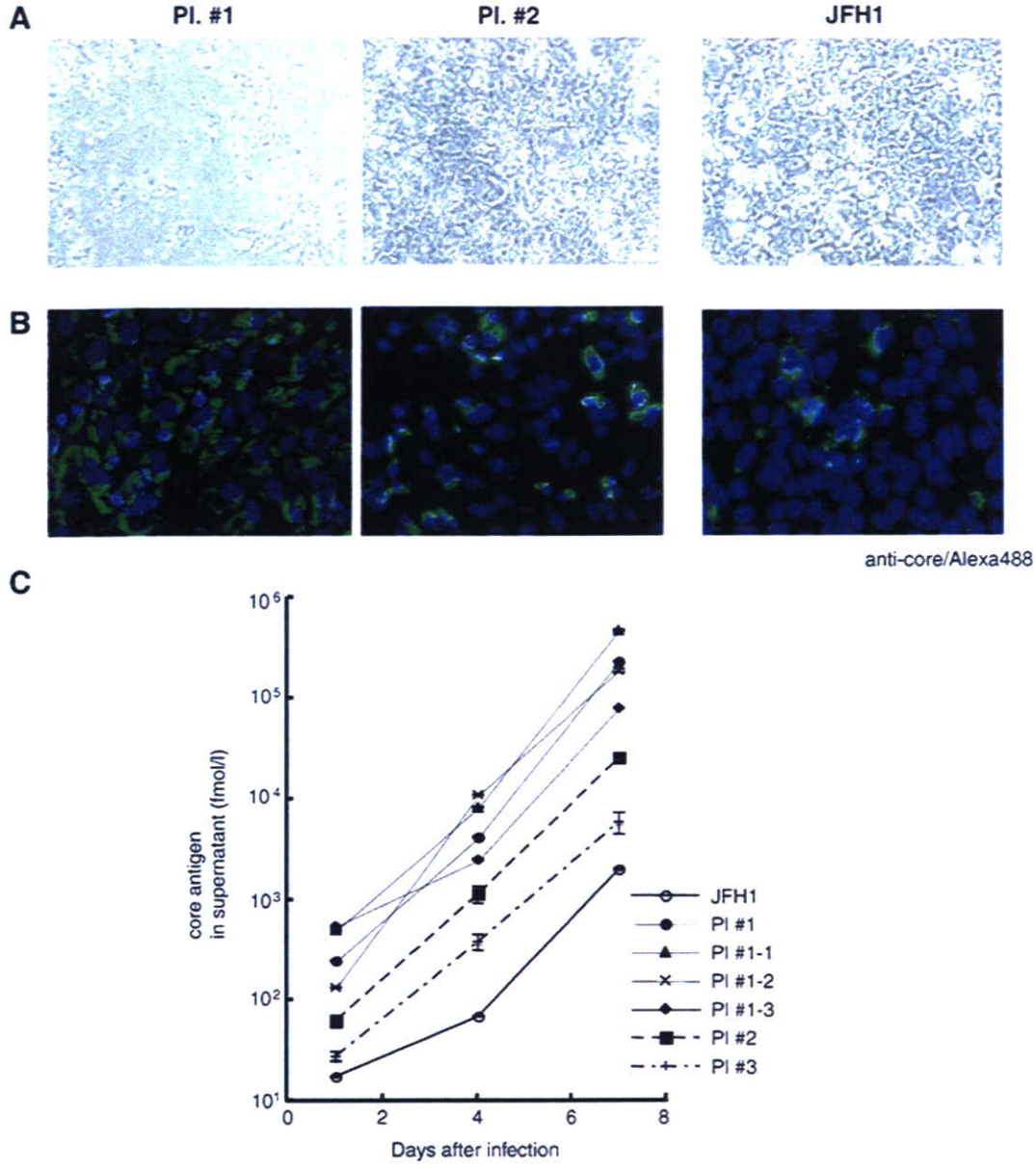

Fig. 8. The isolation of cytopathic plaques. The HCV-JFH1 culture supernatant was transferred at various dilutions onto uninfected Huh-7.5.1 cells. After ~ 5 h incubation, the supernatant was removed then infected cells were cultured in 0.8% methylcellulose-containing medium in 60-mm-diameter plates. Cytopathic plaques were detectable at 8 days after infection. Cells from each plaque were isolated using a cloning cylinder, subcultured, and transferred onto uninfected Huh-7.5.1 cells. (A) Observation by phase-contrast microscopy at 10 days of culture. (B) After 15 days of culture, the supernatant was transferred onto uninfected Huh-7.5.1 cells and an immunofluorescence assay was performed 5 days after infection using anti-core antibody. (C) Supernatants from parental JFH1, plaque-derived viruses (Pl #1, #2, and #3) and the second round isolation of plaques from the Pl #1 subclones (Pl #1-1, #1-2, and #1-3) were inoculated onto Huh-7.5.1 cells with PFU-adjusted doses, respectively. HCV core antigen levels in culture medium were measured on the days indicated. Inoculation and the assays were done in triplicate. The S.D.s were within 4% in each plot.

HCV E2 induces ER stress at lower levels but binds to PERK and inhibits phosphorylation of eIF2-alpha at high levels of expression (Pavio et al., 2003). These reports have shown that HCV may induce ER stress and regulate subsequent intracellular responses to promote its survival in hepatocytes. Consistently with these reports, our findings that HCV-JFH1 induces the expression of an ER chaperon protein and phosphorylation of eIF2-alpha indicates that robust replication of HCV-JFH1 produces unfolded proteins in the ER, leading to activation of ATF6 and stimulation of the transcription of ER chaperon proteins to promote protein folding. HCV-JFH1-induced unfolded proteins also activate PERK, which phosphorylates eIF2-alpha to inhibit the protein translation. Furthermore, the severe ER stress finally activates apoptosis signaling pathways at the early stage of viral infection. Although which HCV-JFH1 gene product is involved in ER stress-mediated apoptosis is not identified in our study, such proteins may contribute to the regulation of ER stress signaling in the host cell that leads to viral survival or cell death.

The plaque assay is often used to quantify virus infectious titers by visualizing the viral-induced CPE. However, due to the noncytopathic nature of HCV and the lack of highly permissive

Table 2
Nucleotide changes and amino acid substitutions in the cytopathic JFH1 subclone

Nucleotide[a]	Amino acid[a]
A1353G	M334V
C2842A	T843K
G3402A	G1017S
A5819G	Synonymous
T7662A	C2438S
C9153T	P2934S
G9232A	G2960D
G9293C	Synonymous
G9295C	R2985P
C9353A	H3000Q
G9355A	S3001N

[a] Nucleotide and amino acid numbers were derived from pJFH1full (Wakita et al., 2005).

host cell lines, detection of HCV-infected cells commonly relied on visualization of the infected focus by immunostaining HCV proteins (Zhong et al., 2005). Disadvantages include the costs of the antibodies and substrate, additional steps for assay and detection, and microscopic examination to count the foci. By using a highly permissive host cell line and optimizing several conditions, we have developed a plaque assay for HCV. Because the HCV-JFH1 strain is not absolutely cytopathic and does not kill all infected cells, the calculated plaque-forming units do not directly reflect HCV infectious titer but rather reflect cytopathogenicity or the percentage of cytopathic clones in the total infectious foci.

The HCV plaque assay revealed that JFH1 infection and replication developed cytopathic and noncytopathic infectious cell foci (Fig. 3B). One would suspect that the different outcomes of HCV replication might be attributable to the clonal heterogeneity of the host cells. However, there are several pieces of evidence that the Huh-7.5.1 cell line, which we used as host, might be a homogenous cell line. Huh-7.5.1 is derived from parental Huh7 cells through two rounds of clonal selection for neomycin resistance that were dependent on permissiveness for the HCV subgenomic replicon (Blight et al., 2002; Zhong et al., 2005). Sumpter et al. have reported that the HCV-permissive feature is due to mutational inactivation of RIG-I, a cytoplasmic double-stranded RNA sensor that induces type-I IFN production (Sumpter et al., 2005). This evidence suggests that the cytopathic HCV replication is attributable to virus factors, in particular, virus genomic alteration and not by clonal variation or evolution of the host cells.

Indeed, the isolation of the plaque-forming HCV subclones and inoculation onto naive cells showed significantly higher replication yields (Fig. 8) and more frequent development of cytopathic plaques (Table 1). These findings indicate that HCV-JFH1 has evolved into cytopathic and noncytopathic subclones. Our results are similar to BVDV infection. BVDV is divided into two biotypes, cytopathic (*cp*) and noncytopathic (*ncp*) strains. Most *cp* strains, which induce strong apoptotic cell death upon infection, develop from the *ncp* strains by RNA recombination such as insertion of cellular sequences, duplications and rearrangements, and deletions and lead to expression of the NS3 protein (Meyers and Thiel, 1996). Kummerer et al. have reported that other *cp* strain had point mutations in NS2 that enhanced cleavage of NS2/3 junction and NS3 production (Kummerer and Meyers, 2000). As for HCV, considering a rapid HCV replication cycle and the poor fidelity of the viral NS5B RNA-dependent RNA polymerase (RdRp) (Bartenschlager and Lohmann, 2000; Kato et al., 2005), evolution of sequence variants may well develop even after a transfection of cloned HCV-RNA. Very recently, *in vitro* permissive subclones of HCV genotype 1a, H77S stain, have been reported, which have five cell culture-adaptive mutations in the NS3, 4A, and 5A regions (Yi et al., 2007). In these clones, introduction of amino acid substitutions in the p7 and NS2 region enhanced production of the virion particles.

Interestingly, sequence analyses of a cytopathic HCV-JFH1 subclone (Pl #1) identified six amino acid substitutions in the NS5B RdRp (Table 2). Three of the six mutations were redundantly appeared in other clones that were independently isolated from the plaques (Table 3). These findings make us speculate that these amino acid substitutions may affect the enzymatic activity of RdRp by altering tertiary structure of the

Table 3
Nucleotide changes and amino acid substitutions in the NS5B regions of the cytopathic JFH1 subclones

Pl #1	#1-1	#1-2	#1-3	Pl #2	Pl #3	Pl #4
						T7623A (S2428T)
T7662A (C2438S)	T7662A (C2438S)	T7662A (C2438S)	T7662A (C2438S)	T7662A (C2438S)	T7662A (C2438S)	
					A7550C	
					C7551A (N2470T)	
						G8259C
						C8260G (A2640R)
C9153T (P2934S)	C9153T (P2934S)	C9153T (P2934S)	C9153T (P2934S)		C9153T (P2934S)	
				G9162T (V2941L)		
					A9201T (I2954F)	
G9232A (G2960D)						
				G9235A (R2965Q)		
G9295C (R2985P)	G9295C (R2985P)		G9295C (R2985P)			
C9353A (H3000Q)	C9353A (H3000Q)					
G9355A (S3001N)	G9355A (S3001N)		G9355A (S3001N)			G9355A (S3001N)

Nucleotide and amino acid numbers were derived from pJFH1full (Wakita et al., 2005).

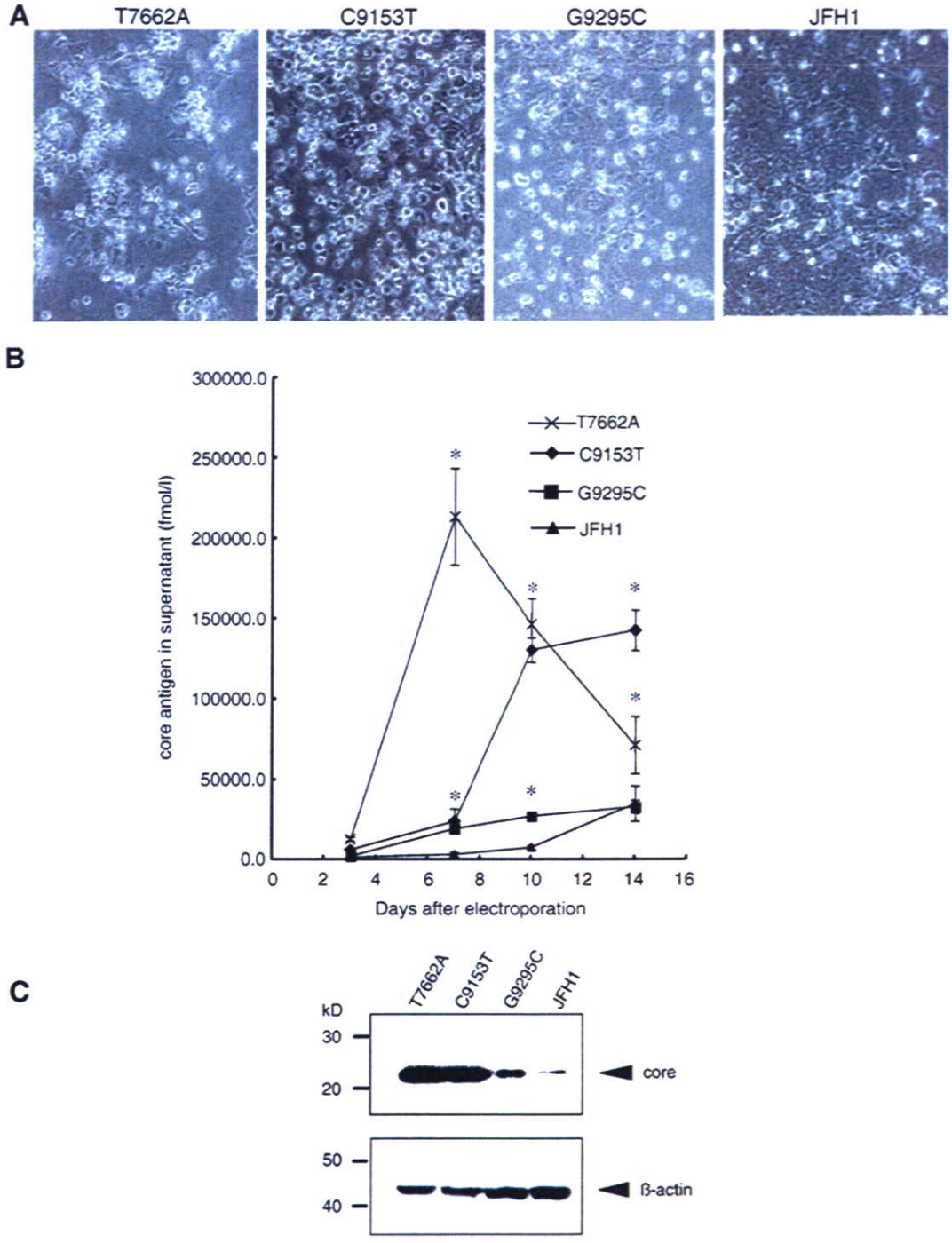

Fig. 9. Introduction of various mutations into the NS5B region of JFH1. The mutations identified in the cytopathic plaque Pl #1; T7662A, C9153T, and G9295C were introduced individually into the parental JFH1. Each JFH1 mutant, T7662A, C9153T, and G9295C, RNA was transfected into Huh-7.5.1 cells by electroporation. The transfected cells were split every 3 to 5 days (see Materials and methods). (A) JFH1 mutants transfected Huh-7.5.1 cells were observed by phase-contrast microscopy at day 7 after transfection. (B) Levels of core antigen in the culture supernatants. The culture supernatants of transfected cells were collected on the days indicated, and the levels of core antigen were measured. Asterisks indicate *p*-values of less than 0.05. (C) The supernatants of JFH1 mutants transfected Huh-7.5.1 cells were transferred onto uninfected Huh-7.5.1 cells. The cells were harvested at 7 days after infection. Western blotting was performed using anti-core and anti-beta-actin.

thumb domain or affect the quaternary structure of the whole HCV replicase complex by altering surface affinity to other nonstructural proteins. Mapping of the amino acid substitutions in the RdRp tertiary structure has shown that the amino acid 2438 was located on the finger domain, and three amino acids, 2934, 2960, and 2985, were located on the outer surface of the thumb domain, which corresponds to the opposite side of the nucleotide tunnel. The other substitutions, 3000 and 3001, were within the domain of the polypeptide linking the polymerase to the membrane anchor (Lesburg et al., 1999). Very

recently, Zhong et al. have reported that long-term culture of HCV-JFH1 of more than 60 days leads to the evolution of certain mutations in the viral genome (Zhong et al., 2006). They identified amino acid changes in Core, E2, NS3, and NS5A regions, and especially E2 mutation increased infectivity and density changes of viruses. In our present study, however, we could not find those mutations in the virus subclones that we have isolated in the plaque assay technique. The discrepancy might be attributable to the presence or absence of HCV-CPE-induced cell clonal alteration of the host Huh-7.5.1 that occurs concomitantly with viral genetic evolution during long-term cell culture. Further analyses may be necessary to determine the most critical regions that regulate the viral replication efficiency and cytopathogenicity.

Interestingly, the mutant virus clones, T7662A (C2438S), C9153T (P2934S), and G9295C (R2985P), showed considerably higher replication efficiency and cytopathogenicity than the wild type JFH1 clone (Fig. 9). These results strongly suggest that certain NS5B mutations in the plaque-purified strains display more replication-efficient and cytopathic phenotypes. The present data are still preliminary. Further studies may be necessary to fully characterize these mutations and their functions, which include introduction of mutations of the HCV region and of the other plaque-purified viruses and combination of the mutations, and to study their effects on virus protein functions. We are at present analyzing derivative JFH1 clones in which other amino acid mutations were introduced.

Several clinical findings have suggested that HCV is not cytopathic and that antiviral immune responses such as cytotoxic T lymphocytes play important roles in HCV pathogenesis (Cerny and Chisari, 1999). On the other hand, apoptotic cell death is the first cellular response to many hepatotoxic events and has been implicated in the pathogenesis of liver diseases, such as viral hepatitis, autoimmune diseases, alcohol-induced injury, cholestasis, hepatocellular carcinoma, and fulminant hepatic failure (Canbay et al., 2004; Ghavami et al., 2005; Patel and Gores, 1995; Rodrigues et al., 2000; Rust and Gores, 2000; Thompson, 1995). Several clinical studies have shown that fulminant hepatic failure (FHF), from which HCV-JFH1 strain was isolated, showed far more hepatocyte apoptosis, as characterized by caspase activation and Fas-FasL expression, than chronic hepatitis and normal populations (Leifeld et al., 2006; Mita et al., 2005; Ryo et al., 2000). The ER stress markers GRP78 and ATF6 are upregulated in the HCV liver tissue as the histological grade advanced. In addition, GRP78 and ATF6 are upregulated as the histological grade increased in hepatocellular carcinoma (HCC) (Shuda et al., 2003) and proteomic analysis of HCC tissue samples has shown significant upregulation of HSP70 and GRP78 (Chuma et al., 2003; Takashima et al., 2003), indicating that these proteins may play important roles in HCV-induced hepatocarcinogenesis.

In conclusion, the cytopathic mutants of HCV-JFH1 strain were isolated by using plaque assay techniques. A mechanism of the cytopathic effects involved ER stress-mediated apoptosis that was triggered by virus infection. That process of cytopathic effects might explain one aspect of HCV-induced liver injury during acute infection. Further analyses of cellular effects on HCV replication may elucidate the pathogenesis of HCV infection and may define novel host factors as targets of antiviral chemotherapeutics.

Materials and methods

Reagents

Recombinant human interferon alpha-2b was from Schering-Plough (Kenilworth, NJ). Beta-mercaptoethanol was from Wako (Osaka, Japan). Anti-CD81 antibody (JS-81) was from BD Biosciences (Franklin Lakes, NJ) (Morikawa et al., 2007).

Cells and cell culture

Huh-7.5.1 cells (Zhong et al., 2005) (kindly provided by Dr Francis V. Chisari) were maintained in Dulbecco's modified minimal essential medium (DMEM, Sigma) supplemented with 2 mmol/l L-glutamine and 10% fetal bovine serum at 37 °C under 5.0% CO_2.

In vitro RNA synthesis and transfection

A plasmid, pJFH1-full (Wakita et al., 2005), which encodes the full-length HCV-JFH1 sequence, and two control plasmids for pJFH1-full were used; pJFH1/GND that is a replication incompetent mutant with a mutation in the NS5B GDD motif and pJFH1/ΔE1-E2 in which a coding region of the HCV envelope proteins was deleted. The HCV RNA was synthesized using the RiboMax Large Scale RNA Production System (Promega, Madison, WI), with the linearized pJFH1 plasmid as template. After DNaseI (RQ-1 RNase-free DNase, Promega) treatment, the transcribed HCV-RNA was purified using ISOGEN (Nippon Gene, Tokyo, Japan). For the RNA transfection, Huh-7.5.1 cells were washed twice, and 5×10^6 cells were resuspended in Opti-MEM I (Invitrogen, Carlsbad, CA) containing 10 μg of HCV RNA, transferred into a 4-mm electroporation cuvette, and subjected to an electric pulse (1050 μF and 270 V) using the Easy Ject system (EquiBio, Mieddlesex, UK). After electroporation, the cell suspension was left for 5 min at room temperature and then incubated under normal culture conditions in a 10-cm diameter cell culture dish. The transfected cells were split every 3 to 5 days. The culture supernatants were subsequently transferred onto uninfected Huh-7.5.1 cells. The levels of HCV replication and viral protein expression were detected by real-time PCR, western blotting, and immunocytochemistry.

HCV subgenomic replicon constructs

HCV subgenomic replicon plasmid pRep-Feo was derived from the HCV-N strain pHCV1bneo-delS (Tanabe et al., 2004) and pSGR-JFH1 was from the HCV-JFH1 strain (Kato et al., 2003). The replicon RNA was synthesized from pRep-Feo or pSGR-JFH1 and transfected into Huh-7.5.1 cells. After culture in the presence of G418 (Wako), cell lines stably expressing the replicon were established.

Real-time RT-PCR analysis

Total cellular RNA was isolated using ISOGEN (Nippon Gene). Two micrograms of total cellular RNA was used to generate cDNA from each sample using SuperScript II (Invitrogen) reverse transcriptase. Expression of mRNA was quantified using Quanti Tect SYBR Green PCR Master Mix (QIAGEN, Valencia, CA) and the ABI 7500 Real-Time PCR System (Applied Biosystems, Foster City, CA). The primers used were as follows: HCV-JFH1 sense (positions 7090 to 7109; 5′-TCA GAC AGA GCC TGA GTC CA-3′), HCV-JFH1 antisense (positions 7404 to 7423; 5′-AGT TGC TGG AGG GCT TCT GA-3′), beta-actin sense (5′-ACA ATG AAG ATC AAG ATC ATT GCT CCT CCT-3′), and beta-actin antisense (5′-TTT GCG GTG GAC GAT GGA GGG GCC GGA CTC-3′).

Quantification of HCV core antigen in the culture supernatant

The culture supernatants of JFH1-RNA transfected Huh-7.5.1 cells were collected on the days indicated, passed through a 0.45 μm filter (MILLEX-HA, Millipore, Bedford, MA), and stored at −80 °C. The levels of core antigen in the culture supernatants were measured using a chemiluminescence enzyme immunoassay (CLEIA) according to the manufacturer's protocol (Lumipulse Ortho HCV Antigen, Ortho-Clinical Diagnostics, Tokyo, Japan).

Western blotting

Western blotting was carried out as described previously (Tanabe et al., 2004; Yokota et al., 2003). Briefly, 10 μg of total cell lysate was separated by SDS–PAGE and blotted onto a polyvinylidene fluoride (PVDF) western blotting membrane. The membrane was incubated with the primary antibodies followed by a peroxidase-labeled anti-IgG antibody and visualized by chemiluminescence using the ECL western blotting Analysis System (Amersham Biosciences, Buckinghamshire, UK). The antibodies used were anti-core mouse monoclonal antibody 2H9 (provided by Dr. Wakita), anti-GRP78 goat monoclonal antibody, anti-GADD153/CHOP rabbit polyclonal antibody (Santa Cruz Biotechnology, Santa Cruz, CA), anti-eIF2-alpha, anti-phospho-eIF2-alpha rabbit polyclonal antibody (Cell Signaling, Danvers, CA), and anti-beta-actin antibody (Sigma).

Immunocytochemistry

HCV-JFH1-transfected or infected Huh-7.5.1 cells were cultured in Lab-Tek® Chamber Slide™ (Nalge Nunc International, Rochester, NY) or on 22-mm-round micro cover glasses (Matsunami, Tokyo, Japan). For detection of HCV-core and GRP78, cells were fixed with cold acetone for 15 min. The cells were incubated with the primary antibodies for 1 h at 37 °C and with Alexa Fluor 488 goat anti-mouse IgG antibody or Alexa Fluor 568 donkey anti-goat IgG antibody (Molecular Probes, Eugene, OR) for 1 h at room temperature. To analyze apoptosis of HCV-JFH1 infected cells, double staining for annexin V-FITC binding and for cellular DNA using propidium iodide (PI) was performed using an annexin V-Fluorescein Staining Kit (Wako, Osaka, Japan). Cells were visualized by a fluorescence microscopy (BZ-8000, KEYENCE, Osaka, Japan).

Plaque assay

Huh-7.5.1 cells were seeded in collagen-coated 60-mm-diameter plates at a density of $2–4 \times 10^5$ cells per plates and were incubated at 37 °C under 5.0% CO_2 (as described above). After overnight incubation, HCV-infected culture supernatants were serially diluted in a final volume of 2 ml per plates and transferred onto the cell monolayers. After ~5 h of incubation, the inocula were removed, and the cell monolayers were overlaid with 8 ml of culture medium (DMEM, 2 mmol/l L-glutamine and 10% fetal bovine serum) that contained 0.8% methylcellulose. After 7 to 12 days of incubation under normal culture conditions, formation of cytopathic plaque was visualized by staining the cell monolayers with 0.08% crystal violet solution (Sigma). The levels of cytotoxicity were evaluated by counting the plaques and calculating the titer (PFU/ml). Similarly, the titers of infectivity were evaluated by performing immunocytochemistry to detect foci of HCV-core-positive cells and calculating the infectious focus-forming units (FFU/ml).

Sequence analyses

The cDNA from the isolated JFH1 plaque was amplified from cytopathic virus-infected Huh-7.5.1 cells by RT-PCR and subjected to direct sequence determination. Nucleotide sequences were read from both strands using Big Dye Terminator Cycle Sequencing Ready Reaction kits (Applied Biosystems) and an automated DNA sequencer (ABI PRISM® 310 Genetic Analyzer; Applied Biosystems).

Establishment of mutant JFH1 clones

In order to introduce various mutations into the NS5B region of JFH1, plasmid pJFH1 was digested with *Hin*dIII and the DNA fragment encompassing nt. 8231 to 9731 was subcloned into the pBluescriptII SK− phagemid vector (Stratagene, La Jolla, CA). The following mutations were introduced into the DNA fragment in the subcloning vector by site-directed mutagenesis (Quick-ChangeII Site-Directed Mutagenesis Kit; Stratagene): C9153T and G9295C, respectively. Finally, these *Hin*dIII–*Hin*dIII fragments were subcloned back into the parental plasmid pJFH1. The mutation T7662A-introduced PCR fragment (nt. 7421–7839) was subcloned into the T-Vector (pGEM-T Easy Vector Systems; Promega) and digested with *Rsr*II and *Bsr*GI. Finally, these *Rsr*II–*Bsr*GI fragments were subcloned back into the parental plasmid.

Statistical analyses

Statistical analyses were performed using the Student's *t*-test, and *p*-values of less than 0.05 were considered as statistically significant.

Acknowledgments

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Targeting Lipid Metabolism in the Treatment of Hepatitis C Virus Infection

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Recently, microdomains of organelle membranes rich in sphingomyelin and cholesterol (called "lipid rafts") have been considered to act as a scaffold for the hepatitis C virus (HCV) replication complex. Using the HCV cell culture system, we investigated the effect of myriocin, a sphingomyelin synthesis inhibitor, on HCV replication. We also investigated the combined effect of myriocin with interferon (IFN) and myriocin with simvastatin. Myriocin suppressed replication of both a genotype 1b subgenomic HCV replicon (Huh7/Rep-Feo) and genotype 2a infectious HCV (JFH-1 HCV) in a dose-dependent manner (for subgenomic HCV-1b, maximum of 79% at 1000 nmol/L; for genomic HCV-2a, maximum of 40% at 1000 nmol/L). Combination treatment with myriocin and IFN or myriocin and simvastatin attenuated HCV RNA replication synergistically in Huh7/Rep-Feo cells. Our data demonstrate that the sphingomyelin synthesis inhibitor strongly suppresses replication of both the subgenomic HCV-1b replicon and the JFH-1 strain of genotype 2a infectious HCV, indicating that lipid metabolism could be a novel target for HCV therapy.

Hepatitis C virus (HCV) is a major etiologic agent of liver diseases, affecting 170 million people worldwide [1]. Fifty-five percent to 85% of acute infections become persistent [2], and at least 20% of patients with chronic HCV infection progress to cirrhosis within 20 years [3]. With therapeutic advances, including the recent combination of pegylated interferon (IFN) plus ribavirin, half of patients can achieve a sustained virologic response [4]. However, the remaining half cannot clear the virus, demonstrating a strong need for HCV-specific therapies.

Positive-strand RNA viruses replicate intracellularly on certain membrane structures, including the endoplasmic reticulum [5], the Golgi apparatus [6], endosomes, and lysosomes [7]. During replication, RNA viruses form distinct replication complexes made of several membrane compartments and viral proteins [8]. In HCV, the membranous web (consisting of vesicles in a membranous matrix) has been described in the cellular matrix of HCV replicon–harboring cells [9, 10]. This membranous web is considered to be the HCV replication complex, consisting of viral and host proteins.

Recent studies suggest that the HCV replication complexes are formed on lipid rafts (which are detergent-insoluble microdomains of intracellular vesicular membranes rich in cholesterol and sphingolipid) [11–13]. It has been reported that viral nonstructural proteins and both positive- and negative-sense HCV RNAs were localized distinctively in a fraction of lipid rafts when subgenomic HCV replicon cells were subjected to membrane flotation analysis [12]. On the other hand, recent studies have demonstrated that agents related to lipid metabolism affect the replication of genotype 1 HCV. Leu et al. [14] reported that polyunsaturated fatty acids exerted strong anti-HCV activity on a subgenomic HCV-1b replicon. Moreover, 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase inhibitors (statins), which prevent cholesterol synthesis, have been shown to suppress replication of ge-

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nomic and subgenomic HCV-1b replicons [15, 16]. Even though the precise mechanism has not been defined, these agents may attenuate HCV replication through the destruction of lipid rafts, according to their pharmacological actions. If this is the mechanism, sphingomyelin, the remaining and essential component of lipid rafts, might play a role in HCV replication. With this in view, recent studies have demonstrated that a sphingomyelin synthesis inhibitor attenuated the replication of a subgenomic HCV-1b replicon in cultured cells [17] and the replication of genomic HCV-1 in a chimeric mouse model [18]. However, investigation of anti-HCV activity in these agents has been limited to genotype 1 HCV, and the combined effect of these agents has not been determined. If they do not target the HCV structure itself but exert their antiviral activity through destruction of the host's lipid raft, it would be plausible to speculate that they might be effective irrespective of the viral isolate, and the combined effect of these agents might be additive or synergistic.

In the present study, we investigated the role played by the sphingomyelin synthesis pathway and the mevalonate pathway in HCV replication, using a subgenomic HCV-1b replicon and the particle-producing cell culture HCV 2a model of JFH-1 HCV [19].

MATERIALS AND METHODS

Cell culture and HCV replicon. The human hepatoma cell lines Huh7 and Huh7.5.1 [20] were maintained in Dulbecco's modified Eagle's medium (Sigma) supplemented with 10% fetal calf serum at 37°C in 5% CO_2. The subgenomic HCV replicon used was derived from Rep-Feo (genotype 1b) [21, 22], and a full-length genomic HCV RNA was derived from genotype 2a JFH-1 HCV [19]. Subgenomic or genomic HCV RNA was synthesized from replicon cDNA–harboring plasmids (pRep-Feo and pJFH-1) by means of T7 polymerase (RiboMax Large Scale RNA Production System; Promega) and transfected into these cells. For the subgenomic replicon, cell lines stably expressing the replicon were established (Huh7/Rep-Feo) in the presence of 500 μg/mL G418.

Reporter plasmids and luciferase assay. pISRE-TA-Rluc expressing the *Renilla* luciferase reporter gene under control of the IFN-stimulated response element (ISRE) was constructed by replacing the firefly luciferase gene with the *Renilla* luciferase gene of pISRE-TA-Luc, purchased from Invitrogen. Luciferase activity was quantified using the Bright-Glo or Dual-Luciferase assay system (both from Promega) and a luminometer (AB-2250; ATTO). Assays were performed in triplicate, and the results were expressed as mean ± SD percentages of the control values. QuantiLum recombinant luciferase (Promega) was used as the positive control for the analysis.

Reagents. The reagents used included myriocin (Biomol), IFN-α 2b (Santa Cruz Biotechnology), phytosphingosine hydrochloride (Sigma), 2-hydroxypropyl-β-cyclodextrin (2-HP-β-CyD; Sigma), and simvastatin (Cosmobio).

Northern blotting. Total cellular RNA was extracted from cells by means of Isogen (Wako). The RNA was separated by denaturing agarose-formaldehyde gel electrophoresis and transferred to a membrane from a NorthernMax kit (Ambion). The membrane was hybridized with a digoxigenin-labeled probe that was specific for the nonstructural replicon sequence. The signals were detected in a chemiluminescence reaction by using a digoxigenin detection kit (Roche) and were visualized by using an LAS-1000 imaging system (Fuji Film).

Western blotting. Ten micrograms of total cell lysate was separated using NuPAGE 4%–12% Bis-Tris gel (Invitrogen) and was blotted onto an Immobilon polyvinylidene difluoride membrane (Roche). The membrane was incubated with an anti-core monoclonal antibody (MAb; Affinity Bioreagents), an anti-NS3 MAb (Virogen), an anti-NS5A MAb (gift from Burckstummer, Robert Koch Institute), or a anti–β-catenin MAb (Sigma). Detection was done in a chemiluminescence reaction (ECL; Amersham).

Dimethylthiazol carboxymethoxyphenyl sulfophenyl tetrazolium (MTS) assays. To evaluate cytotoxicity, MTS assays were performed using a CellTiter 96 Aqueous One Solution Cell Proliferation Assay (Promega), in accordance with the manufacturer's instructions.

Thin-layer chromatography (TLC). The lipid fraction of cells treated with myriocin was extracted using the method of Bligh and Dyer [23], and total lipids from the cells treated with myriocin were extracted with 3 mL of chloroform. The extracts were spotted onto silica gel TLC plates (Merck) and were chromatographed with chloroform-methanol-water (65:25:4 [vol/vol/vol]). The plate was visualized with a molybdenum spray.

Real-time reverse-transcription polymerase chain reaction (RT-PCR). TaqMan RT-PCR targeting the 5' untranslated region was used for the quantitation of intracellular genomic JFH-1 HCV RNA. The sequences of the sense and antisense primers and the TaqMan probe were 5'-TGCGGAACCGGTGAGTACA-3', 5'-CTTAAGGTTTAGGATTCGTGCTCAT-3', and 5'-(FAM)CACCCTATCAGGCAGTACCACAAGGCC(TAMRA)-3', respectively. The method has been described elsewhere [24].

Short interfering RNA (siRNA) analysis. The sequence encoding the LCB1 subunit of serine palmitoyltransferase (SPT) was selected as the target for siRNA (sense, 5'-AACAACAUCGUUUCAGGUCCUTT-3'; antisense, 5'-AGGGCCUGAAACGAUGUUGTT-3'). siRNA targeting enhanced green fluorescent protein (GFP) was used as the negative control (sense, 5'-CUUACGCUGAGUACUUCGATT-3'; antisense, 5'-UCGAAGUACUCAGCGUAATT-3'). (Underlined letters indicate deoxyribonucleotides.)

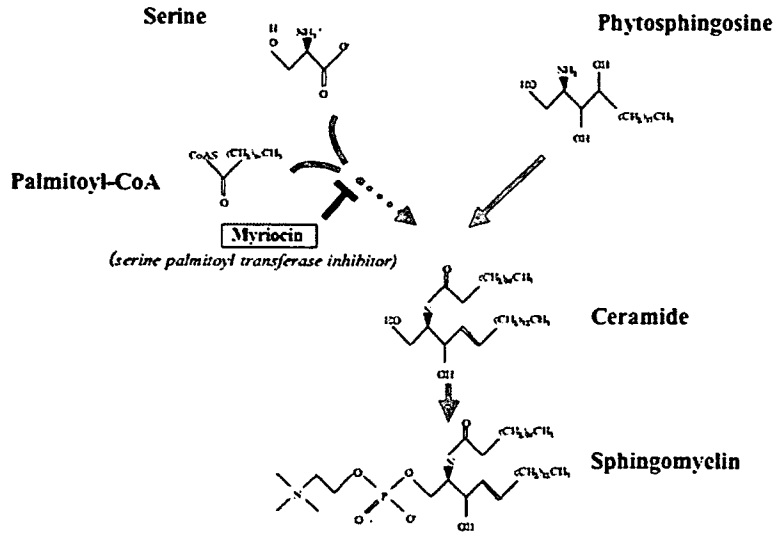

Figure 1. The sphingomyelin synthesis pathway. Serine palmitoyltransferase catalyzes the first committed step of sphingomyelin biosynthesis from serine and palmitoyl-coenzyme A (CoA). Myriocin inhibits the catalyzing activity of serine palmitoyltransferase. Phytosphingosine is known to work as a precursor of ceramide in both mammalian and fungal cells.

Statistical analyses. Statistical analyses were performed using Student's *t* test; statistically significant differences were defined as those for which $P < .05$.

RESULTS

Specific suppression of the replication of a subgenomic HCV-1b replicon by an inhibitor of sphingomyelin synthesis. To clarify the role played by the sphingomyelin synthesis pathway in HCV replication, we added myriocin, a specific inhibitor of SPT that catalyzes the first committed step of sphingomyelin biosynthesis (figure 1), to the medium of Huh7/Rep-Feo cells. The luciferase activity, reflecting replication of the subgenomic HCV-1b replicon, dropped to 37% and 21% of the control at myriocin concentrations of 100 and 1000 nmol/L, respectively (figure 2*A*, *upper panel*), but myriocin did not cause toxicity to the cultured cells (figure 2*A*, *lower panel*). The result indicates that the decrease in HCV replication is due to a specific suppressive effect of myriocin and not to the cytotoxicity of myriocin. Northern hybridization analysis also demonstrated a substantial reduction of the subgenomic HCV replicon RNA in Huh7/Rep-Feo cells treated with myriocin in a dose-dependent manner (figure 2*B*). Similarly, Western blot analysis demonstrated a decrease in HCV NS5A after treatment with myriocin (figure 2*C*).

No enhancement of ISRE promoter activity after myriocin treatment. To determine whether the effect of myriocin in suppressing the subgenomic HCV replicon was associated with the activation of IFN-stimulated genes, the ISRE–*Renilla* luciferase plasmid was transfected into Huh7/Rep-Feo cells, and these cells were cultured with various concentrations of myriocin. As a positive control for the enhancement of ISRE reporter activity, the ISRE–*Renilla* luciferase–transfected cells were cultured with IFN. Myriocin had no significant effect on ISRE promoter activity, whereas IFN significantly up-regulated ISRE activity (figure 2*D*, *upper panel*). In contrast, firefly luciferase activity in the Huh7/Rep-Feo cells, reflecting HCV replication, was inhibited by both IFN and myriocin in a dose-dependent manner (figure 2*D*, *lower panel*). These results demonstrate that the action of myriocin on HCV replication is independent of the IFN pathway.

Decrease in the sphingomyelin content of Huh7 cells after myriocin treatment. To clarify whether myriocin really inhibits the biosynthesis of sphingomyelin in Huh7 cells, we treated Huh7 cells with 100 nmol/L myriocin and analyzed the change in the cellular phospholipid composition by TLC. As demonstrated in figure 2*E*, the cellular sphingomyelin content decreased after myriocin treatment, but no significant change was observed in other cellular phospholipids.

Restoration of HCV replication by addition of phytosphingosine. To confirm that suppression of HCV RNA replication was due to depletion of sphingomyelin, we incubated replicon cells with phytosphingosine, a precursor of ceramide in mammalian and fungal cells, in the presence of myriocin. Treatment with phytosphingosine restored HCV replication in a dose-dependent manner (figure 2*F*, *upper panel*). On the other hand, phytosphingosine by itself did not have any effect on HCV replication (figure 2*F*, *lower panel*). This result indicates that inhibition of HCV replication was the direct result of depletion of sphingomyelin.

Suppression of HCV replication by knocking down SPT with siRNA. Next, we determined whether inhibition of SPT expression suppresses HCV replication by knocking down SPT with siRNA. As demonstrated in the upper panel of

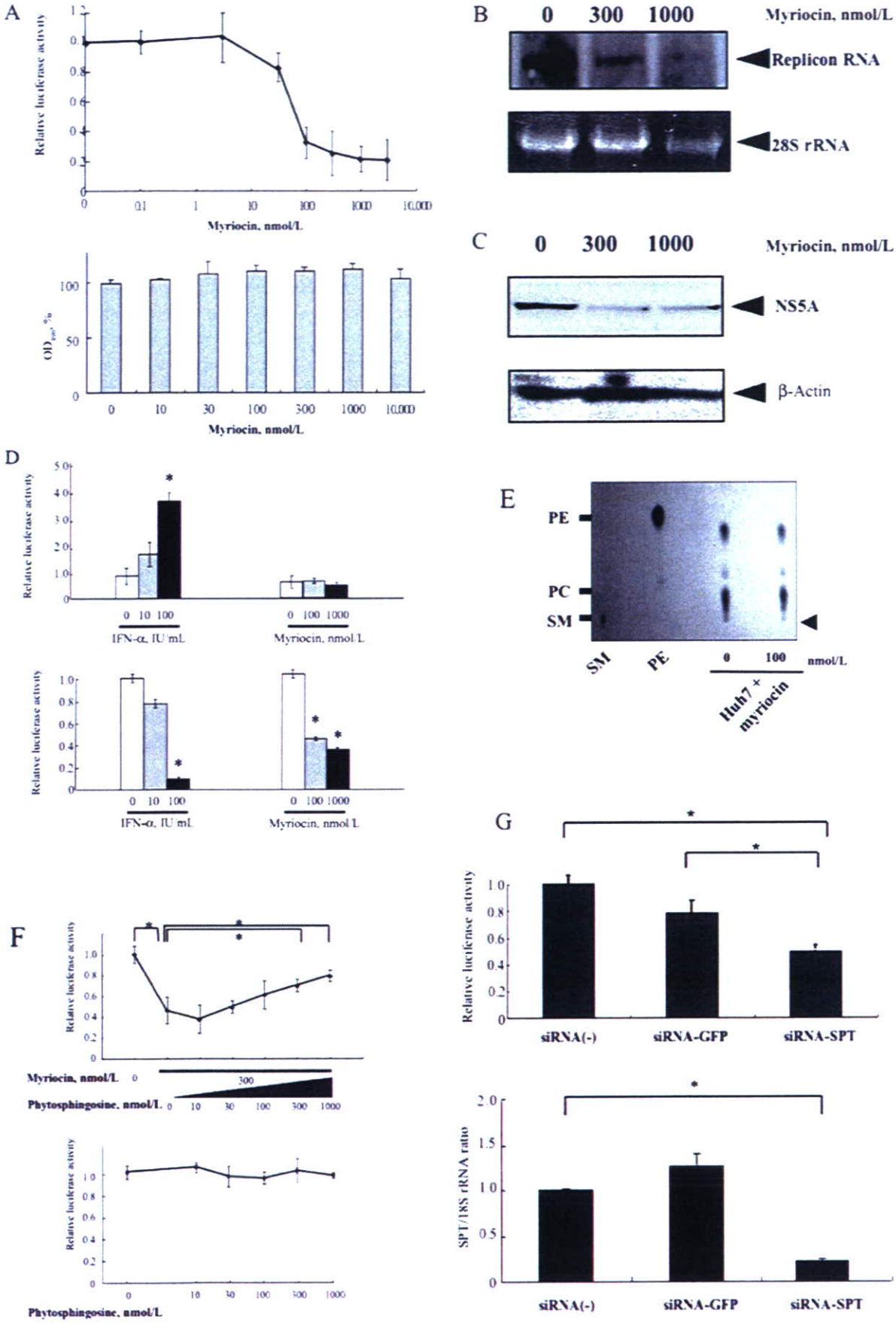
A
Relative luciferase activity
Myriocin, nmol/L
B
0 300 1000
Myriocin, nmol/L
Replicon RNA
28S rRNA
C
0 300 1000
Myriocin, nmol/L
NS5A
β-Actin
D
Relative luciferase activity
IFN-α, IU/mL
Myriocin, nmol/L
E
PE
PC
SM
nmol/L
Huh7 + myriocin
F
Relative luciferase activity
Myriocin, nmol/L
Phytosphingosine, nmol/L
G
Relative luciferase activity
siRNA(-)
siRNA-GFP
siRNA-SPT
SPT/18S rRNA ratio

figure 2G, HCV replication was suppressed significantly by siRNA targeting SPT compared with no siRNA or siRNA targeting GFP (negative control). We confirmed with real-time PCR that the siRNA targeting SPT significantly decreased expression of SPT mRNA (figure 2G, *lower panel*). This result indicates that the SPT enzyme plays an important role in HCV replication.

Inhibition of the replication of a subgenomic HCV-1b replicon by an HMG-CoA reductase inhibitor (simvastatin). HMG-CoA reductase inhibitors have been reported to suppress replication of subgenomic and genomic HCV-1b replicons [15, 16]. Because cholesterol is another important component of lipid rafts, it may be speculated that depletion of cholesterol by HMG-CoA reductase inhibitors disrupts the lipid raft, affecting the ability of the HCV replicon to replicate in Huh7 cells. To confirm the effect of HMG-CoA reductase inhibitors on the subgenomic HCV-1b replicon, we examined the effect of simvastatin by means of Huh7/Rep-Feo cells. Cultures of Huh7/Rep-Feo cells with simvastatin at concentrations of 0–100 μmol/L showed a dose-dependent reduction of the subgenomic HCV-1b replicon (figure 3, *upper panel*). The MTS assay showed that treatment with simvastatin had no toxic effect on Huh7/Rep-Feo cells in the dose range used (figure 3, *lower panel*). These results demonstrated that simvastatin specifically suppressed replication of a subgenomic HCV-1b replicon. However, because recent studies showed that statins suppress HCV replication through inhibition of geranylgeranylation of certain proteins rather than inhibition of cholesterol synthesis [15], we also examined the effect on HCV replication of 2-HP-β-CyD, an agent known to deplete cholesterol directly from membranes. As demonstrated in figure 4A, 2-HP-β-CyD also suppressed HCV replication without cytotoxicity. To confirm that 2-HP-β-CyD did not inhibit firefly luciferase activity nonspecifically rather than by suppressing HCV RNA, we incubated recombinant firefly luciferase with various concentrations of 2-HP-β-CyD in the culture medium, and the medium was subjected to luciferase analysis. As demonstrated in figure 4B, 2-HP-β-CyD did not affect luciferase activity. These results indicate that cholesterol itself plays an important role in HCV replication.

Synergistic inhibitory effects of myriocin with IFN, simvastatin with IFN, and myriocin with simvastatin. We carried out the following assay to determine whether myriocin and IFN have a synergistic inhibitory effect on HCV replication. Huh7/Rep-Feo cells were treated with combinations of myriocin and IFN at various concentrations. The relative dose-inhibition curves of IFN were plotted for each fixed concentration of myriocin (0, 30, 100, and 300 nmol/L). As demonstrated in the upper panel of figure 5A, the curves shifted to the left with increasing concentrations of myriocin, demonstrating the synergy of the 2 drugs against the subgenomic HCV-1b replicon. Isobologram analysis also confirmed the synergy (figure 5A, *lower panel*). To determine whether this synergistic effect was associated with up-regulation of the IFN-stimulated gene responses, we investigated the combined effect of myriocin and IFN on ISRE activity. As demonstrated in figure 5B (*upper panel, right*), myriocin did not enhance the ISRE–*Renilla* luciferase activity induced by IFN, but

Figure 2. Specific inhibition of the replication of a subgenomic hepatitis C virus (HCV) genotype 1b replicon by myriocin. *A*, Inhibition of HCV replicon replication by myriocin. By use of Huh7/Rep-Feo cells expressing a selectable chimeric luciferase reporter Feo gene, the intracellular replication level of an HCV replicon was quantified on the basis of luciferase activity [22, 25]. Huh7/Rep-Feo cells were cultured with various concentrations of myriocin. After 96 h of treatment, the luciferase assay was performed, as described in Materials and Methods (*upper panel*). In the dimethylthiazol carboxymethoxyphenyl sulfophenyl tetrazolium (MTS) assay, Huh7/Rep-Feo cells were cultured with various concentrations of myriocin for 96 h (*lower panel*). Data are means ± SDs of triplicates from 2 independent experiments. *B*, Northern hybridization. Huh7/Rep-Feo cells were cultured with various concentrations of myriocin and harvested at 96 h after administration. Ten micrograms of total cellular RNA was electrophoresed in each lane. The membrane containing the HCV replicon RNA was hybridized using a digoxigenin-labeled probe specific for the replicon sequence (*upper panel*), and 28S human ribosomal RNA (rRNA) was used as an internal control (*lower panel*). Lane 1, no myriocin; lane 2, 300 nmol/L myriocin; lane 3, 1000 nmol/L myriocin. *C*, Western blotting. Ten micrograms of total cellular protein was electrophoresed in each lane. Anti-NS5A monoclonal antibody was used as the primary antibody to detect HCV proteins (*upper panel*), and β-actin was used as an internal control (*lower panel*). Lane 1, no myriocin; lane 2, 300 nmol/L myriocin; and lane 3, 1000 nmol/L myriocin. *D*, No enhancement of interferon (IFN)–stimulated response element (ISRE) promoter activity by myriocin. To investigate whether the effect of myriocin was associated with the activation of IFN-stimulated genes, the ISRE–*Renilla* luciferase plasmid was transfected into Huh7/Rep-Feo cells in the presence of myriocin. The upper panel demonstrates the ISRE–*Renilla* luciferase activity at 48 h after transfection. The lower panel demonstrates the firefly luciferase activity of the Huh7/Rep-Feo cells, reflecting HCV replication. Data are means ± SDs of triplicates from 2 independent experiments. $^*P < .05$. *E*, Decrease in the sphingomyelin (SM) content of Huh7 cells after myriocin treatment. The change in the cellular phospholipid content was analyzed by thin-layer chromatography. Huh7 cells were cultured alone or with 100 nmol/L myriocin for 96 h. PC, phosphatidylcholine; PE, phosphatidylethanolamine. *F*, Restoration of the HCV replication that was suppressed by myriocin after the addition of phytosphingosine. Huh7/Rep-Feo cells were cultured with myriocin alone or with various concentrations of phytosphingosine. The luciferase assay was performed after 72 h of treatment (*upper panel*). Huh7/Rep-Feo cells were also cultured with phytosphingosine alone as indicated for 72 h (*lower panel*). Data are means ± SDs of triplicates from 2 independent experiments. $^*P < .05$. *G*, Suppression of HCV replication by knocking down of serine palmitoyltransferase (SPT) with short interfering RNA (siRNA). Huh7/Rep-Feo cells were transfected with 10 nmol/L siRNA oligonucleotides targeting the LCB1 subunit of SPT or control siRNA targeting green fluorescent protein (GFP). The luciferase activity of the HCV replicon was measured 72 h after transfection (*upper panel*). SPT mRNA expression at 72 h after siRNA transfection was analyzed by real-time polymerase chain reaction. The SPT mRNA level was measured relative to 18S rRNA (*lower panel*). Values are shown as ratios to negative control levels and as the means ± SDs of triplicates from 2 independent experiments. siRNA(−), no siRNA. $^*P < .05$.

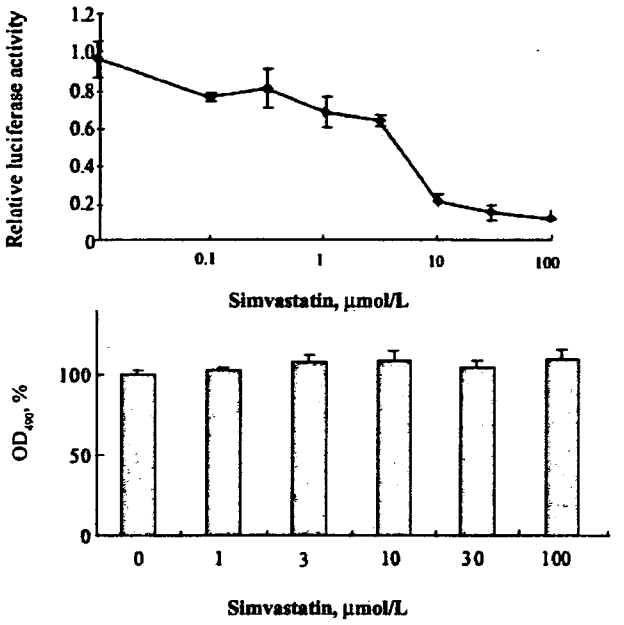

Figure 3. Inhibition of replication of a subgenomic hepatitis C virus genotype 1b replicon by simvastatin. Huh7/Rep-Feo cells were cultured with various concentrations of simvastatin, and the luciferase assay was performed after 48 h of treatment *(upper panel)*. The dimethylthiazol carboxymethoxyphenyl sulfophenyl tetrazolium assay was performed after Huh7/Rep-Feo cells were cultured with various concentrations of simvastatin for 48 h *(lower panel)*. Data are means ± SDs of triplicates from 2 independent experiments.

it significantly enhanced IFN-induced suppression of the firefly luciferase activity reflecting HCV replication *(lower panel, right)*. This demonstrated that the synergistic effect was not caused by up-regulation of the IFN-stimulated genes. We also assessed the synergy of simvastatin with IFN and of myriocin with simvastatin. In each case, the 2 drugs showed synergistic effects at the concentrations indicated (figure 5*C* and 5*D*). In all cases, the MTS reduction values at the drug concentrations used in this assay did not show any significant decrease (data not shown). These results indicate that the synergistic effects on HCV replication of IFN with myriocin, IFN with simvastatin, and myriocin with simvastatin were exerted through their pharmacological effects and were not due to the augmentation of cytotoxicity.

Suppression of JFH-1 HCV replication by myriocin and simavastatin. The experiments described thus far were done using the subgenomic HCV-1b replicon system. Recently, Wakita et al. [19] established an infectious HCV model in cultured cells. This system, known as the JFH-1 system and based on genotype 2a HCV, secretes viral particles into the medium, and the medium is infectious for chimpanzees. This JFH-1 system completely mimics HCV infection in vivo and is considered more suitable for analyzing the effect of drugs. Therefore, we examined the effect of myriocin and simvastatin using the JFH-1 system. Huh7.5.1/JFH-1 HCV cells were cultured for 96 h with 1000 nmol/L myriocin, 10 μmol/L simvastatin, 1000 IU/mL IFN, and a combination of 1000 nmol/L myriocin and 10 μmol/L simvastatin. The intracellular JFH-1 HCV RNA titer was analyzed using real-time RT-PCR. As demonstrated in figure 6*A*, intracellular JFH-1 HCV RNA treated with myriocin or simvastatin decreased to 60% of control in 96 h, demonstrating that the inhibitory effect of myriocin and simvastatin on replication was not restricted to the subgenomic HCV-1b replicon. When both agents were used in combination, JFH-1 HCV RNA also

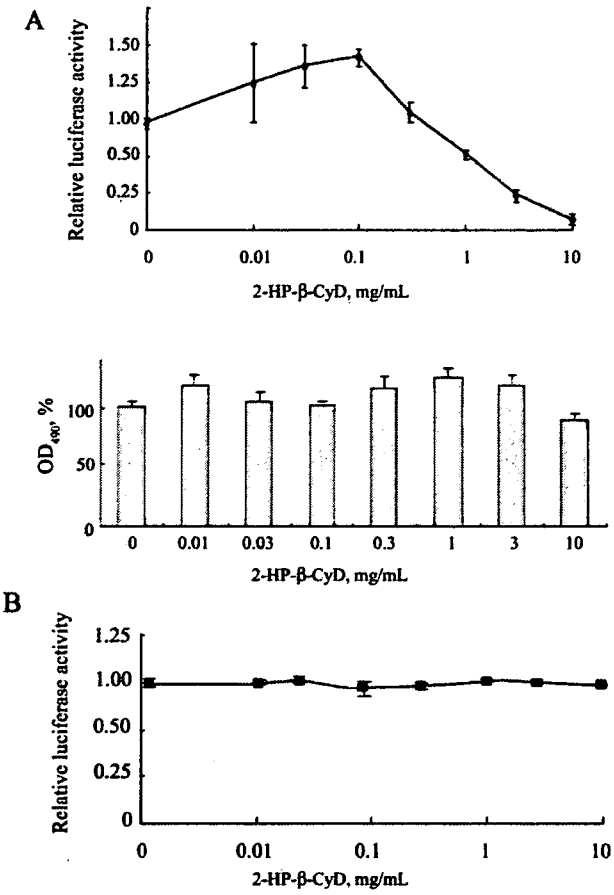

Figure 4. Inhibition of replication of a subgenomic hepatitis C virus genotype 1b replicon by 2-hydroxypropyl-β-cyclodextrin (2-HP-β-CyD). *A*, Huh7/Rep-Feo cells cultured with various concentrations of 2-HP-β-CyD for 48 h. The luciferase assay was performed after 48 h of treatment *(upper panel)*. The dimethylthiazol carboxymethoxyphenyl sulfophenyl tetrazolium assay was performed after Huh7/Rep-Feo cells were cultured with various concentrations of 2-HP-β-CyD for 48 h *(lower panel)*. Data are means ± SDs of triplicates from 2 independent experiments. *B*, Recombinant firefly luciferase incubated with various concentrations of 2-HP-β-CyD in the culture medium at 37°C for 48 h. The medium was collected and subjected to luciferase analysis. Data are means ± SDs of triplicates from 2 independent experiments.

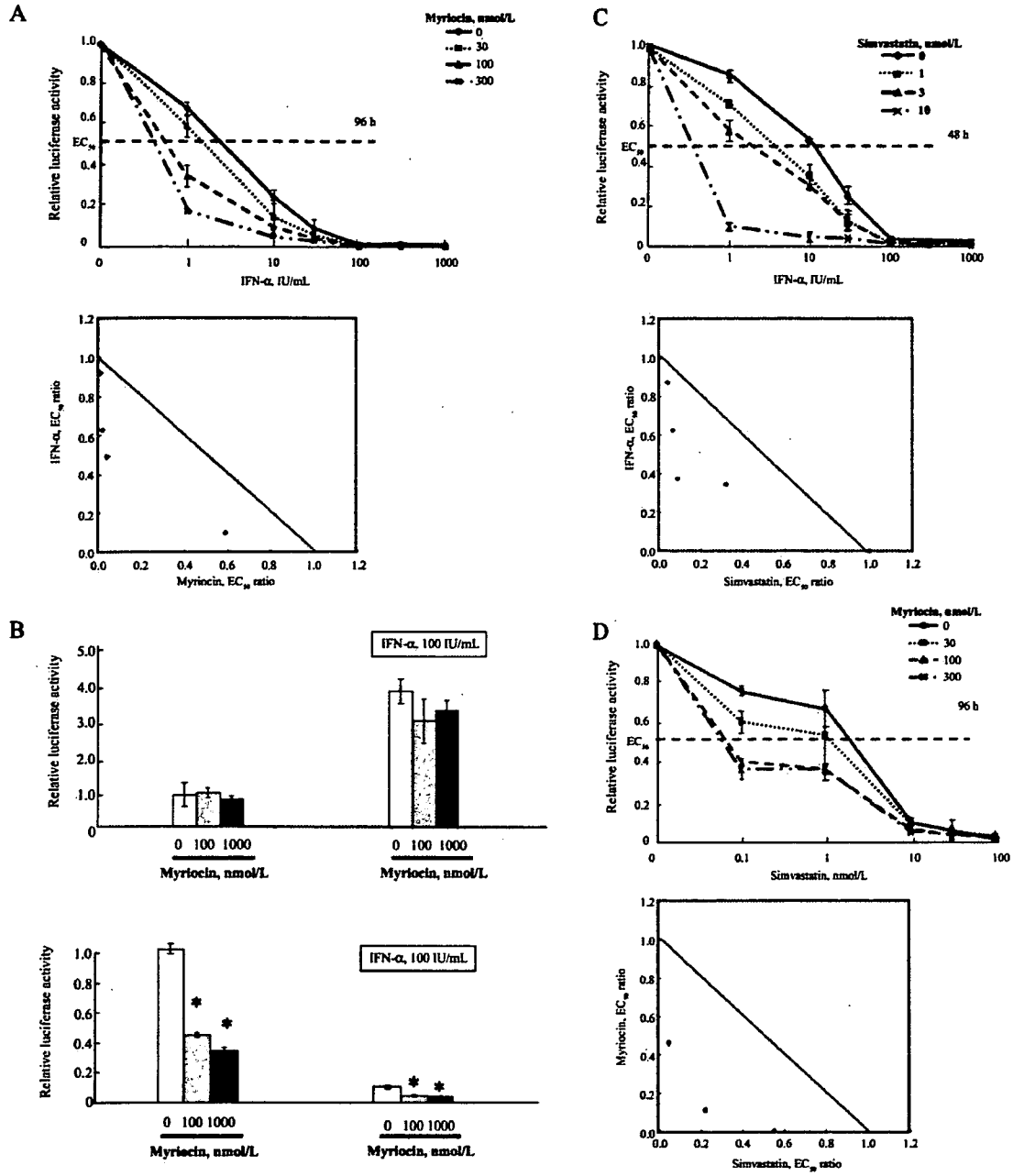

Figure 5. Synergistic inhibitory effects of myriocin with interferon (IFN), simvastatin with IFN, and myriocin with simvastatin. *A*, Synergistic inhibitory effect of myriocin with IFN on hepatitis C virus replication. Huh7/Rep-Feo cells were treated with combinations of myriocin and IFN at various concentrations. The upper panel shows the relative dose-inhibition curves of IFN plotted for each fixed concentration of myriocin (0, 30, 100, and 300 nmol/L). The lower panel shows the isobologram analysis for the combination of myriocin with IFN. *B*, IFN-stimulated response element (ISRE) promoter activity induced by a combination of myriocin with IFN. Huh7/Rep-Feo cells transfected with ISRE–*Renilla* luciferase were cultured with various concentrations of myriocin alone *(left)* or with 100 IU/mL IFN *(right)*. The upper panel demonstrates the ISRE–*Renilla* luciferase activity at 48 h after transfection. The lower panel demonstrates the firefly luciferase activity of the Huh7/Rep-Feo cells, reflecting hepatitis C virus (HCV). Data are means ± SDs of triplicates from 2 independent experiments. $*P < .05$. *C*, Synergistic inhibitory effect of simvastatin with IFN on HCV replication. *D*, Synergistic inhibitory effect of simvastatin and myriocin on HCV replication.

decreased to almost 60% of the control at 48 and 96 h after treatment. However, no evident synergistic inhibitory effect was observed (figure 6*A*). To clarify the inhibitory effect of myriocin on JFH-1 HCV, we performed Western blot analysis for JFH-1 HCV proteins. As demonstrated in figure 6*B*, a substantial decrease in the core and NS3 proteins of JFH-1 HCV was observed 96 h after treatment with myriocin, confirming the RT-PCR results (figure 6*B*).

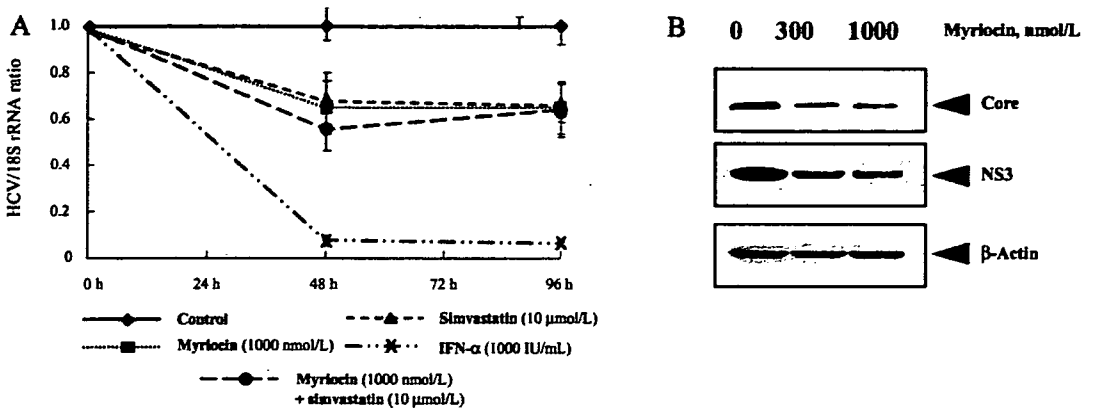

Figure 6. Suppression of JFH-1 hepatitis C virus (HCV) replication by myriocin and simvastatin. *A*, Cells containing JFH-1 HCV treated for 96 h with 1000 nmol/L myriocin, 10 μmol/L simvastatin, 1000 IU/mL IFN, or a combination of 1000 nmol/L myriocin and 10 μmol/L simvastatin. The cells were collected at 48 and 96 h, and the JFH-1 HCV RNA level relative to 18S rRNA was analyzed by real-time polymerase chain reaction. Values are shown as the ratios to negative control values (cells receiving no treatment) and as means ± SDs. *B*, Western blotting. Cells containing JFH-1 HCV were treated with 300 or 1000 nmol/L of myriocin and harvested at 96 h after administration. Ten micrograms of total cellular protein was electrophoresed in each lane. Anti-core monoclonal antibody (MAb) and anti-NS3 MAb were used as the primary antibodies to detect JFH-1 HCV proteins. β-Actin was detected as an internal control. Lane 1, no myriocin; lane 2, 300 nmol/L myriocin; and lane 3, 1000 nmol/L myriocin.

DISCUSSION

In the present study, we demonstrated that the sphingomyelin synthesis inhibitor myriocin suppressed not only replication of a subgenomic HCV-1b replicon but also replication of the JFH-1 strain of infectious genotype 2a HCV. We also demonstrated that simvastatin suppressed replication of both a subgenomic HCV-1b replicon and JFH-1 HCV. When a subgenomic HCV-1b replicon was used, the anti-HCV activity of both myriocin and simvastatin was enhanced synergistically with IFN. Moreover, when myriocin and simvastatin were used together, their anti-HCV activity was enhanced synergistically.

What is the mechanism by which myriocin suppresses viral replication? Because myriocin is a specific inhibitor of SPT, which catalyzes the first committed step of sphingomyelin biosynthesis, we speculated that myriocin exerts its action by inhibiting production of downstream substrates, especially sphingomyelin. The findings that siRNA targeted against SPT decreased HCV replication and that HCV replication was restored by addition of phytosphingosine, a precursor of sphingomyelin, demonstrated that the effect was specific to SPT activity. Moreover, the fact that treatment of Huh7 cells with myriocin did not enhance the ISRE promoter activity indicated that the inhibitory effects of myriocin were independent of those of IFN. It is known that intracellular replication of most RNA viruses occurs on certain membrane structures—including the endoplasmic reticulum, the Golgi apparatus, endosomes, and lysosomes—by making replication complexes at these sites [5–7]. For HCV, it has been reported by several groups that in vitro replication activity is located in the membrane fractions of cultured cells [26–28]. In addition, newly synthesized HCV RNA and the nonstructural proteins in replicon cells were colocalized in detergent-resistant membrane structures, most likely lipid rafts [18]. Caveolin-2, a lipid raft protein, was also shown to colocalize with the nonstructural proteins [18]. According to these findings, the HCV replication complex machinery is considered to form on a lipid raft. Therefore, because sphingomyelin is the major component of the lipid raft, it is plausible to speculate that myriocin disrupted lipid raft formation and inhibited HCV replication.

Cholesterol is another major component of lipid rafts and might also be targeted for anti-HCV therapy. Because cholesterol is synthesized in the mevalonate pathway, an inhibitor of the pathway might act to disrupt lipid rafts. In accordance with this concept, statins, which are HMG-CoA reductase inhibitors, already have been reported to suppress the replication of genomic and subgenomic HCV-1b replicons [15, 16]. In the present study, we also confirmed that simvastatin suppressed replication of a subgenomic HCV-1b replicon without toxicity. Moreover, we showed for the first time that the suppressive effect was also observed in an infectious HCV-2a model of JFH-1 HCV. Meanwhile, recent studies found that the effect of statins was attributable to inhibition of geranylgeranylation rather than depletion of cholesterol, because addition of geranylgeraniol rescued HCV suppression induced by statins [15]. However, although geranylgeranylation might play a role in HCV regulation, the importance of cholesterol itself has not yet been determined. To clarify further the role played by cholesterol in HCV replication, we investigated the effect of 2-HP-β-CyD, which is known to deplete cholesterol directly from cells. As demonstrated in figure 4, specific suppression of HCV replication by 2-HP-β-CyD indicated the importance of cholesterol itself for HCV replication. It is unlikely that these agents suppressed replication of the subgenomic replicon through inhibi-

tion of encephalomyocarditis virus internal ribosome entry site (EMCV-IRES) activity, because they also significantly suppressed replication of a full-length genomic HCV (JFH-1 HCV) that does not include EMCV-IRES (figure 6*A*; data for 2-HP-β-CyD not shown).

Although we observed an inhibitory effect of myriocin and simvastatin on both the subgenomic HCV-1b replicon and JFH-1 HCV, there was a difference in efficacy between the 2 HCV systems; the subgenomic HCV-1b replicon was more sensitive to and was more strongly inhibited by either agent alone or in combination, compared with JFH-1 HCV. This result was unexpected, because we had speculated that these agents might be effective irrespective of the viral isolate if these agents targeted not the virus itself but rather host factors, such as lipid rafts. However, there are several differences between these 2 systems, and we cannot directly compare the results. In particular, the subgenomic HCV replicon lacks viral structural proteins and has only an HCV RNA intracellular replication step, whereas JFH-1 HCV includes all steps of the HCV life cycle. We do not know the precise target of the agents, and further studies are still needed.

Is it really possible to use these agents in clinical HCV treatment? Especially because statins have been used in the treatment of hyperlipidemia for many years worldwide with proven safety, it would be ideal if we could use statins as one therapeutic application for anti-HCV therapy. Most recently, O'Leary et al. [29] undertook a human pilot study and treated 10 patients with atorvastatin for 12 weeks; they reported that there was no statistically significant change in HCV RNA levels compared with pretreatment levels. The reason for the discrepancy between in vitro and in vivo findings is unknown. However, as also discussed by O'Leary et al., the most plausible explanation for this discrepancy is that the plasma concentrations of atorvastatin after a conventionally approved dose were unlikely to reach those found to be effective in cell culture medium. According to their calculations, to inhibit HCV RNA replication the plasma atorvastatin concentration should be 3 logs higher than that achieved by a conventional dose. However, even though it would be difficult to inhibit HCV RNA replication with statins alone, a clinical antiviral effect might be still achieved if statins were used in combination with IFN (or myriocin), because a synergistic effect was observed in our in vitro study. To determine the synergistic effect in vivo, however, further clinical trials are needed. On the other hand, although promising in vitro, myriocin has not yet been used for human clinical diseases, and its safety has not been established. However, in chimeric mice, the plasma myriocin concentration equivalent to culture medium effectively inhibited HCV RNA replication, and drug toxicity was not observed at this concentration [30]. This finding suggested the possibility that myriocin could be used in vivo, although further studies are needed.

In conclusion, we have demonstrated that inhibition of the sphingomyelin synthesis pathway and the mevalonate pathway both effectively suppressed HCV replication in vitro, indicating that lipid metabolism could be an important target for new anti-HCV therapies.

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Griseofulvin, an oral antifungal agent, suppresses HCV replication in vitro.

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Running title: Griseofulvin suppresses HCV RNA replication.

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ABSTRACT

Hepatitis C virus (HCV), which infects an estimated 170 million people worldwide, is a major cause of chronic liver disease. Currently standard therapy for chronic hepatitis C is based on pegylated interferon (IFN)-α in combination with ribavirin. However, success rates remain at about 50%. Therefore, alternative agents are needed for the treatment of HCV infection. Here, using an HCV-1b subgenomic replicon cell culture system (Huh7/Rep-Feo), we found that griseofulvin, an oral antifungal agent, suppressed HCV RNA replication and protein expression in a dose dependent manner. We also found that griseofulvin suppressed the replication of infectious HCV JFH-1. A combination of IFN-α and griseofulvin exhibited a synergistic inhibitory effect in Huh7/Rep-Feo cells. Furthermore, we found that griseofulvin blocked the cell cycle at G2/M in the HCV subgenomic replicon cells, but did not inhibit HCV internal ribosome entry site (IRES)-dependent translation. In conclusion, our results suggest that griseofulvin may represent a new approach to the development of a novel therapy for HCV infection.

KEY WORD: Cell cycle, Griseofulvin, HCV IRES, HCV replicon, JFH-1

INTRODUCTION

Hepatitis C virus (HCV) is an etiologic agent of chronic liver disease (1, 2) and it is estimated that approximately 170 million people worldwide are infected with the virus. Chronic hepatitis C can lead to severe liver diseases, including fibrosis, cirrhosis and hepatocellular carcinoma (3). With advancements in HCV therapy, including the most recent combination of pegylated-IFN α and ribavirin, up to one half of patients achieve a sustained virologic response. However, the remainder cannot clear the virus, demonstrating a great need for more powerful therapeutic modalities (4).

Investigations have been hampered by the lack of an efficient HCV cell culture system. In 1999, the establishment of an HCV subgenomic replicon cell culture system improved the situation. The subgenomic replicon RNA is composed of the HCV 5'-untranslated region (UTR) containing the internal ribosomal entry site (IRES), a neomycin phosphotransferase (neo) gene and the HCV nonstructural (NS) proteins 3 through 5B under the control of an encephalomyocarditis virus (EMCV) IRES, followed by the HCV 3'-UTR (5). An HCV replicon carrying, in addition to the selectable marker, a gene encoding luciferase, can be used to screen a large number of compounds for antiviral activity (6, 7, 8). The recent development of an in vitro HCV