 mM after oral administration of 5 g of BCAA. However, in the Honda et al. study, the BCAA concentration at which STAT1 was efficiently phosphorylated was more than 4 mM, whereas at 2 mM or less, no obvious increase in phospho-STAT1 was observed. Therefore, we may have detected no change in phospho-STAT1 due to BCAA levels used in this study. Thus, BCAA may be capable of suppressing HCV genome replication at a low concentration by inhibiting HCV IRES activity while decreasing virus replication by augmentation of IFN signaling at high concentrations.

Although BCAA suppressed replication of HCV replicon, they increased HCVcc production in infected cells. The life cycle of HCV has many steps that are required to achieve infection, such as attachment to the cell surface, endocytosis of the virus, uncoating and releasing genome RNA, RNA replication, polyprotein synthesis and processing, viral assembly, and release of progeny virus. Among these, the HCV replicon system only represents the steps of genome RNA replication and non-structural protein synthesis in the cells, and BCAA affects these by impairing protein synthesis via suppression of HCV IRES activity. However, HCVcc replication requires all of these steps. We assumed that the increase of HCVcc due to BCAA indicated that some step(s) must be upregulated by BCAA to the extent of overcoming the decreased genome replication. The study of particle formation-deficient viruses suggested that virus assembly or some downstream step in the virus life cycle was critical for the augmentation of HCVcc by BCAA. A single-cycle virus production assay indicated that the production of an infectious virus was prominent in the presence of BCAA, while virus secretion was not strongly affected. Although HCV genome replication was suppressed by BCAA, more infectious virus particles were secreted into the media, and they could have re-infected the Huh7 cells. We suggest that the abundant infectious HCV in BCAA-supplemented medium causes amplification of the virus during repetition of such re-infection, which leads to an accumulation of HCV in the cells, and thus, the abundance of HCV RNA in the cells with BCAA medium overcomes that without BCAA. Further investigation is needed on the detailed mechanisms defining how BCAA regulates HCV particle formation. Clarification of this process could contribute to new insights into HCV replication and could also suggest a basis for treatment of HCV patients.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.bbrc.2013.06.051.

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PLOS ONE

Inhibitory Effects of Caffeic Acid Phenethyl Ester Derivatives on Replication of Hepatitis C Virus

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Abstract

Caffeic acid phenethyl ester (CAPE) has been reported as a multifunctional compound. In this report, we tested the effect of CAPE and its derivatives on hepatitis C virus (HCV) replication in order to develop an effective anti-HCV compound. CAPE and CAPE derivatives exhibited anti-HCV activity against an HCV replicon cell line of genotype 1b with EC_{50} values in a range from 1.0 to 109.6 μM. Analyses of chemical structure and antiviral activity suggested that the length of the n-alkyl side chain and catechol moiety are responsible for the anti-HCV activity of these compounds. Caffeic acid n-octyl ester exhibited the highest anti-HCV activity among the tested derivatives with an EC_{50} value of 1.0 μM and an SI value of 63.1 by using the replicon cell line derived from genotype 1b strain Con1. Treatment with caffeic acid n-octyl ester inhibited HCV replication of genotype 2a at a similar level to that of genotype 1b irrespectively of interferon signaling. Caffeic acid n-octyl ester could synergistically enhance the anti-HCV activities of interferon-alpha 2b, daclatasvir, and VX-222, but neither telaprevir nor danoprevir. These results suggest that caffeic acid n-octyl ester is a potential candidate for novel anti-HCV chemotherapy drugs.

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Introduction

Hepatitis C virus (HCV) is well known as a major causative agent of chronic liver disease including cirrhosis and hepatocellular carcinoma and is thought to persistently infect 170 million patients worldwide [1]. HCV belongs to the genus *Hepacivirus* of the family *Flaviviridae* and possesses a viral genome that is characterized by a single positive strand RNA with a nucleotide length of 9.6 kb [2]. The single polypeptide coded by the genome is composed of 3,000 amino acids and is cleaved by host and viral proteases, resulting in 10 proteins, which are classified into structural and nonstructural proteins [3]. The viral genome is transcribed by a replication complex consisting of NS3 to NS5B and host factors [4]. NS3 forms a complex with NS4A and becomes a fully active form to cleave the C-terminal parts of the nonstructural proteins. The advanced NS3/4A protease inhibitors, telaprevir and boceprevir, have been employed in the treatment of chronic hepatitis C patients infected with genotype 1 [5]. Sustained virologic response (SVR) was reportedly 80% in patients infected with genotype 1 following triple combination therapy with pegylated interferon, ribavirin, and telaprevir [6], although the therapy exhibits side effects including rash, severe cutaneous eruption, influenza-like symptoms, cytopenias, depression, and anemia [7]. In addition, there is the possibility of the emergence of drug-resistant viruses following treatment with those anti-HCV drugs [8] Thus, further study is required for development of safer and more effective anti-HCV compounds.

Several recent reports indicate that silbinin [9], epigallocatechin-3-gallate [10], curcumin [11], quercetin [12] and proanthocyanidins [13], which all originate from natural sources, have exhibited inhibitory activity against HCV replication in cultured cells. Caffeic acid phenethyl ester (CAPE) is an active component included in propolis prepared from honeybee hives, and has a similar structure to flavonoids (Fig. 1A). CAPE has multifunctional properties containing anti-inflammatory [14], antiviral [15], anticarcinogenic [16], and immunomodulatory activities [15]. CAPE also inhibits enzymatic activities of endogenous and viral proteins [17–19] and transcriptional activity of NF-kappaB [14,20]. In addition, CAPE could suppress HCV replication enhanced by using the NF-kappaB activation activity of morphine [21], although it has been unknown which of moieties including CAPE is responsible for anti-HCV activity. Furthermore, it is not clear whether chemical modification of CAPE could enhance anti-HCV activity or not. In this report, we examined the effect of

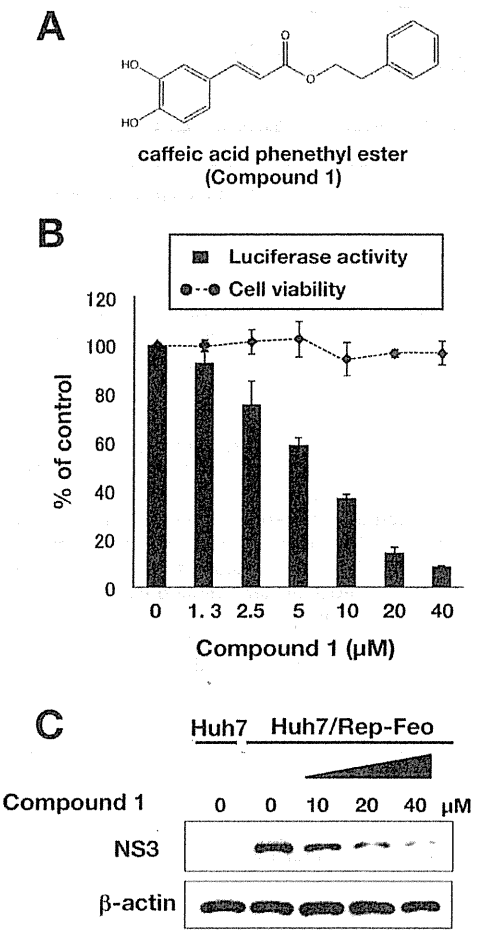

Figure 1. Effect of CAPE on viral replication in the replicon cell line of genotype 1b. (A) Molecular structure of CAPE. (B) Huh7/Rep-Feo cells were incubated for 72 h in a medium containing various concentrations of CAPE. Luciferase and cytotoxicity assays were carried out by the method described in Materials and Methods. Error bars indicate standard deviation. The data represent results from three independent experiments. (C) Protein extract was prepared from Huh7/Rep-Feo cells treated for 72 h with the indicated concentration of CAPE and it was then was subjected to Western blotting using antibodies to NS3 and beta-actin.
doi:10.1371/journal.pone.0082299.g001

CAPE derivatives on HCV proliferation to develop more effective and safer anti-HCV compounds.

Results

Effect of CAPE on HCV RNA replication in HCV subgenomic replicon cells

CAPE is composed of ester of caffeic acid and phenethyl alcohol (Fig. 1A). We examined the effect of CAPE (compound **1**) on both viral replication and cell growth in the HCV subgenomic replicon cell line Huh7/Rep-Feo. The replicon cell line was treated with various concentrations of compound **1**. The replication level of the HCV RNA was measured as an enzymatic activity of luciferase, which is bicistronically, encoded on the replicon RNA. Compound **1** suppressed HCV RNA replication at concentrations from 1.3 to 40 μM in a dose-dependent manner, but did not affect cell viability (Fig. 1B). HCV NS3, which is a viral protease, was decreased at the protein level by treatment with CAPE in a dose-dependent manner, corresponding to the viral replication, whereas beta-actin was not changed in the replicon cell line (Fig. 1C). Based on the calculation using a dose dependency of CAPE, compound **1** exhibited an EC_{50} value of 9.0 μM and a CC_{50} value of 136.1 μM, giving a selectivity index estimate (SI) of 17.9 (Table 1). These results suggest that treatment with CAPE inhibits HCV replication in HCV subgenomic replicon cells.

Structure-activity relationship of CAPE analogues

To clarify the structure-activity relationship of CAPE analogues, we examined the effect of hydroxyl groups on the aromatic ring (catechol moiety), the alkenyl moieties on alpha, beta-unsaturated esters, and the ester parts as follows (Figure S1).

We tested whether commercially available CAPE-related compounds **2** to **6** (Fig. S1) affected HCV replication (Table 1). All these compounds showed weaker inhibitory activity than CAPE (**1**), but are not toxic. Compound **2**, which is the acid component of CAPE, showed a slightly lower value of EC_{50} than compound **3**, which is the compound **2** derivative replaced a hydroxyl group with a methoxyl group of catechol moiety, while compound **4**, which is the derivative lacking two hydroxyl groups within catechol moiety, exhibits a higher value of EC_{50} than compounds **1** and **2**. These data suggest that the catechol moiety of CAPE is required for anti-HCV activity. Interestingly, compounds **5** and **6**, which are natural products including polyhydroxylated acid moieties in the ester parts, showed much weaker inhibitions than compound **1** and exhibits low *Clog P* values. The position of hydroxyl group or/and the structure of the ester part may affect the inhibitory activity and/or hydrophobicity.

We next examined the effects of caffeic acid ester compounds **7** to **11**, which include various lengths of alkyl side chains, on HCV replication (Table 2 and Figure S2). The EC_{50} values decreased in the order methyl ester (compound **7**), n-butyl ester (compound **8**), n-hexyl ester (compound **9**), and n-octyl ester (compound **10**), suggesting that elongation of the n-alkyl side chain increased the inhibitory activity. However, the EC_{50} value of n-dodecyl ester (compound **11**) was higher than that of compound **10**. Thus, n-octyl ester (compound **10**) showed the lowest EC_{50} value and the highest SI among the tested compounds shown in Tables 1 and 2. Compounds **7** to **11** gradually increased own *Clog P* values,

Table 1. Effect of CAPE (**1**) and related compounds **2–6** on HCV replication.

Compound (Number)	EC_{50} [a] (μM)	CC_{50} [b] (μM)	SI [c]	*Clog P* [d]
CAPE (**1**)	9.0±0.7	136.1±1.9	17.9	3.30
caffeic acid (**2**)	36.6±6.7	>320	>8.7	0.98
ferulic acid (**3**)	71.9±5.8	>320	>4.5	1.42
cinnamic acid henethyl ester (**4**)	86.1±6.3	>320	>3.7	4.56
chlorogenic acid (**5**)	103.0±3.4	>320	>3.1	−0.96
rosmarinic acid (**6**)	109.6±1.1	>320	>2.9	1.10

a: Fifty percent effective concentration based on the inhibition of HCV replication.
b: Fifty percent cytotoxicity concentration based on the reduction in cell viability.
c: Selectivity index (CC_{50}/EC_{50}).
d: Determined with ChemDraw software (Chem Bio Office Ultra, 2008).
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corresponding to length of n-alkyl side chain (Fig. 2A). Compounds **10** and **11** exhibit EC_{50} values of 2.7 and 5.9 μM, respectively, SI values of 29.6 and 9.80, respectively, and *Clog P* values of 4.90 and 5.96, respectively, suggesting that high hydrophobic property of n-alkyl side chain decreases anti-HCV activity. The appropriate *Clog P* value of caffeic acid ester containing unsaturated side chain may be around 5.

Dihydrocaffeic acid methyl ester (compound **12**) showed less activity than caffeic acid methyl ester (compound **7**) regardless of values of *Clog P* value and CC_{50}, suggesting that the alpha, beta-unsaturated part attached to ester affects the anti-HCV activity level (Table 3 and Figure S3).

We further examined the effect of the hydroxyl groups on the aromatic ring on HCV replication (Table 4 and Figure S4). The EC_{50} values of *O*-methylated caffeic acid n-octyl esters (compounds **13** and **14**) were higher than that of compound **10**. Compounds **15** including 3, 4-di-*O*-methylated caffeic acid n-octyl ester exhibited higher EC_{50} than values of compounds **10**, **13** and **14**. However, addition of a third hydroxyl group to 3, 4, 5-trihydroxy derivative (compound **16**) of compound **10** resulted in a reduction of anti-HCV activity. Furthermore, *Clog P* values of compound **10**, **13**, **14, 15** and **16** were not correlated with anti-HCV activity (EC_{50} value) (Fig. 2B). These results suggest that the catechol moiety plays an important role in anti-HCV activity, and that the 4-hydroxy moiety is more important for the activity than the 3-hydroxy moiety.

Thus, compound **10**, which exhibits the lowest EC_{50} value and the highest SI value, is the most effective compound among CAPE analogues used in this study.

Effect of CAPE derivatives on virus production

The structure of compound **10** is shown in Fig. 3A. Treatment with compound **10** reduced HCV replication and NS3 protein in a dose-dependent manner at a higher anti-HCV level than

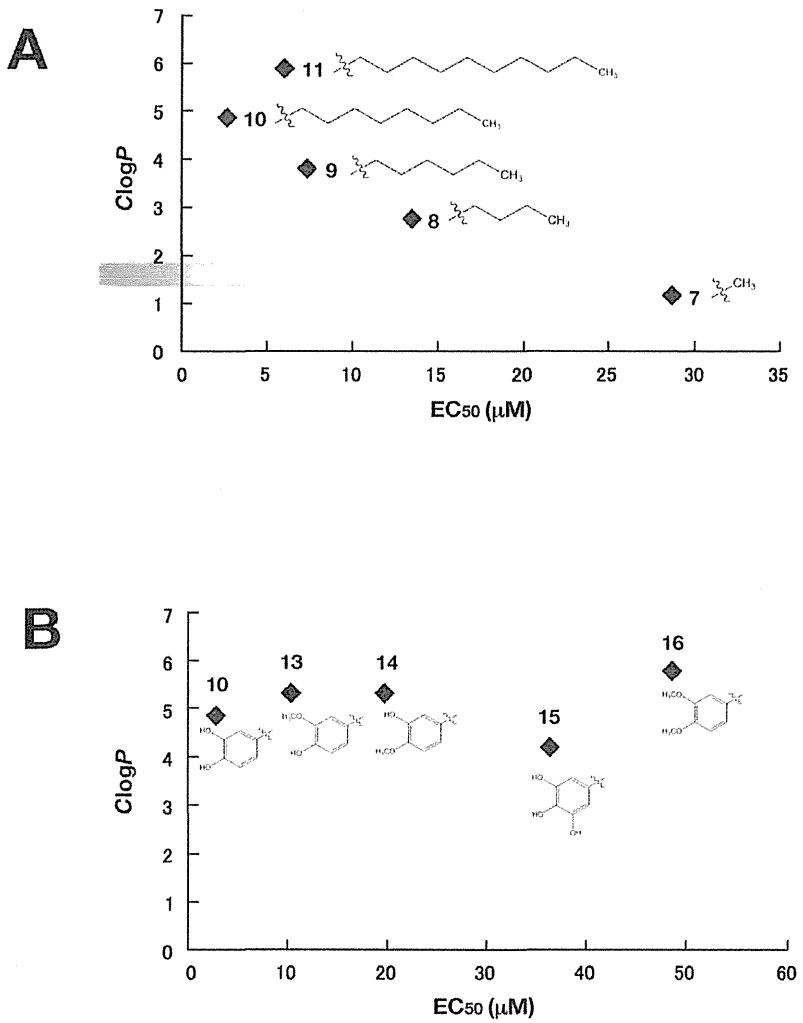

Figure 2. Correlation between the inhibitory effect on HCV replication *and* Clog *P* of CAPE analogues. Values of *x*-axis indicate EC_{50} values of CAPE analogues, while values of *y*-axis show *Clog P* values. (A) Correlation between the inhibitory effect on HCV replication and *Clog P* of CAPE analogues (Compound 7–11). (B) Correlation between the inhibitory effect on HCV replication and *Clog P* of CAPE analogues (Compound 10 and 13–16).
doi:10.1371/journal.pone.0082299.g002

Table 2. Effect of caffeic acid esters **7, 9–14**, including **1**, on HCV replication.

Compound No.	R	EC_{50} [a] (μM)	CC_{50} [b] (μM)	SI [c]	*Clog P* [d]
7	CH_3	28.6±1.2	122.1±5.0	4.2	1.20
8	C_4H_9	13.5±2.1	39.0±1.1	2.9	2.79
9	C_6H_{13}	7.3±0.2	37.6±1.2	5.1	3.85
10	C_8H_{17}	2.7±0.1	71.7±8.5	26.6	4.90
11	$C_{10}H_{21}$	5.9±0.9	57.9±2.9	9.8	5.96
1	$(CH_2)_2Ph$	9.0±0.7	136.1±1.9	17.9	3.30

The basic structure and side moieties are shown in Figure S2.
a: Fifty percent effective concentration based on the inhibition of HCV replication.
b: Fifty percent cytotoxicity concentration based on the reduction in cell viability.
c: Selectivity index (CC_{50}/EC_{50}).
d: Determined with ChemDraw software (Chem Bio Office Ultra, 2008).
doi:10.1371/journal.pone.0082299.t002

compound **1** (Figs. 3B and C), but not effect enzymatic activities of firefly and *Renilla* luciferases (Fig. 3D) and IRES-dependent translation (Fig. 3E), suggesting that inhibition of HCV replication by compound **10** is not due to offtarget effect. We evaluated the inhibitory effect of compound **10** on three different subgenomic replicon cell lines (1b: N strain, Con1 strain, 2a: JFH-1 strain) and one full genome replicon cell line (1b: O strain). Compound **10** inhibited the viral replication of all replicon cell lines at similar level, and exhibited the lowest EC_{50} value of 1.0 μM and an SI value of 63.1 by using Con1 replicon cells (Table 5). We next examined the effect of compound **10** on virus production by using HCVcc, since subgenomic replicon mimics HCV replication, but not the whole viral cycle. The Huh7 OK1 cell line, which is highly permissive to the HCV JFH1 strain [22], was infected with HCVcc and then treated with compound **10** at 24 h post-infection. The supernatant was harvested 72 h post-infection from the culture supernatant and then the RNA that prepared from the supernatant was estimated by real time qRT-PCR. Figure 3F shows that treatment with compound **10** reduced HCV viral production (EC_{50} = 1.8±0.4 μM) in a similar way to the data obtained by using a replicon cell line. To clarify whether or not compound **10** inhibited HCV replication via interferon-signaling pathway, we analyzed ISRE activity and the expression of interferon stimulated gene (ISG) by using reporter assay and RT-PCR, respectively. The replicon cells were harvested at 48 h post-treatment. There were no significant effects of compound **1**, **6** and **10** on ISRE-promoter activities, while interferon alpha 2b significantly enhanced it as a positive control (Fig.4 A). The data of the RT-PCR analysis showed that the transcriptional expressions of ISGs including Mx1, MxA, IFIT4, ISG15, OAS1, OAS2, and OAS3 were induced with interferon alpha 2b, but not with compound **1**, **6** and **10** (Fig. 4B). These data suggest that the CAPE derivatives have an inhibitory effect on virus production and replication, irrespective of interferon signaling induction.

Synergistic effect of caffeic acid n-octyl ester on interferon and direct-acting antiviral agents

To estimate the effects of drug combinations on anti-HCV activity, we examined the antiviral activity of compound **10** in combination with IFN-α 2b, telaprevir (NS3 protease inhibitor), danoprevir (NS3 protease inhibitor), daclatasvir (NS5A inhibitor) or VX-222 (NS5B polymerase inhibitor). Con1 LUN Sb #26 replicon cells were treated with compound **10** in combination with

Table 3. Effect of caffeic acid esters **7**and **8** on HCV replication.

Compound No.	EC_{50} [a] (μM)	CC_{50} [b] (μM)	SI [c]	*Clog P* [d]
7	28.6±1.2	122.1±5.0	4.2	1.20
12	77.0±1.6	140.7±3.4	1.8	1.02

Chemical structures of both compounds are shown in Figure S3
a: Fifty percent effective concentration based on the inhibition of HCV replication.
b: Fifty percent cytotoxicity concentration based on the reduction in cell viability.
c: Selectivity index (CC_{50}/EC_{50}).
d: Determined with ChemDraw software (Chem Bio Office Ultra, 2008).
doi:10.1371/journal.pone.0082299.t003

each anti-HCV agent at various concentration rations for 72 h. The effect of each drug combination on HCV replication was analyzed by using CalcuSyn. An explanatory diagram of isobologram was shown at a right end of lower panels of Fig. 5A as described in Materials and Methods. As shown in the resulting isobologram, all plots of the calculated EC_{90} values of compound **10** with IFN-alpha 2b, daclatasvir, or VX-222 are located under the additive line, while the plots of compound **10** with telaprevir, or danoprevir are located above the additive line and closed to the additive line (Fig. 5A). Additionally, we determined the degree of inhibition for each drug combination was analyzed as the combination index (CI) calculation at 50, 75 and 90% of effective concentrations by using CalcuSyn. An explanatory diagram was shown at a right end of lower panels of Fig. 5B as described in Materials and Methods. On the basis of the CalcuSyn analysis, the combination of compound **10** with daclatasvir exhibited strong synergistic effect on inhibition of HCV replication in the replicon cells (Fig. 5B, upper middle). The combination of compound **10** with VX-222 exhibited an additive to synergistic effect, suggesting that it trends toward synergistic (Fig. 5B, upper right), and with IFN-alpha 2b exhibited an antagonistic to synergistic effect, suggesting that it trends toward synergistic (Fig. 5B, upper left). In contrast, the combination of compound **10** with telaprevir resulted in antagonistic effect (Fig. 5B, lower left), and with danoprevir resulted in an antagonistic to additive effect, suggesting it trends toward antagonistic (Fig. 5B, lower middle). These calculated data

Table 4. Effect of octyl esters **10** and **13–16** on HCV replication.

Compound No.	R^1, R^2, R^3	EC_{50} [a] (μM)	CC_{50} [b] (μM)	SI [c]	*Clog P* [d]
10	$R^1=R^2=R^3=H$	2.7±0.1	71.7±8.5	26.6	4.90
13	$R^1=CH_3$, $R^2=R^3=H$	10.2±1.1	60.3±1.6	5.9	5.35
14	$R^1=R^3=H$, $R^2=CH_3$	19.6±0.8	59.2±1.4	3	5.35
15	$R^1=R^2=CH_3$, $R^3=H$	48.5±1.7	212.4±6.9	4.4	5.82
16	$R^1=R^2=H$, $R^3=OH$	36.3±2.9	59.8±6.9	1.6	4.24

The basic structure and side moieties are shown in Figure S4.
a: Fifty percent effective concentration based on the inhibition of HCV replication.
b: Fifty percent cytotoxicity concentration based on the reduction in cell viability.
c: Selectivity index (CC_{50}/EC_{50}).
d: Determined with ChemDraw software (Chem Bio Office Ultra, 2008).
doi:10.1371/journal.pone.0082299.t004

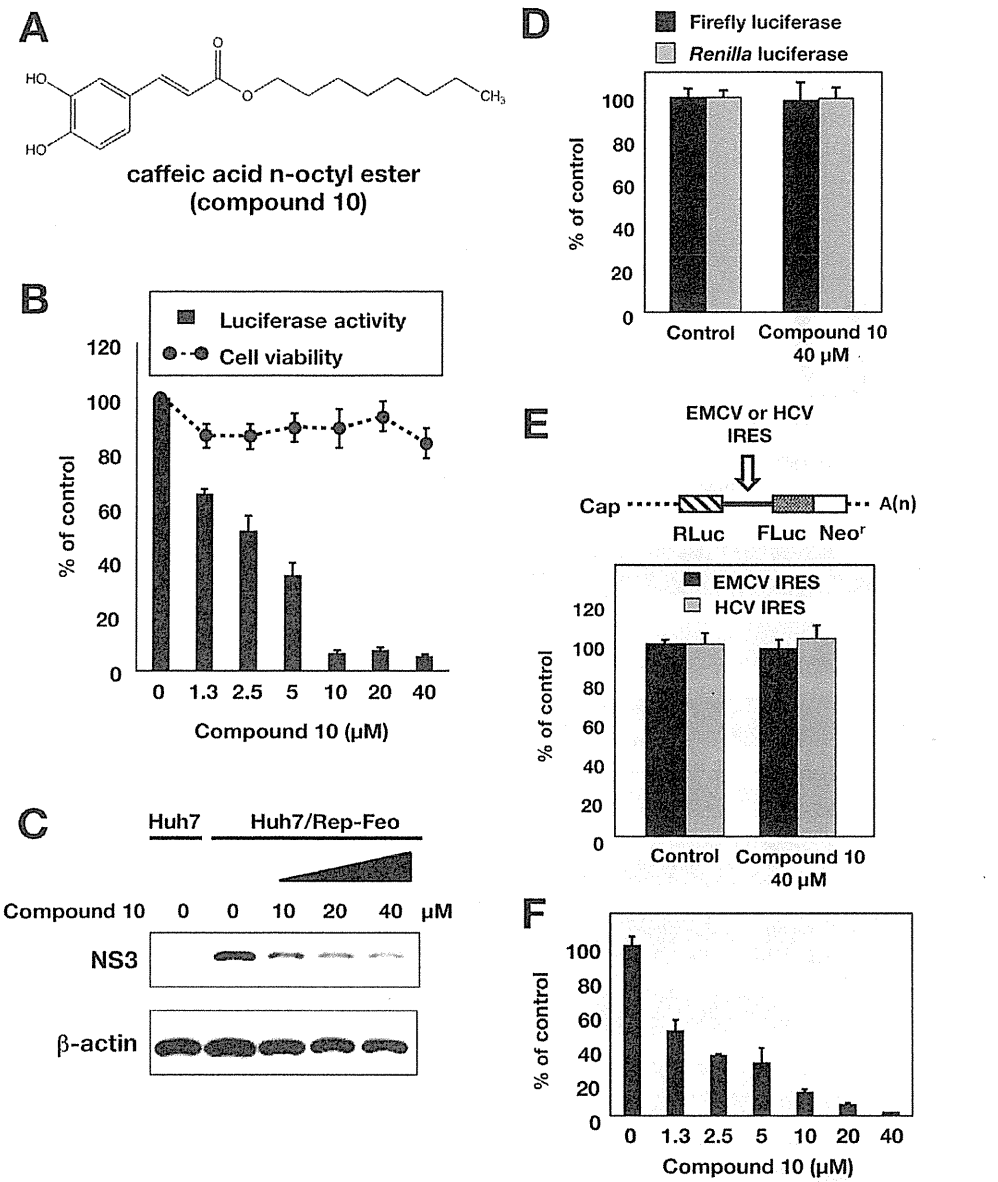

Figure 3. Effect of compound 10 on the viral replication in the replicon cell line and HCVcc. (A) Molecular structure of compound **10**. (B) Huh7/Rep-Feo cells were incubated for 72 h in a medium containing various concentrations of compound **10**. Luciferase and cytotoxicity assays were carried out by the method described in Materials and Methods. Error bars indicate standard deviation. The data represent three independent experiments. (C) Protein extract was prepared from Huh7/Rep-Feo cells treated for 72 h with the indicated concentration of compound **10** and it was then subjected to Western blotting using antibodies to NS3 and beta-actin. (D) Huh7 cell line was transfected with pEF Fluc IN encoding firefly luciferase or pEF Rluc IN encoding *Renilla* luciferase. Both transfected cell lines were incubated with DMSO (Control) or 40 μg/ml compound **10**. Firefly or *Renilla* luciferase activity was measured 72 h post-treatment. Luciferase activity was normalized with protein concentration. Error bars indicate standard deviation. The data were represented from three independent experiments. (E) Schematic structure of RNA transcribed from the plasmids was shown (Top). The bicistronic gene is transcribed under the control of elongation factor 1α (EF1α) promoter. The upstream cistron encoding *Renilla* luciferase (RLuc) is translated by a cap-dependent mechanism. The downstream cistron encodes the fusion protein (Feo), which consists of the firefly luciferase (Fluc) and neomycin phosphotransferase (Neo^r), and is translated under the control of the EMCV or HCV IRES. Huh7 cell line was transfected with each plasmid and incubated for 72 h post-treatment with DMSO (control) or 40 μg/ml of compound **10**. Firefly and *Renilla* luciferase activities were measured. Relative ratio of Firefly luciferase activity to *Renilla* luciferase activity was represented as percentage of the control condition. Error bars indicate standard deviation. The data were represented from three independent experiments. (F) Huh7 OK1 cell line was infected with HCVcc derived from JFH-1 strain and then treated with several concentrations of compound **10** at 24 h post-infection. The resulting cells were harvested 72 h post-infection. The viral RNA of supernatant was purified and estimated by the method described in Materials and Methods. Error bars indicate standard deviation. The data represent three independent experiments. Treatment with DMSO corresponds to '0'.
doi:10.1371/journal.pone.0082299.g003

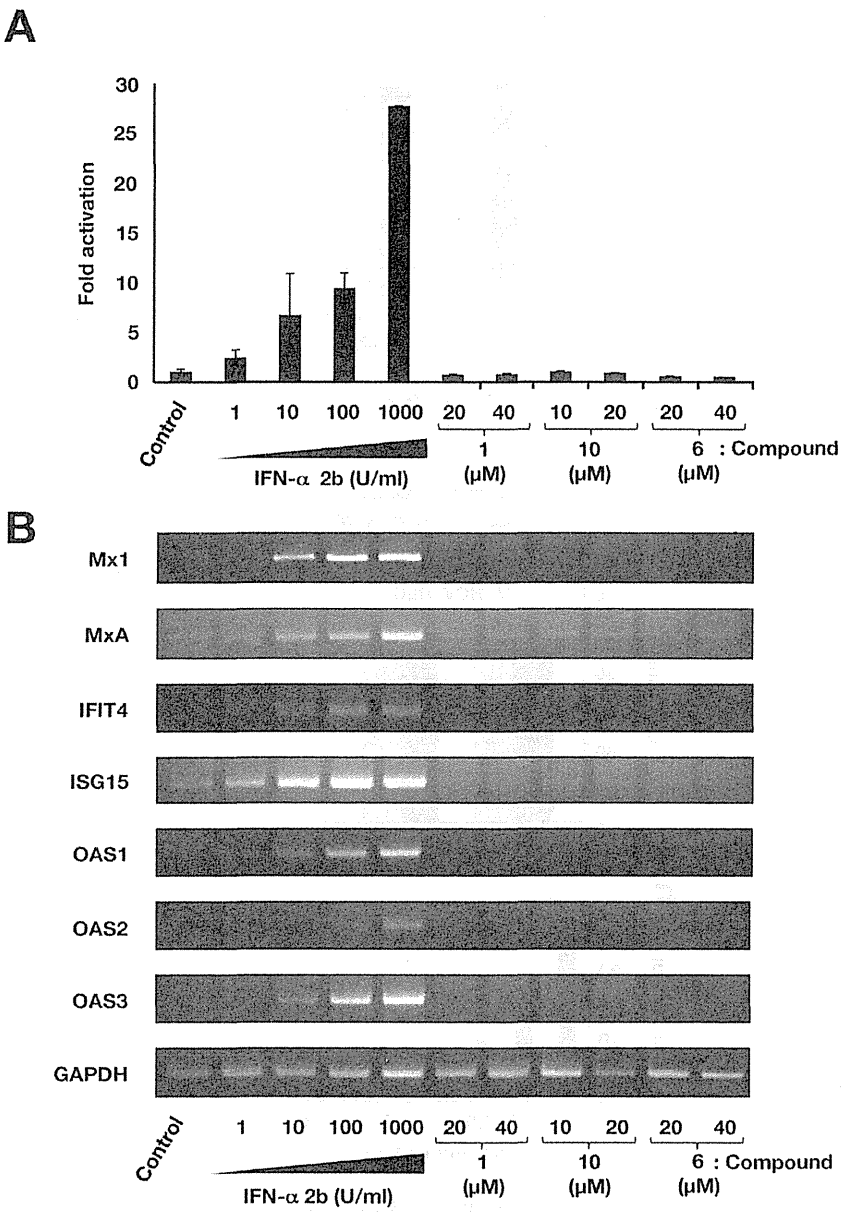

Figure 4. Effect of CAPE derivatives on the interferon-signaling pathway. (A) Plasmids pISRE-TA-Luc and phRG-TK were co-transfect into Huh7 OK1 cells. The transfected cells were cultured with 1, 10, 100, or 1000 U/mL of interferon-alpha 2b, and compounds **1**, **6** and **10**. Treatment with DMSO corresponds to '0'. After 48 h of treatment, luciferase activities were measured, and the value were normalized against *Renilla* luciferase activities. Error bars indicate standard deviation. The data represent three independent experiments. (B) Huh7 replicon cell line of genotype 1b was treated with 1, 10, 100, or 1000 U/mL of interferon-alpha 2b, and compounds **1**, **6** and **10** for 48 h. Treatment with DMSO corresponds to the control. The mRNAs of Mx1, MxA, IFIT4, ISG15, OAS1, OAS2, OAS3, and GAPDH as an internal control were detected by RT-PCR.
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of combination tests suggest that daclatasvir, IFN-alpha 2b, and VX-222 synergistically, but telaprevir and danoprevir antagonistically, inhibit HCV replication in combination with compound **10**.

Discussion

CAPE is an active component of propolis, which possesses broad-spectrum biological activities [14–19]. In this study, CAPE suppressed HCV RNA replication in a dose-dependent manner (Fig. 1A and B). Treatment with CAPE inhibited HCV replication with an EC_{50} of 9.0 μM and an SI of 17.9 in Huh7/Rep-Feo cells (Table 1). The treatment of the replicon cell line with CAPE did not induce expression of the IFN-inducible gene (Fig. 4), suggesting that the inhibition of HCV replication by CAPE is independent of the IFN signaling pathway.

Table 5. Anti-HCV activity of compound **10** in replicon cell lines of genotypes 1b and 2a.

Cell line	Replicon type	Strain (Genotype)	EC_{50} [a] (μM)	CC_{50} [b] (μM)	SI [c]
Huh7 Rep/Feo-1b	Subgenome	N (1b)	2.7±0.1	71.7±8.5	26.6
Con1 LUN Sb #26	Subgenome	Con1 (1b)	1.0±0.1	63.1±3.1	63.1
Huh7 Rep/Reo-2a	Subgenome	JFH1 (2a)	1.0±0.3	60.0±2.3	60.0
OR6	Full genome	O (1b)	1.5±0.4	61.7±0.6	41.1

a: Fifty percent effective concentration based on the inhibition of HCV replication.
b: Fifty percent cytotoxicity concentration based on the inhibition of HCV replication.
c: Selectivity Index (CC_{50}/EC_{50}).
doi:10.1371/journal.pone.0082299.t005

We also examined the effect of CAPE derivatives on HCV replication. Our data suggest that the n-alkyl side chain and catechol moiety of the CAPE derivative are critical in its anti-HCV activity (Tables 2 and 3). The EC_{50} value of the derivative decreased dependently on the length of the n-alkyl side chain until reaching octyl ester length (Table 2), while longer chains than octyl ester of a derivative led to an increase in the EC_{50} value and *Clog P* value. Compound **10**, Caffeic acid n-octyl ester, exhibited the highest anti-HCV activity among the tested compounds with an EC_{50} value of 2.7 μM and an SI value of 26.6. Cyclosporine A and its analogues could suppress the viral replication of genotype 1b at a higher level than that of genotype 2a [23]. Interestingly, compound **10** could inhibit HCV replication of genotype 1b and 2a at a similar level, irrespective of expression of the interferon-inducible gene (Fig. 4). CAPE and its derivatives may therefore possess a mechanism different from cyclosporine A and its analogues with respect to anti-HCV activity.

CAPE has been reported to be an inhibitor of NF-kappaB [14,20]. Lee et al. reported that the catechol moiety in CAPE was important for inhibition of NF-kappaB activation [24]. The data shown in Table 3 suggest that the catechol moiety in CAPE is critical to the anti-HCV activity of compound **10**. Previous studies have implicated the inhibition of NF-kappaB in anti-HCV activity. Treatment with an extract prepared from *Acacia confusa* [25] or San-Huang-Xie-Xin-Tang [26] could suppress HCV replication and inhibit NF-kappaB activation. However, Chen et al. reported that curcumin-mediated inhibition of NF-kappaB did not contribute to anti-HCV activity [11]. Furthermore, treatment with *N*′-(Morpholine-4carbonyloxy)-2(naphthalene-1-yl) acetimidamide could activate NF-kappaB and downstream gene expression in the same Huh7/Rep-Feo replicon cell line as the cell line used in this study and exhibited potent inhibition of HCV replication without interferon signaling [27]. These reports support the notion that CAPE derivatives do not mainly target NF-kappaB activity as part of their anti-HCV activity.

Several host proteins have been reported to regulate function of NS5A, leading to supporting HCV replication (review in [2,28]). Daclatasvir exhibited potent synergistic effect on anti-HCV activity in combination of compound **10** (Fig. 5). Anti-HCV activity of compound **10** might associate with intrinsic functions of host factors that interact with NS5A. NS3 protease inhibitors exhibited antagonistic effect in combination of compound **10** (Fig. 5). The inhibitory effect of compound **10** might be mediated by the activation of an unknown endogenous protease that is nonspecifically suppressed by NS3 protease inhibitors. Further study to clarify the mechanism by which compound **10** suppresses HCV replication might contribute to identification of a novel host factor as a drug target for development of the effective compound supporting an effect of other anti-HCV drugs.

In conclusion, we showed that CAPE and its analogue possess a significant inhibitory effect against HCV replication. The length of n-alkyl side chains and the catechol moiety of CAPE are critical to its inhibitory activity against HCV replication. The most effective derivative among the tested compounds was caffeic acid n-octyl ester, which exhibited an EC_{50} value of 1 μM and an SI value of 63.1 in the replicon cell line of genotype 1b strain Con1. Treatment with caffeic acid n-octyl ester reduced the viral replication of genotype 1b and 2a at a similar level and inhibited viral production of HCVcc. Treatment with caffeic acid n-octyl ester could synergistically enhance the anti-HCV activities of IFN-α 2b, daclatasvir, and VX-222, but neither telaprevir nor danoprevir. Further investigation to clarify the mechanism of anti-HCV activity and further modification of the compound to improve anti-HCV activity will lead to novel therapeutic strategies to treat chronic hepatitis C virus infection.

Materials and Methods

Compounds

Boldface numbers in this text indicate the compound numbers shown in Tables. All chemical structures of compounds used in this study are shown in figure S1. CAPE (**1**), caffeic acid (**2**), ferulic acid (**3**), and chlorogenic acid (**5**) and were purchased from Sigma-Aldrich (St. Louis, MO, USA). Cinnamic acid phenethyl ester (**4**) was from Tokyo Chemical Industry (Tokyo, Japan). Rosmarinic acid (**6**) was from Wako Pure Chemical (Tokyo, Japan). Caffeic acid n-octyl ester (n-octyl caffeate) (**10**), 3-O-methylcaffeic acid n-octyl ester (n-octyl-3-methylcaffeate) (**13**), 4-O-methylcaffeic acid n-octyl ester (n-octyl-3-methylcaffeate) (**14**), and 3, 4-O-dimethyl-caffeic acid n-octyl ester (n-octyl-3, 4-methylcaffeate) (**15**) were from LKT Laboratories (St. Paul, MN, USA).

Caffeic acid esters **7**, **8**, **9**, and **11** were synthesized by preparing caffeic acid chloride followed by treatment with corresponding alcohols [29]. Dihydrocaffeic acid ester **12** was prepared by hydrogenation of **7**. Compound **16** is a newly synthesized ester. Spectroscopic data of known esters **7–9**, and **11** prepared here were identical to those reported [30-32] Interferon alfa-2b (IFN-α 2b) was obtained from MSD (Tokyo, Japan). Telaprevir and daclatasvir were purchased from Selleckchem (Houston, TX, USA). Danoprevir and VX-222 were from AdooQ BioScience (Irvine, CA, USA).

Chemistry of 3,4,5-Trihydroxycinnamic acid n-octyl ester

3,4,5-Trihydroxycinnamic acid n-octyl ester (**16**) was prepared by condensation of corresponding benzaldehydes with malonic acid n-octyl monoester [33]. A solution of malonic acid n-octyl monoester (432 mg, 2 mmol), 3,4,5-trihydroxybenzaldehyde (462 mg, 3 mmol) and piperidine (0.2 mL) in pyridine (2 mL)

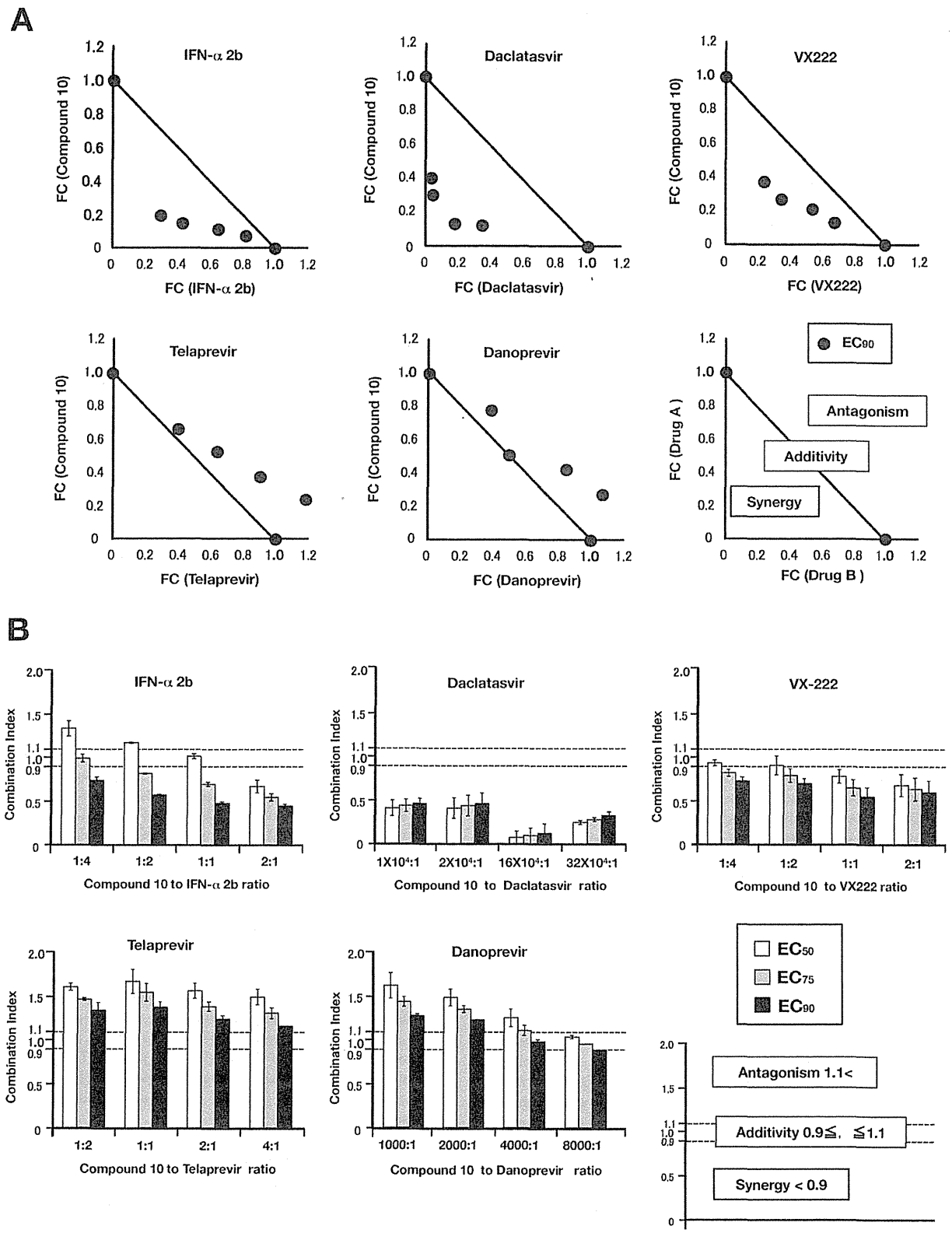
A
IFN-α 2b
FC (Compound 10)
FC (IFN-α 2b)
Daclatasvir
FC (Daclatasvir)
VX222
FC (VX222)
Telaprevir
FC (Telaprevir)
Danoprevir
FC (Danoprevir)
EC90
Antagonism
Additivity
Synergy
FC (Drug A)
FC (Drug B)
B
IFN-α 2b
Combination Index
Compound 10 to IFN-α 2b ratio
Daclatasvir
1X10⁴:1
2X10⁴:1
16X10⁴:1
32X10⁴:1
Compound 10 to Daclatasvir ratio
VX-222
Compound 10 to VX222 ratio
Telaprevir
Compound 10 to Telaprevir ratio
Danoprevir
1000:1
2000:1
4000:1
8000:1
Compound 10 to Danoprevir ratio
EC50
EC75
EC90
Antagonism 1.1<
Additivity 0.9≦, ≦1.1
Synergy < 0.9

Figure 5. Synergistic effect analyses for the combination of compound 10 with IFN-α 2b, daclatasvir, VX-222, telaprevir, or danoprevir. The Huh7 cell line, including the subgenomic replicon RNA of genotype 1b strain Con1, was treated for 72h with combinations of compound 10 and IFN-α 2b, daclatasvir, VX-222, telaprevir, or danoprevir. Luciferase assay were carried out as described in Materials and Methods. (A) The calculated EC_{90} values for combination were plotted as the fractional concentration (FC) of compound 10 and one of IFN-α 2b, daclatasvir, VX-222, telaprevir, and danoprevir on the *x* and *y* axes, respectively. Synergy, antagonism and additivity are indicated in a representative graph as a right end of lower graphs and are described in Materials and Methods. (B) Combination indexes of compound 10 with IFN-α 2b, daclatasvir, VX-222, telaprevir, or danoprevir at the EC50, EC75, and EC90 values were measured at various drug rations. Synergy, antagonism and additivity are indicated in a representative graph as a right end of lower graphs and are described in Materials and Methods.
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was heated at 70°C for 1 h. The reaction mixture was concentrated under a vacuum to give a residue, which was dissolved in $CHCl_3$-IPA (3:1, v/v) and then washed with 10% HCl and water. The organic layer was dried over Na_2SO_4 and evaporated to give a residue, which was purified by silica gel column chromatography using AcOEt-hexane (1:1, v/v) as eluent to give the corresponding n-octyl ester (85 mg, 13.8%) as a pale powder. FT-IR vmax (KBr): 3389, 3239, 2923, 1675, 1627, 1606 cm^{-1}. ^1H NMR (400MHz, CD_3OD) δ: 0.86 (3H, t, J= 7.2 Hz), 1.20–1.40 (10H, m), 1.65 (2H, quintet, J= 6.4 Hz), 4.11, (2H, t, J= 6.4 Hz), 6.16 (2H, d, J= 15.6 Hz), 6.55 (2H, s), 7.40 (2H, d, J= 15.6 Hz). 13C NMR (100 Hz, CD_3OD) δ: 14.4, 23.7, 27.1, 29.8, 30.3, 30.4, 32.9, 65.6, 108.5, 115.3, 126.6, 137.5, 147.1, 169.4. CI MS *m/z*: 309 (M^++H). High-resolution CI MS calcd. for $C_{17}H_{25}O_5$ (M^++H) for 309.1702. Found: 309.1686.

Replicon cell lines and virus infection

The Huh7/Rep-Feo cell line, which harbors the subgenomic replicon RNA composed of HCV IRES, the gene of the fusion protein consisting of neomycin phosphotransferase and firefly luciferase, EMCV IRES and a nonstructural gene of genotype 1b strain N in order in Huh7 cell line, was previously established [34]. Thus, the luciferase activity corresponds to the level of HCV RNA replication. The cell line was maintained in Dulbecco's modified Eagle medium containing 10% fetal calf serum and 0.5 mg/mL G418 and cultured in absence of G418 when they were treated with compounds. The Lunet/Con1LUN Sb #26 cell line, which harbors the subgenomic replicon RNA of the Con1 strain (genotype 1b), was described previously [35]. The OR6 cell line, which harbors the full genomic replicon RNA of the O strain (genotype 1b), was described previously [36]. The HCV replicon cell line derived from the genotype 2a strain JFH1 was described previously [37]. The viral RNA derived from the plasmid pJFH1 was transcribed and introduced into Huh7OK1 cells according to the method of Wakita et al. [38]. The virus was amplified by the several times passages. The cells were infected with the virus at a multiplicity of infection (moi) of 1 and then treated with each compound at 24 h post-infection. The culture supernatants were harvested 72 h post-treatment to estimate the viral RNA as described below.

Determination of luciferase activity in HCV replicon cells

The replicon cells were seeded at 2×10^4 cells per well in a 48-well plate 24 h before treatment. Compounds were added to the culture medium to give various concentrations. The resulting cells were harvested 72 h post-treatment and lysed with cell culture lysis reagent (Promega, Madison, WI). The luciferase activity of each cell lysate was estimated using a luciferase assay system (Promega). The resulting luminescence was detected by a Luminescencer-JNR AB-2100 (ATTO, Tokyo, Japan).

Determination of Cytotoxicity in HCV replicon cells

The replicon cells were seeded at a density of 1×10^4 cells per well in a 96-well plate and then incubated at 37°C for 24 h. Compounds were added to the culture medium to give various concentrations and were then harvested 72 h post-treatment. Cell viability was measured using a dimethylthiazol carboxymethoxyphenylsulfophenyl tetrazolium (MTS) assay with a CellTiter 96 aqueous one-solution cell proliferation assay kit (Promega).

Western Blotting

Western blotting was carried out by the method described previously [39]. The antibodies to NS3 (clone 8G-2, mousemonoclonal, Abcam, Cambridge, UK), and beta-actin were purchased from Cell Signaling Technology (rabbit polyclonal, Danvers, MA, USA) and were used as the primary antibodies in this study.

RNA analysis

Total RNAs were prepared from cells by using the RNAqueous-4PCR kit (Life Technologies, Carlsbad, CA). Viral RNA were prepared from culture supernatants by using the QIAamp Viral RNA mini kit (QIAGEN, Hilden, Germany). The viral RNA genome was estimated by the qRT-PCR method described previously [40]. RT-PCR was carried out by the method described previously [41] which was slightly modified at the PCR step. The PCR samples were incubated once for 10 min at 95°C for an initial activation step of the AmpliTaq Gold DNA Polymerase (Life Technologies), and then subjected to an amplification step of 30 repeats of the cycle consisting of three segments as follow: 0.5 min at 95°C, 1 min at 55°C and 1 min at 72°C. The primers used in this study were as follows: Mx1: 5′-AGCCACTGGACTGACGACTT-3′ and 5′-GAGGGCTGAAAATCCCTTTC-3′;

MxA: 5′-GTCAGGAGTTGCCCTTCCCA-3′ and 5′-ATTCCCATTCCTTCCCCGG-3′;

IFIT4: 5′-CCCTTCAGGCATAGGCAGTA-3′ and 5′-CTCCTACCCGTCACAACCAC -3′; ISG15: 5′-CGCAGATCACCCAGAAGAT-3′ and 5′-GCCCTTGTTATTCCTCACCA-3′;

OAS1: 5′-CAAGCTCAAGAGCCTCATCC-3′ and 5′-TGGGCTGTGTTGAAATGTGT-3′;

OAS2: 5′-ACAGCTGAAAGCCTTTTGGA-3′ and 5′-GCATTAAAGGCAGGAAGCAC-3′;

OAS3: 5′-CACTGACATCCCAGACGATG-3′ and 5′-GATCAGGCTCTTCAGCTTGGC-3′;

GAPDH: 5′-GAAGGTGAAGGTCGGAGTC and 5′- GAAGATGGTGATGGGATTTC-3′

Effects on activities of internal ribosome entry site (IRES) and luciferases

Huh7 OK1 cells were transfected with pEF.Rluc.HCV.IRES.-Feo or pEF.Rluc.EMCV.IRES.Feo [39]. These transfected cells were seeded at 2×10^4 cells per well in a 48-well plate 24 h before treatment, treated with DMSO or compound **10**, and then harvested at 72 h post-treatment. The firefly luciferase activities were measured with a luciferase assay system (Promega). The total protein concentration was measured using the BCA Protein Assay Reagent Kit (Thermo Scientific, Rockford, IL, USA) to normalize

luciferase activity. To evaluate the interferon response, Huh7OK1 cells were seeded on a 48 well plate at a density of 2×10^4 cells per well, and transfected with pISRE-TA-Luc (Takara bio, Shiga, Japan) and phRG-TK (Promega). These transfected cells were incubated in the presence of compounds, IFN-α 2b, or DMSO, and then harvested at 48 h post-treatment. The firefly luciferase and *Renilla* luciferase activities were quantified by using Dual luciferase reporter assay system (Promega).

Prediction of Clog*P* for compounds

The *Clog*P value deduced from chemical structure roughly corresponds to a value of hydrophobicity. The *Clog*P values of compounds used in this study were calculated using the computer software Chem Bio Office Ultra 2008 (PerkinElmer, Cambridge, MA, USA).

Synergistic effect of caffeic acid n-octyl ester on anti-HCV activities of other drugs

The effects of drug-drug combinations were evaluated by using the Con1 LUN Sb #26 replicon cells, and were analyzed by using the computer software CalcuSyn (Biosoft, Cambridge, United Kingdom). Dose inhibition curves of two different drugs were plotted with each other. In each drug combination, EC_{90} values of several combinations of two different drugs were plotted as the fractional concentration (FC) of both drugs on the *x* and *y*-axes. Additivity indicates the line linked between 1.0 FC value points of both drugs in the absence of each other. Synergy and antagonism are indicated by values plotted under and above, respectively, an additivity line. The explanatory diagram of isobologram is shown in a right end of lower panels of Figure 5A. Combination indexes (CIs) were calculated at the EC_{50}, EC_{75}, and EC_{90} by using CalcuSyn. A CI value of less than 0.9 indicates synergy. A CI value ranging from 0.9 to 1.1 indicates additivity. A CI value of more than 1.1 indicates antagonism. The explanatory diagram was shown in a right end of lower panels of Figure 5B.

Supporting Information

Figure S1 Molecular structure of CAPE and commercial CAPE-related compounds. CAPE structure is divided into three parts: (I) the catechol moiety, (II) the alkenyl moiety on alpha, beta -unsaturated ester, and (III) the ester part. Molecular structures of CAPE and its commercial derivatives are shown.
(TIF)

Figure S2 The basic structure and side moieties of compounds shown in Table 2. Each compound structure is represented on the basis of the basic structure (top).
(TIF)

Figure S3 The molecular structures of compounds 7 and 12, which are shown in Table 3. Both compounds are different in alpha, beta-unsaturated or saturated part attached to ester.
(TIF)

Figure S4 The basic structure and side moieties of compounds shown in Table 4. Each compound structure is represented on the basis of the basic structure (top).
(TIF)

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Author Contributions

Conceived and designed the experiments: MT KM. Performed the experiments: H. Shen AY MN HY MS H. Shindo SM. Analyzed the data: HK TT NE. Contributed reagents/materials/analysis tools: YF MI NK NS. Wrote the paper: H. Shen AY MT KM.

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VIRAL HEPATITIS

Ca^{2+}/S100 proteins regulate HCV virus NS5A–FKBP8/FKBP38 interaction and HCV virus RNA replication

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Abstract

Background & Aim: FKBP8/FKBP38 is a unique FK506-binding protein with a C-terminal membrane anchor and localizes at the outer membranes of mitochondria and the endoplasmic reticulum. Similar to some immunophilins, such as FKBP51, FKBP52 and Cyclophilin 40, FKBP8/FKBP38 contain a putative Calmodulin-binding domain and a tetratricopeptide-repeat (TPR) domain for the binding of Hsp90. Both Hsp90 and the non-structural protein 5A (NS5A) of the hepatitis C virus (HCV) interact specifically with FKBP8/FKBP38 through its TPR domain, and the ternary complex formation plays a critical role in HCV RNA replication. The goal of this study is to evaluate that the host factor inhibits the ternary complex formation and the replication of HCV *in vitro* and *in vivo*. *Methods:* S100 proteins, FKBP38, FKBP8, HCV NS5A, Hsp90, and calmodulin were expressed in E.coli and purified. *In vitro* binding studies were performed by GST pull-down, S-tag pull-down and surface plasmon resonance analyses. The effect of S100 proteins on HCV replication was analysed by Western blotting using an HCV NS3 antibody following transfection of S100 proteins into the HCV replicon harbouring cell line (sO cells). *Results: In vitro* binding studies showed that S100A1, S100A2, S100A6, S100B and S100P directly interacted with FKBP8/FKBP38 in a Ca^{2+}-dependent manner and inhibited the FKBP8/FKBP38–Hsp90 and FKBP8/FKBP38–NS5A interactions. Furthermore, overexpression of S100A1, S100A2 and S100A6 in sO cells resulted in the efficient inhibition of HCV replication. *Conclusion:* The association of the S100 proteins with FKBP8/FKBP38 provides a novel Ca^{2+}-dependent regulatory role in HCV replication through the NS5A–host protein interaction.

Hepatitis C virus (HCV) infection is a major cause of chronic liver disease, which frequently progresses to cirrhosis and hepatocellular carcinoma (1, 2). HCV represents a global public health problem, affecting approximately 170 million people worldwide, which is more than 3% of the world population (3, 4). HCV is a member of the positive strand RNA viruses, belongs to the family Flaviviridae, genus Hepacivirus, and contains a genome of approximately 9.6 kb in length, which encodes a large polyprotein precursor of approximately 3000 amino acids (5, 6). The polyprotein is cleaved by host and viral proteases to release the individual enzymes and proteins that mediate virus replication, assembly and release, producing viral structural proteins (Core, E1 and E2), a putative viropore protein (p7) and non-structural proteins (NS2, NS3, NS4A, NS4B, NS5A and NS5B) (5, 6). Importantly, the NS5A of HCV plays a critical role in HCV replication and is an attractive target for antiviral therapy of HCV infection (7). NS5A is a multifunctional 56–58 kDa serine phosphoprotein and interacts with a number of cellular proteins thereby affecting numerous host functions, including the modulation of signal transduction pathways, suppression of apoptosis and modulation of transcription (8–10). Recently, FK506-binding protein 8 (FKBP8)/FK506-binding protein 38 (FKBP38) was shown to interact with NS5A and to regulate HCV replication (11, 12),

*These authors contributed equally to this work.

suggesting that the immunophilins are promising therapies for chronic hepatitis C. FKBP8/FKBP38 binds to both NS5A and heat-shock protein 90 (Hsp90) through the tetratricopeptide-repeat (TPR) domain, and the ternary complex (FKBP8/FKBP38–Hsp90–NS5A) plays a critical role in HCV replication (11, 12). TPRs are loosely conserved 34 amino acid helix–turn–helix sequence motifs that mediate protein–protein interactions (13). This property enables TPR-containing proteins to function as scaffold proteins and allows them to be involved in a variety of cellular functions (14, 15).

The S100 protein family is composed of at least 25 members that share two EF-hand motifs, a 25–65% amino acid sequence homology and a molecular weight of 10–12 kDa (16–18).

Recently, we demonstrated that S100A2 and S100A6 interacted with the TPR domains of Hsp70/Hsp90-organizing protein (Hop), kinesin light chain (KLC) and Tom70 in a Ca^{2+}-dependent manner, leading to the dissociation of the Hsp90–Hop–Hsp70, KLC–JIP1 and Tom70–Hsps interactions *in vitro* and *in vivo* (19). Further studies have revealed an interaction of S100A1 and S100A2 bound to FK506-binding protein 52 (FKBP52) and cyclophilin 40 (Cyp40), which contain a TPR domain; in the presence of Ca^{2+}, this interaction led to the inhibition of the Cyp40–Hsp90 and FKBP52–Hsp90 interactions (20).

Because S100 proteins interact with TPR motifs (19, 20), we explored the potential role for S100 proteins in the regulation of the FKBP8/FKBP38–HSP90 and/or FKBP8/FKBP38–NS5A interactions and thereby the control of HCV replication. In this study, we demonstrate that Ca^{2+}/S100 proteins modulate replication of HCV via two different mechanisms. Firstly, S100A1, S100A2, S100A6, S100B and S100P interact with the TPR domain of FKBP8/FKBP38 and compete with Hsp90 binding to FKBP38. Secondly, these S100 proteins inhibit the interaction between NS5A and FKBP8/FKBP38. Using HCV replicon harbouring cells (sO cell: HCV O strain of genotype 1b) (21, 22), the overexpression of S100A1, S100A2 and S100A6 with A23187 treatment has shown a significant decrease in NS3 expression. These observations indicate that Ca^{2+}/S100 proteins could modulate HCV replication by inhibiting the interaction between FKBP8/FKBP38 and its binding partners.

Materials and methods

Materials

Phenyl–Sepharose and glutathione–Sepharose were purchased from GE Healthcare (Little Chalfont, Buckinghamshire, UK). Nickel–nitrilotriacetic acid agarose was purchased from Qiagen. S-protein agarose was purchased from Merck. Antibodies were obtained as follows: anti-S100A1 (Novus Biologicals, Littleton, Colorado, USA), anti-S100A2 (ANOVA, Santa Clara, CA, USA), anti-S100A6 (Proteintech Group Inc., Chicago, IL, USA), Anti-HCVNS3 (Leica Microsystems, Wetzlar, Germany), anti-β-actin (BioVision, Milpitas, CA, USA) and horseradish peroxidase-conjugated antimouse or antirabbit IgG antibody (GE Healthcare). All other chemicals were obtained from standard commercial sources.

Plasmids

The following plasmids were previously described: pME18S-S100A1, -S100A2, -S100A6, pET-Calmodulin (pET-CaM), pET-CaM-Glutathione-S-transferase (pET-CaM-GST) and pET16b-Hsp90 (19, 20, 23, 24). Human FKBP38 and FKBP8 complementary DNAs (cDNAs) were purchased from Open Biosystems and subcloned into pET30a. For the expression of FKBP38 C-terminal deletion mutants, polymerase chain reaction (PCR) fragments encoding residues 1–166, −297, −315, −325 and −335 were also cloned into pET30a. To create a plasmid of the pET30a-FKBP38 carboxylate clamp mutant (K250E/R254E), the plasmid was generated using inverse PCR using pET30a-FKBP38 (1–335) as a template. pETUbHis-NS5A was kindly provided by Dr Craig E. Cameron (25). The sequence integrity of the all inserts was confirmed through automated sequence analysis (Applied Biosystems, Foster City, CA, USA).

Preparation of recombinant proteins

All recombinant proteins were produced in *Escherichia coli* strain BL21(DE3) or BL21(DE3) CodonPlus-RIL (Novagen, Darmstadt, Germany). S100 proteins (S100A1, S100A2, S100A4, S100A6, S100A10, S100A11, S100A12, S100B and S100P) were expressed and prepared as described previously (26, 27). Calmodulin (CaM) was prepared as described by Hayashi and colleagues (28). C-terminally GST-tagged CaM linked by a Gly_6 spacer (CaM-GST) was prepared as described (23, 24). A C-terminally His-tagged NS5A, lacking the N-terminal 32 amino acid residues of the membrane-anchoring region (NS5A-His), was expressed via the pET-ubiquitin expression system, in which the NS5A-His was fused with ubiquitin at the C-terminus and was cleaved by a ubiquitin-specific protease, Ubp1, in *E. coli* as described by Huang and colleagues (25). The His-tagged Hsp90 and NS5A were purified via the nickel–nitrilotriacetic acid (NTA)-agarose method according to the manufacturer's protocol. Protein expression of N-terminally His_6 and S-tagged FKBP38 (His_6-S-tag-FKBP38) and FKBP8 (His_6-S-tag-FKBP8) was induced with the addition of isopropyl β-D-thiogalactopyranoside to a final concentration of 1 mM and further incubation at 16°C for 4 h. The His_6-S-tag-FKBP38 mutants (1–166, −297, −315, −325) and the His_6-S-tag-FKBP8 mutants (1–382) were purified using NTA agarose. The His_6-S-tag-FKBP38 (1–335), His_6-S-tag-FKBP8 (1–392) and His_6-S-tag-FKBP38-K250E/R254E mutants were purified with CaM-GST-coupled glutathione–Sepharose

columns as follows. The bacterial pellet from 200 ml of culture was resuspended in 10 ml of Buffer A (20 mM Tris-HCl, 200 mM NaCl and 5 mM dithiothreitol, pH 7.5), lysed using ultrasonic disruption and centrifuged at 35 000 *g* for 30 min at 4°C. The purified CaM-GST (3 mg) and $CaCl_2$ (2 mM final concentration) were mixed with the supernatant. The resulting mixture was applied to a glutathione – Sepharose column (1 ml bed volume; GE Healthcare) and then the column was washed with 5 ml of Buffer A supplemented with 0.2 mM $CaCl_2$. His_6-S-tag-FKBP38 or His_6-S-tag-FKBP8 was eluted using Buffer A supplemented with 0.5 mM ethylene glycol tetraacetic acid (EGTA). The concentration and purity of the isolated proteins were determined with a Bradford assay (Bio-Rad, Hercules, CA, USA) and Sodium dodecyl sulphate–polyacrylamide gel electrophoresis (SDS-PAGE).

Pull-down assay

To assess the binding of S100 proteins, Hsp90 and NS5A to FKBP8/FKBP38, His_6-S-tag-FKBP8/FKBP38 and either S100 proteins, Hsp90 or NS5A, were mixed with S-protein-agarose beads (20 μl) in Buffer B (20 mM Tris-HCl, 150 mM NaCl and 0.02% Tween 20, pH 7.5) in the presence of 1 mM $CaCl_2$ or EGTA. The reaction mixtures (200 μl) were incubated for 60 min at 25°C. After the resin was washed three times with 1.0 ml of Buffer B, the resin was boiled in SDS-sample buffer (30 μl). Next, the samples were subjected to SDS-PAGE and visualized with Coomassie Blue staining. The details of the experimental conditions are described in the figure legends.

Surface Plasmon Resonance (SPR)

Binding kinetics were analysed using a SPR Biacore 2000 system (Biacore AB, Little Chalfont, Buckinghamshire, UK). CM5 research grade chips, N-hydroxysuccinimide and 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (Biacore amine coupling kit) were used for the amine coupling of the recombinant N-terminally His_6 and S-tagged FKBP8 (His_6-S-tag-FKBP8) (4540RU) to the dextran surface of the CM5 chip. Recombinant S100A1, S100A2, S100A6, S100B, S100P and CaM (1.25 μM, 625 nM, 313 nM, 156 nM and 78 nM respectively) were injected over the sensor surface at a flow rate of 20 μl/min in HBS-P buffer (10 mM Hepes, 150 mM NaCl and 0.005% Surfactant P20, pH 7.4) containing 1 mM $CaCl_2$. The S100 proteins were allowed to interact with the surface of the sensor chip for 2.5 min, after which HBS-P buffer was injected over the sensor surface to monitor the dissociation of the S100 protein. At intervals based on the sample injection, an FKBP8-coupled sensor chip was regenerated with HBS-P buffer supplemented with 2.5 mM EGTA and 0.75% n-Octyl-ß-D-glucopyranoside. The response curves were prepared for fit using a subtraction of the signal generated simultaneously on the control flow cell. Biacore sensorgram curves were evaluated in BIAevaluation 4.1 using a 1:2 binding model for the S100 proteins. A 1:1 Langmuir model was used for the CaM binding.

Cell culture, transfection and preparation of cell lysates

HuH-7-derived cells harbouring HCV replicon harbouring cells (sO cells) were maintained in Dulbecco's Modified Eagle's medium (Invitrogen, Carlsbad, CA, USA) containing 0.3 mg/ml G418 (Promega, Fitchburg, MA, USA) supplemented with 10% fetal bovine serum (Invitrogen) in a humidified 5% CO_2 incubator at 37°C as described (21). Transient transfections were performed using Fugene 6 (Roche, Mannheim, Germany) according to the manufacturer's instructions. The sO cells (10 cm dish) were transfected with pME18S-S100A1, pME18S-S100A2 or pME18S-S100A6 (each 7 μg). After 8 h of incubation with the transfection reagents, the medium was changed and cells were grown until 100% confluent. Next, the cells were treated with or without A23187 (5 μM) for 6, 12 and 24 h and were then lysed via the addition of 1 ml of the lysis buffer (20 mM Tris-HCl, 150 mM NaCl, 0.5 mM ethylenediaminetetraacetic acid (EDTA), 0.5% Nonidet-P40, 10% glycerol, pH 7.5), briefly sonicated and centrifuged at 15 000 *g* for 30 min at 4°C. The supernatants were subjected to SDS-PAGE, followed by Western blot analysis.

Results

Interaction between the members of the S100 protein family and FKBP38

Previously, we demonstrated that S100A1, S100A2 and S100A6 interacted with the TPR domains of Hop, Tom70, CyP40, FKBP52 and KLC in a Ca^{2+}-dependent manner and led to the disruption of the TPR protein –client protein interactions *in vitro* and *in vivo* (9, 20). Because S100 proteins interact with TPR motifs, we explored the potential role of S100 proteins in regulating the functions of FKBP8/FKBP38. Firstly, we examined the interaction of the S100 proteins with FKBP8/FKBP38. FKBP8/FKBP38, a TPR-containing non-canonical member of the immunosuppressive drug FK506-binding protein (FKBP) family, consists of four structural and functional domains. The FK506-binding domain is located in the N-terminal half, followed by a TPR domain, a putative CaM-binding site and a transmembrane domain. Human FKBP8 is identical to FKBP38 except for the extra 58 amino acid residues at the N-terminus. The domain structure organization of FKBP8/FKBP38 is shown in Figure 1a. Because our preliminary binding analyses demonstrated that the last 10 residues immediately upstream of the transmembrane domain (^{326}AWSIPWKWLF^{335}) in FKBP38, but not the putative CaM-binding site, compose the actual