NS4B has been reported to induce an unfolded protein response or ER stress (Zheng *et al.*, 2005). Accumulation of unfolded or misfolded proteins in the ER is detected by three ER sensor proteins, ATF6, IRE-1 and PKR-like ER kinase (PERK), and triggers the unfolded protein response as a stress response and induces expression of molecular chaperon proteins, global shut-off of protein translation and apoptotic cell death (Mori, 2000). Therefore, it may be possible that transgenic overexpression of NS4B induces ER stress and suppresses overall protein synthesis, including that of IFNs. In our experiments, however, NS4B suppressed the ISRE-mediated IFN gene activation but did not suppress non-specific protein expression, as demonstrated by *Renilla* luciferase activity in the control plasmid driven by the herpes simplex thymidine kinase promoter. In addition, the growth and viability of cells that overexpressed NS4B did not differ from untransfected cells or from those transfected with the other HCV proteins. IL-8 overproduction induced by ER stress was not observed in our NS4B-overexpressing cells (Fig. 4c). These findings indicated that the inhibitory effect of NS4B is specific to the IFN induction pathway and is not a non-specific effect through ER stress.

In conclusion, we have shown that dsRNA-induced IFN expression was suppressed by NS4B. These virus–host interactions probably contribute to HCV persistence and to the pathogenesis of HCV-associated liver disease.

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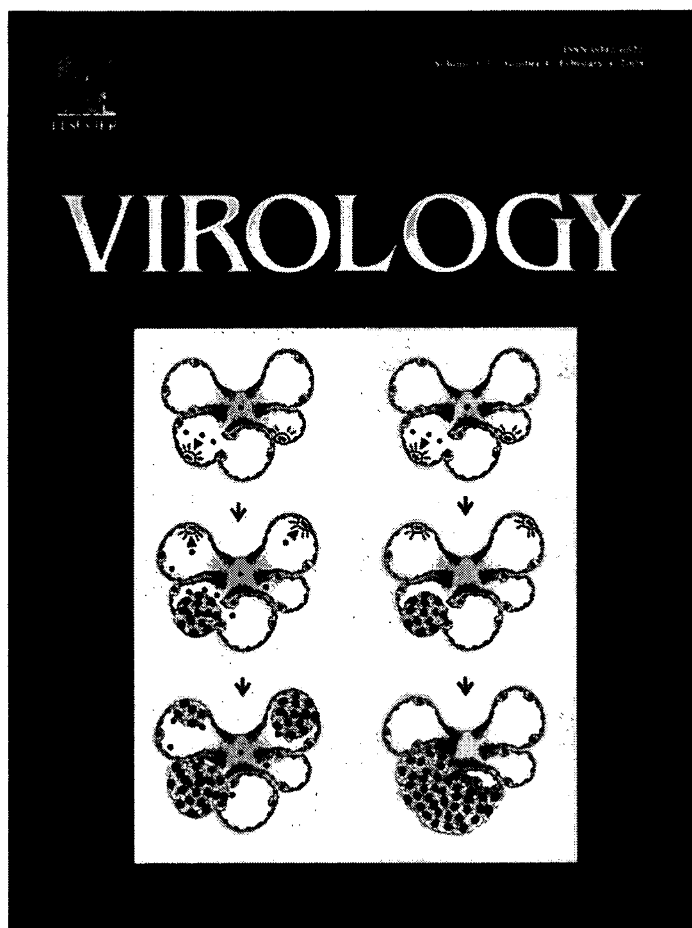

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Development of plaque assays for hepatitis C virus-JFH1 strain and isolation of mutants with enhanced cytopathogenicity and replication capacity

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Abstract

HCV culture *in vitro* results in massive cell death, which suggests the presence of HCV-induced cytopathic effects. Therefore, we investigated its mechanisms and viral nucleotide sequences involved in this effect using HCV-JFH1 cell culture and a newly developed HCV plaque assay technique. The plaque assay developed cytopathic plaques, depending on the titer of the inoculum. In the virus-infected cells, the ER stress markers, GRP78 and phosphorylated eIF2-alpha, were overexpressed. Cells in the plaques were strongly positive for an apoptosis marker, annexin V. Isolated virus subclones from individual plaque showed greater replication efficiency and cytopathogenicity than the parental virus. The plaque-purified virus had 9 amino acid substitutions, of which 5 were clustered in the C terminal of the NS5B region. Taken together, the cytopathic effect of HCV infection involves ER-stress-induced apoptotic cell death. Certain HCV genomic structures may determine the viral replication capacity and cytopathogenicity.
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Keywords: HCV-JFH1; HCV cell culture; Plaque assay; ER stress; Unfolded protein responses; Apoptosis; NS5B RNA-dependent RNA polymerase

Introduction

Molecular analyses of the HCV life cycle, virus–host interactions, and mechanisms of liver cell damage by the virus are not understood completely, mainly because of the lack of cell culture systems. These problems have been partly overcome by the development of the HCV subgenomic replicon (Lohmann et al., 1999) and HCV cell culture systems (Lindenbach et al., 2005; Wakita et al., 2005; Zhong et al., 2005). The HCV-JFH1 strain, which is a genotype 2a clone derived from a Japanese fulminant hepatitis patient that can replicate efficiently in Huh7 cells (Kato et al., 2003; Kato et al., 2001), has contributed to the establishment of the HCV cell culture system. Furthermore, the Huh7-derived cell lines, Huh-7.5 cells, Huh-7.5.1, and Lunet cells allow production of higher viral titers and have a higher permissiveness for HCV (Koutsoudakis et al., 2007; Lindenbach et al., 2005; Zhong et al., 2005). The HCV-JFH1 cell culture system now allows us to study the complete HCV life cycle: virus–cell entry, translation, protein processing, RNA replication, virion assembly, and virus release.

HCV belongs to the family *Flaviviridae*. One of the characteristics of the *Flaviviridae* is that they cause cytopathic effects (CPE). The viruses have positive strand RNA genomes of ~10 kilobases that encode a polyprotein of ~3000 amino acids.

Abbreviations: HCV, hepatitis C virus; IFN, interferon; CPE, cytopathic effect; ER, endoplasmic reticulum; UPR, unfolded protein response; PFU, plaque-forming unit; FFU, focus-forming unit; RdRp, RNA-dependent RNA polymerase.

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The protein is post-translationally processed by cellular and viral proteases into at least 10 mature proteins. The viral nonstructural proteins accumulate in the ER and direct genomic replication and viral protein synthesis (Bartenschlager and Lohmann, 2000; Jordan et al., 2002; Mottola et al., 2002). It has been reported that Japanese encephalitis virus (JEV), bovine viral diarrhea virus (BVDV), and dengue viruses (DEN) cause apoptotic cell death (Despres et al., 1996; He, 2006; Jordan et al., 2002; Su et al., 2002). In addition, certain amino acid substitutions in the viral structural or nonstructural proteins affect the replication and cytopathogenicity of these viruses substantially (Blight et al., 2000; Maekawa et al., 2004; Mendez et al., 1998). It has been recently reported that HCV-JFH1-transfected Huh-7.5.1 cells died when all of the cells were infected and intracellular HCV-RNA reached maximum levels (Zhong et al., 2006). These findings suggest HCV-induced cytopathogenicity. However, the mechanisms have not been well documented.

In the present study, we investigated the cellular effects of HCV infection and replication using the HCV-JFH1 cell culture system. Here, we report that HCV-JFH1-transfected and infected cells show substantial CPE that are characterized by massive apoptotic cell death with the expression of several ER stress-induced proteins. Taking advantage of the CPE, we developed a plaque assay for HCV in cell culture and isolated subclones of HCV that showed enhanced replication and cytopathogenicity. We have demonstrated that these viral characters were determined by mutations at certain positions in the structural and nonstructural regions of the HCV genome, especially the NS5B region.

Results

Production of infectious HCV-JFH1 by JFH1-RNA transfected cells

After transfection of HCV-JFH1 RNA into Huh-7.5.1 cells, intracellular HCV RNA and HCV antigen were continuously detectable in the cell culture (Fig. 1A). Furthermore, the culture supernatant from the transfected cells was positive for core protein, which reached maximum levels at 14 days post-transfection and was continuously detectable during the cell culture (Fig. 1A, black bar). The culture supernatant was readily infectable to naive Huh-7.5.1 cells (data not shown). Immunofluorescence assay showed that 48% of the JFH1-RNA-transfected cells and 42% of the virus-infected cells were positive for HCV core protein. These results demonstrate that the transcript of HCV-JFH1 clone replicates efficiently and produces infectious virus particles in cells, as reported previously (Wakita et al., 2005; Zhong et al., 2005).

Hepatitis C virus infection induced cytopathic effects in vitro

By the seventh day post-transfection, the production of virus decreased concomitant with massive cell death and then cell growth gradually recovered. At 14–16 days post-transfection, the levels of HCV-RNA and core antigen reached maximum (Fig. 1). In the JFH1 mutants JFH1/GND and JFH1/ΔE1-E2-RNA-transfected Huh-7.5.1 cells, the viral replication and host cell death were not observed. The massive cell death after HCV-

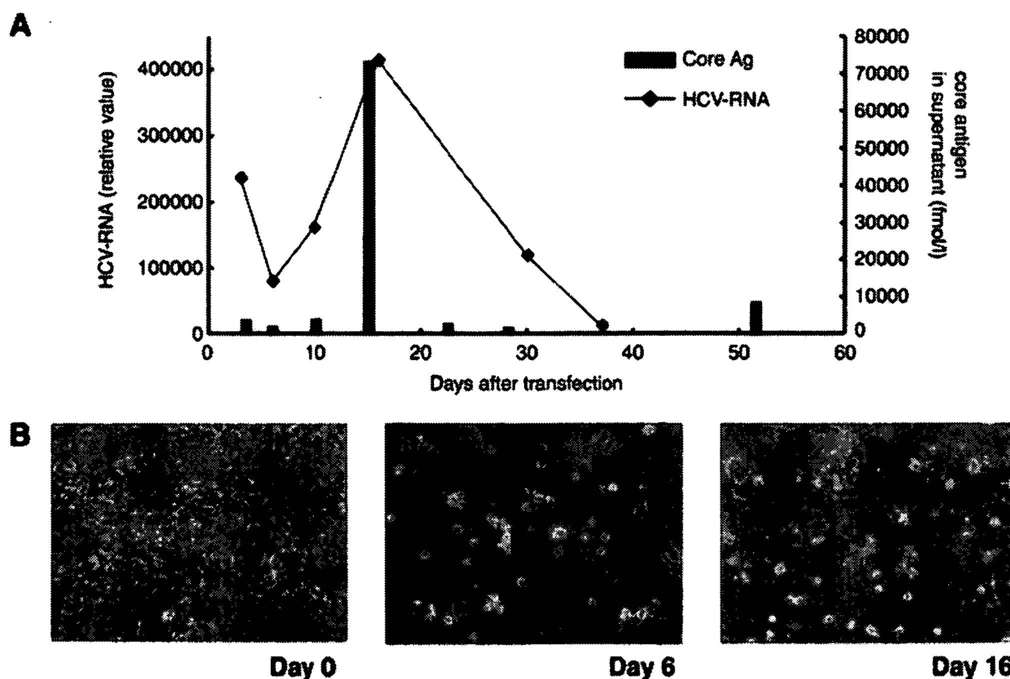

Fig. 1. Replication of HCV-JFH1 RNA in JFH1-transfected and infected Huh-7.5.1 cells. (A) Levels of HCV-RNA in JFH1 RNA-transfected cells. After transfection of the *in vitro* transcribed JFH1-RNA into Huh-7.5.1 cells, total cellular RNA was isolated on indicated days and quantified by real-time RT-PCR. Furthermore, the culture supernatant of JFH1-RNA transfected Huh-7.5.1 cells was collected on the days indicated and the levels of core antigen in the culture supernatant were measured (black bar). (B) HCV-JFH1-transfected Huh-7.5.1 cells (the left panel, day 0; the middle panel, day 6; the right panel, day 16).

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JFH1 transfection led us to suspect the occurrence of CPE, produced in host cells by HCV infection and replication. A plaque assay was performed (see Materials and methods) to investigate the morphological CPE following HCV-JFH1 infection. Culture supernatants from JFH1-transfected cells were diluted serially and inoculated onto uninfected Huh-7.5.1

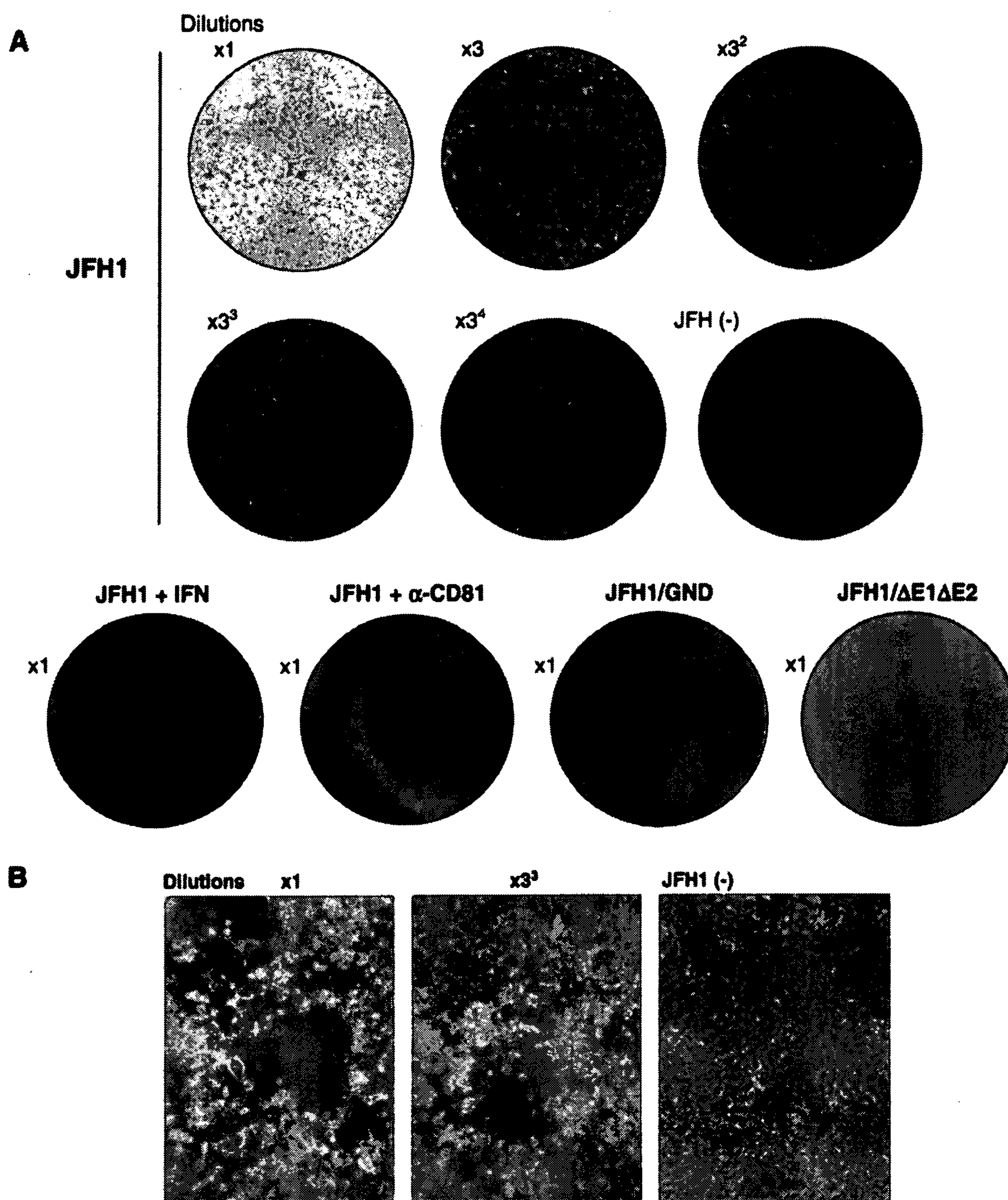

Fig. 2. The cytopathic effects of HCV-JFH1 *in vitro*. (A) Plaque assay. Upper panel, Huh-7.5.1 cells were seeded in collagen-coated 60-mm-diameter plates at density of 4×10^5 cells per plates and were incubated at 37 °C under 5.0% CO_2 (as described above). After overnight incubation, HCV-infected culture 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 infected cells were overlaid with 8 ml of culture medium containing 0.8% methylcellulose and incubated under normal conditions. After 7 days culture, formation of cytopathic plaque was visualized by staining with 0.08% crystal violet solution. Lower panel, JFH1+IFN; after infection of the virus supernatant, the cells were cultured in the presence of 50 U/ml interferon-alpha. JFH1+a-CD81, Huh-7.5.1 cells were pretreated with 10 μg/plate of anti-CD81 antibody. After incubation at 37 °C for 30 min, anti-CD81 was removed, the cells were washed with PBS, and the HCV-JFH1 culture supernatant was transferred. After ~5 h incubation, the supernatant was removed and the infected cells were overlaid with 8 ml of culture medium containing 0.8% methylcellulose and controls for the plaque assay were also performed with the JFH1/GND or JFH1/ΔE1-E2 culture supernatant. (B) The cytopathic plaques were observed by phase-contrast microscopy at day 7 after HCV-JFH1 infection.

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cells. The cells were subsequently cultured in medium containing agarose. Almost 10 days after the inoculation, viable cells were stained and plaques were visualized (Fig. 2A, upper panel). HCV-inoculated cell cultures developed plaques as unstained areas that were accompanied by round cells in the periphery (Fig. 2B). The formation of cytopathic plaques was not observed in a parental Huh7 cell line (data not shown). Immunocytochemistry of the foci revealed the presence of HCV core-positive cells surrounding the cytopathic plaques (Fig. 3A). Culture of the HCV-inoculated cells in the presence of interferon-alpha (50 U/ml) completely abolished the formation of plaques (Fig. 2A, lower panel). Uninfected Huh-7.5.1 cells (Fig. 2A, upper panel), Huh-7.5.1 cells treated with anti-CD81 antibody before HCV-JFH1 infection and JFH1/GND or JFH1/ΔE1-E2-transfected cell cultures did not develop plaques (Fig. 2A, lower panel). These findings suggest that HCV-infected cells develop cytopathic plaques depending on the quantity of the inoculums and that HCV replication, viral protein expression and the propagation of viral particles were the features of these plaques.

HCV-JFH1 infection induced host-cell apoptosis

We next determined whether the cytopathic effects of HCV-JFH1 replication include process of apoptotic cell death. Cells including plaques were double-stained with annexin V-FITC and PI. The ligand of annexin V, phosphatidylserine, is normally confined to the cytoplasmic leaflets of the plasma membrane. In the early phase of apoptosis, phosphatidylserine is exposed on the outer surface of the plasma membrane, which enables detection of FITC-labeled annexin V. As shown in Fig. 4, the fluorescence of annexin V was observed in the cells around the plaques. Foci of apoptotic cells were scattered in the plaques. On the other hand, the expression of annexin V was slightly detectable in the subgenomic replicon-harboring cells, though they were at the same level as the uninfected Huh-7.5.1 cells and the cell death was not observed. Therefore, the cells that express HCV subgenomic replicons did not induce apoptotic cell death. These findings demonstrate that the cytopathic effects of HCV replication and the particle formation induce apoptotic cell death.

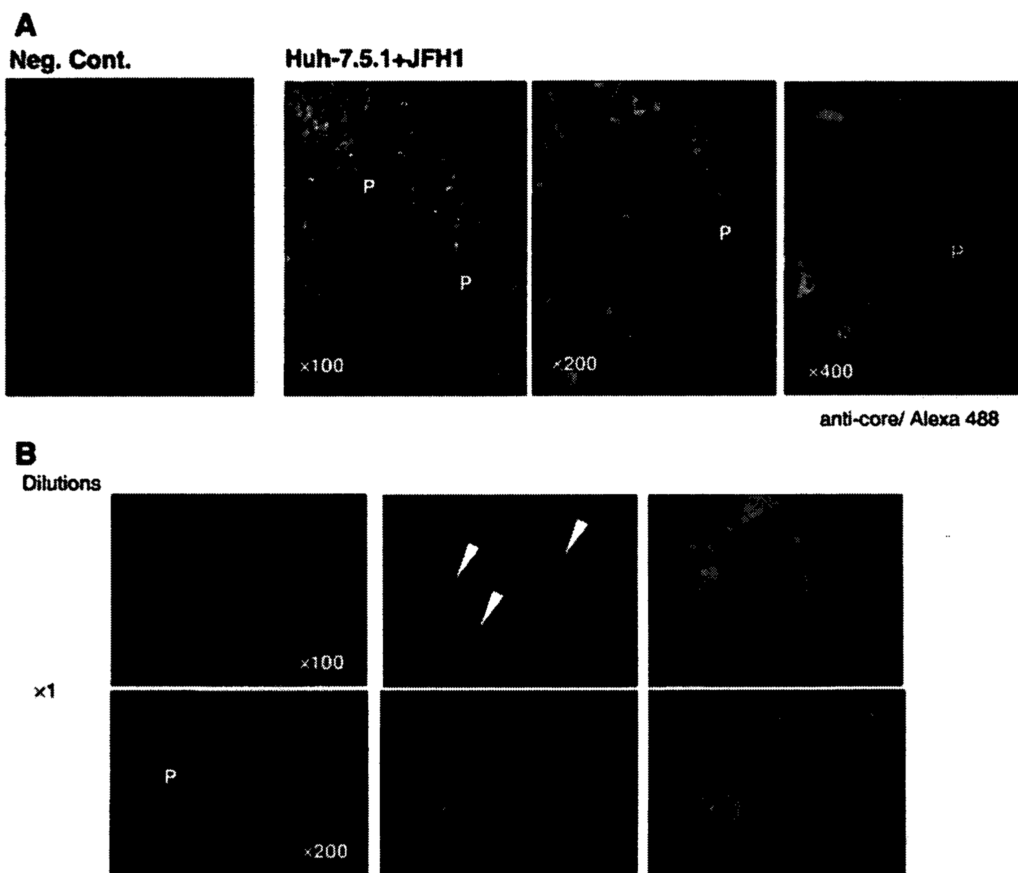

Fig. 3. Immunofluorescence detection of HCV core protein in cytopathic plaques. (A) The HCV-JFH1 culture supernatant was transferred onto uninfected Huh-7.5.1 cells, plated on 22 mm-round micro cover glasses in 60-mm-diameter plates at density of 2×10^5 cells per plate. After ~5 h incubation, the supernatant was replaced with medium containing 0.8% methylcellulose. Immunocytochemistry was performed 12 days after infection. A 'P' indicates a cytopathic plaque. (B) Immunofluorescence detection of HCV-positive foci and 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 and the infected cells were cultured in 60-mm-diameter plate with medium containing 0.8% methylcellulose. Immunocytochemistry was performed 5 days after infection using mouse anti-core antibody. The infectivity and cytotoxicity were quantified by counting HCV-positive foci (FFU/ml) and cytopathic plaque (PFU/ml) respectively. White arrowheads indicate HCV-positive foci.

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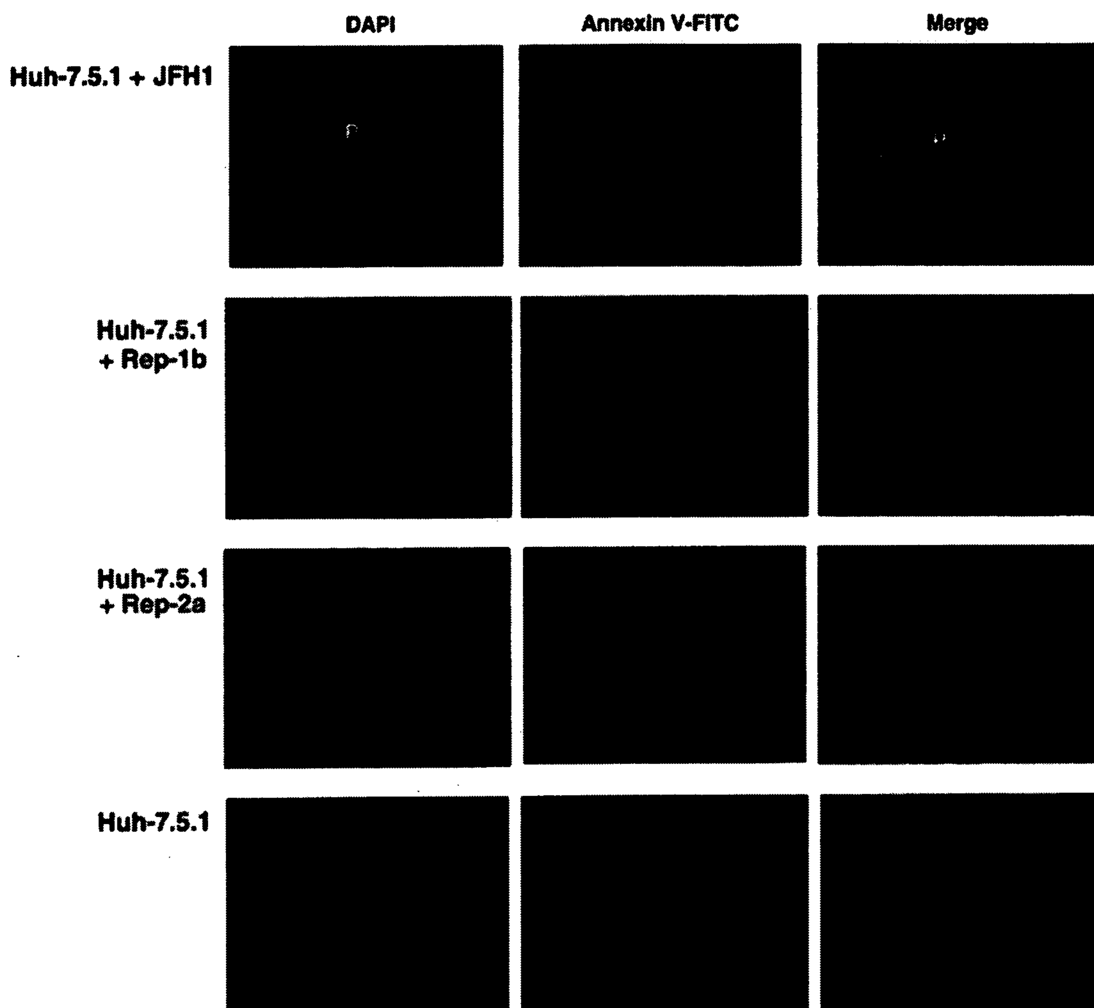

Fig. 4. HCV-JFH1 infection induces apoptosis and leads to plaque formation. The HCV-JFH1 culture supernatant was transferred onto uninfected Huh-7.5.1 cells plated on 22-mm round micro cover glasses in 60-mm-diameter plates at density of 2×10^5 cells per plate. After ~5 h incubation, the supernatant was replaced with medium containing 0.8% methylcellulose. Thirteen days after infection, cover glasses were incubated with 100 µl of staining solution containing Annexin V-FITC at room temperature for 10 to 15 min. The cells that express HCV subgenomic replicons were also incubated and stained with Annexin V-FITC. Rep 1b, Rep-Feo; Rep 2a, SGR-JFH1 (see Materials and methods).

JFH1 replication activates expression of ER stress-related proteins

Cellular stresses such as virus infections prevent protein folding and maturation in the endoplasmic reticulum (ER) and result in the accumulation of misfolded proteins (ER stress) (Kaufman, 1999; Pahl, 1999), triggering the unfolded protein response (UPR). The UPR leads to global shut-off of protein translation and to apoptotic cell death (Ferri and Kroemer, 2001; Mori, 2000; Munro and Pelham, 1986). We and other groups have previously reported that subgenomic or genomic HCV replication induces ER stress and triggers UPR (Nakagawa et al., 2005; Tardif et al., 2002). Therefore, we next studied expression of the ER stress-related proteins, GRP78 and phosphorylated eIF2-alpha, in JFH1-infected cells (Fig. 5). GRP78 is one of the ER chaperones whose expression is induced by ER stress through cleavage and nuclear translocation of ATF6. The eIF2-alpha is phosphorylated by PER-like ER kinase (PERK) on ER stress, causing direct global inhibition of initiation of protein translation (Harding et al., 1999). Huh-7.5.1 cells were infected with HCV-JFH1 supernatant and harvested on the fourth and seventh days post-infection (Fig. 5). As the expression of HCV core protein increased, expression levels of GRP78 and phosphorylated eIF2-alpha also increased substantially. Suppression of virus replication by interferon-alpha treatment led to a decrease of cellular GRP78 and phosphorylated eIF2-alpha. Interferon-alpha treatment did not eliminate the expression of HCV completely, though the levels of core and phosphorylated eIF2-alpha expression apparently decreased compared with the JFH-1 infected Huh-7.5.1 cells at seventh days post-infection. These findings demonstrated that HCV-JFH1 infection induced ER stress.

Persistence of ER stress activates apoptosis signaling pathways, including the induction of C/EBP homologous protein (CHOP) and activation of JNK kinase and caspase12, leading to cell death (Ferri and Kroemer, 2001). As shown in Fig. 5, the

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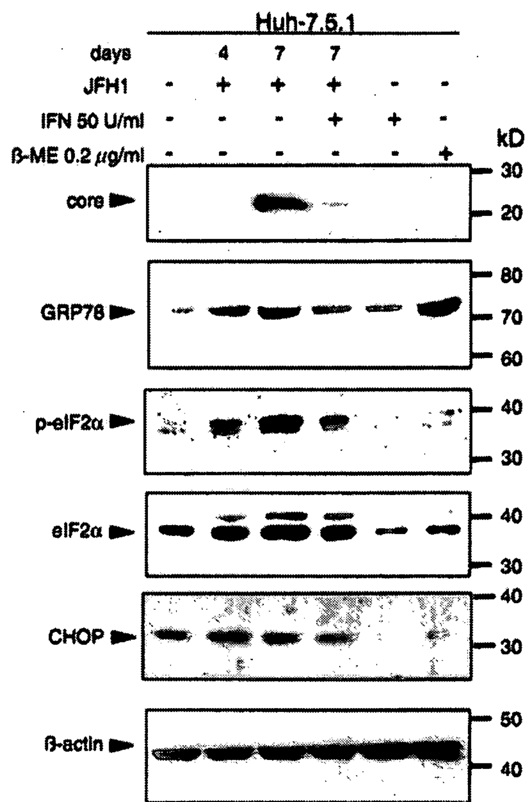

Fig. 5. Expression of ER stress-related proteins in HCV-JFH1 infected cells. The supernatant of JFH1-transfected Huh-7.5.1 cells was transferred onto uninfected Huh-7.5.1 cells. The cells were harvested at 4 and 7 days after infection. The JFH1-infected cells were also cultured with interferon (50 U/ml) or 2-mercaptoethanol (0.2 µg/ml) and harvested after 48 h after treatment. 2-Mercaptoethanol was used as a positive control to induce ER stress (Nakagawa et al., 2005). Western blotting was performed using anti-core, anti-GRP78, anti-phospho-eIF2-alpha (p-eIF2α), anti-eIF2-alpha, anti-GADD153/CHOP, and anti-beta-actin antibodies. β-ME, 2-mercaptoethanol.

level of CHOP expression was apparently increased in JFH1-infected Huh-7.5.1 cells.

To determine whether ER stress contributes to the formation of cytopathic plaques, JFH1-infected cells were incubated in methylcellulose-containing medium and double immunofluorescence staining of the plaques was performed. As shown in Fig. 6, overexpression of GRP78 was colocalized with HCV-core-positive cells with and without CPE. Together with the result shown in Fig. 4, these findings suggest that ER stress is induced in the HCV-JFH1-infected cells and these responses may be involved in development of apoptosis and the formation of cytopathic plaques.

A cytopathic clone could be isolated and this had acquired a high infection efficiency and increased cytopathogenicity

The plaque assay enabled differential quantification of viral infectivity and cytopathogenicity by the immunofluorescence detection of HCV core protein in JFH1-infected, plaque-developed cultures. The number of plaques, as well as infectious foci, was linearly proportional to the dilution of an inoculum (Fig. 7B). It was revealed that only a few populations of HCV-positive foci developed cytopathic plaques (Fig. 3B and Table 1). The infectious focus-forming units and plaque-forming units were 5.6×10^3 FFU/ml and 9.7×10^2 PFU/ml, respectively (Table 1).

To determine whether the difference between the cytopathic and noncytopathic HCV-JFH1 replication might be attributable to viral factors, we isolated clones from each cytopathic plaque. JFH1-infected Huh-7.5.1 cells were incubated in DMEM containing methylcellulose. Cytopathic plaques became visible at ~1 week after inoculation. We isolated cells from each plaque using a cloning cylinder, subcultured, and transferred supernatant onto uninfected Huh-7.5.1 cells. To our surprise, infection of naive cells with plaque-derived supernatants led to massive cell death at 10 days post-infection (Fig. 8A). The supernatant of these cells was transferred again onto uninfected Huh-7.5.1 cells again. Immunofluorescence assay revealed that almost 100% of the cells were positive for HCV core protein (Fig. 8B). The infectivity and cytopathogenicity of this isolated plaque (Pl #1) were 4.9×10^3 FFU/ml and 3.0×10^3 PFU/ml respectively (Table 1), much higher than the parental JFH1 clone. Moreover, the ratio of PFU to FFU in a plaque-isolated clone (Pl #1) was significantly higher than that of parental JFH1 clone (0.58 and 0.17 respectively) (Table 1 and Figs. 7B and C). We next performed an infection experiment of the parental JFH1 and a plaque-derived clone by adjusting infectious titers of the inocula by HCV core antigen levels. As shown in Fig. 8C, virus from cytopathic plaque (Pl #1, #2, #3) showed significantly higher elevation of core antigen levels in supernatants than the parental JFH1 in every time point. The second round isolation of plaques from the Pl #1 subclone (Pl #1-1, #1-2 and #1-3 in the Table 3) showed consistently higher replication efficiency and cytopathogenicity. These results indicated that JFH1 subclones isolated from cytopathic plaques showed significantly higher infection efficiency and greater cytopathic effects than the original JFH1.

The isolated plaque had amino acid substitutions clustered in the NS5B region

To determine whether there are viral mutations in the cytopathic JFH1 subclone (Pl #1), we performed sequence analyses. As shown in Table 2, 11 nucleotide changes were found in the cytopathic plaque, and 9 of these were non-synonymous mutations (81.8%). In particular, 6 of the 11 mutations (9153, 9232, 9293, 9295, 9353, and 9355) were clustered in the C terminal half of the NS5B region. We also performed sequence analyses of the Pl #1-isolated subclones, Pl #1-1, #1-2, and #1-3, and other clones that had been independently isolated from different plaques, Pl #2, #3, and #4 (Table 3). Those subclones showed similar mutations within NS5B region. The C2438S, P2934S, and S3001N substitutions were redundantly appeared in the 4 plaque-isolated clones and in all three Pl #1-derived subclones. In contrast, no mutations were found in the virus from infectious foci without plaque formation. These results showed an evidence that certain amino acid mutations were directly associated with the viral replication efficiency and cytopathogenicity.

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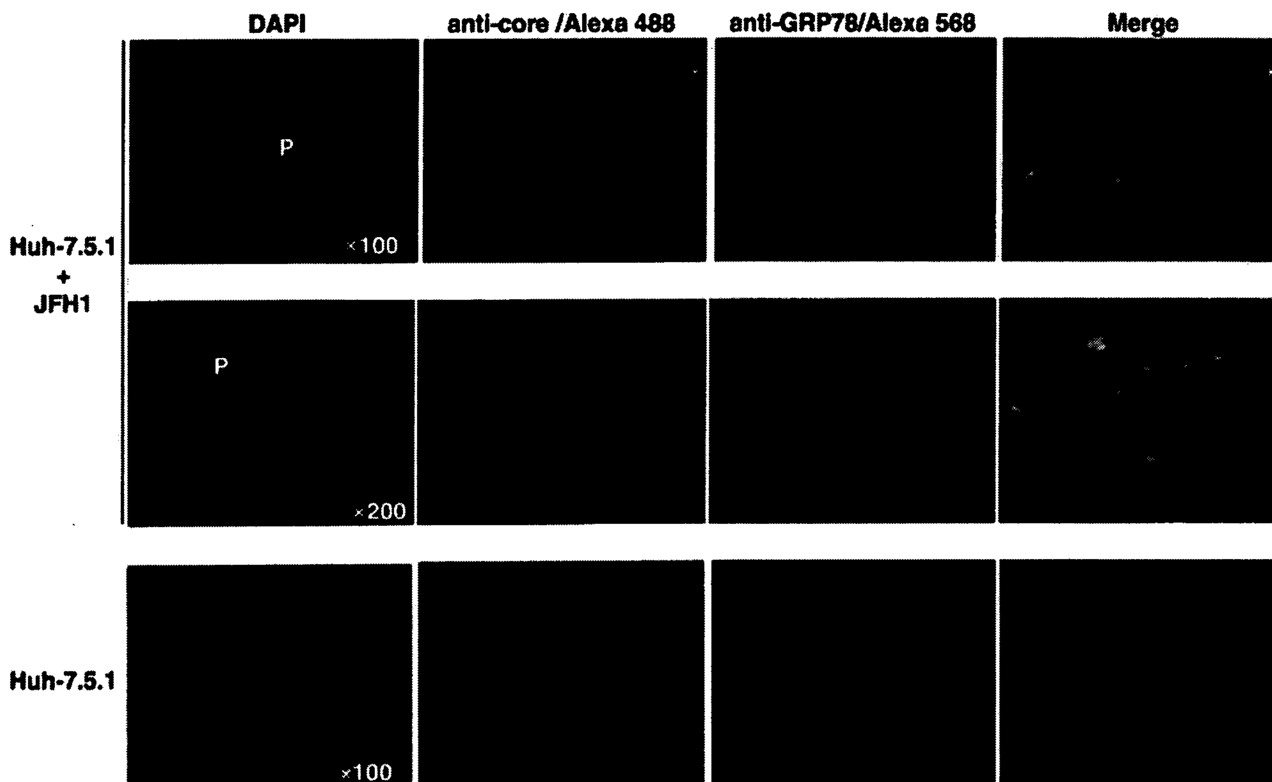

Fig. 6. Co-expression of HCV core and GRP78 in the cytopathic plaque. The HCV-JFH1 culture supernatant was transferred onto uninfected Huh-7.5.1 cells plated on 22-mm round micro cover glasses in 60-mm-diameter plates at density of 4×10^5 cells per plate. After ~5 h incubation, the supernatant was replaced with medium containing 0.8% methylcellulose. Double immunofluorescence was performed 10 days after infection using mouse anti-core antibody and goat-anti-GRP78 antibody.

Introduction of NS5B mutations in JFH1 clone showed higher replication efficiency and cytopathogenicity

We finally investigated on phenotypes of the amino acid mutations identified in the isolated cytopathic subclones. We constructed mutant clones from the wild type JFH1 plasmid, in which three amino acid mutations in NS5B region were individually introduced; T7662A, C9153T, and G9295C (see Tables 2 and 3). Transfection of the mutant HCV-RNAs showed that all mutants developed massive cell death on 10 days after transfection and that their extents of the CPE were apparently greater than the wild type JFH1 clone (Fig. 9A). The levels of core antigen in the culture medium were significantly higher in the mutant clones than in the wild type (Fig. 9B). Furthermore, the expression levels of cellular HCV core protein were significantly higher in the mutant clones than in the wild type with the order of T7662>C9153≫G9295C>JFH1 (Fig. 9C).

Discussions

Our results show that replication of HCV-JFH1 resulted in morphologic changes to the host cells, which are characterized by massive cell death (Figs. 1–3). These observations suggested that HCV infection and replication could cause CPE on the host cells. The development of the CPE involved virus protein-induced ER stress and subsequent apoptotic cell death (Figs. 4–6). The JFH1/ΔE1-E2 with deletion of the HCV envelope proteins-infected Huh-7.5.1 cells did not induce the CPE (Fig. 2A), which indicates that the key factors of plaque formation are not only viral replication but also the propagation of virus particles and re-infection. We took advantage of the HCV-induced CPE and developed a plaque assay using highly permissive Huh-7.5.1 cells. The assay revealed that the HCV-induced cytopathogenicity varied between infectious foci with cytopathic and noncytopathic infection (Fig. 3B). Interestingly, isolated JFH1 subclones from the plaques showed significantly increased infectivity and cytopathogenicity (Table 1 and Fig. 8). Viral genetic analyses showed nine amino acid substitutions; among them five were clustered in the C terminal half of the NS5B region, which might contribute to virus replication efficiency and cytopathogenicity (Table 2).

Cytopathic effects are key characteristics of the *Flaviviridae* that include Japanese encephalitis virus (JEV) (Vaughn and Hoke, 1992), West Nile Virus (Borisevich et al., 2006), yellow fever virus (Quaresma et al., 2006), dengue virus (DEN) (Despres et al., 1993), and bovine viral diarrhea virus (BVDV) (Mendez et al., 1998) and also of viruses such as adenovirus (Shinoura et al., 1999), Epstein–Barr virus (Sato et al., 1989), poliovirus (Yanagiya et al., 2005), and influenza virus (Hinshaw et al., 1994). The *Flaviviridae* utilizes the ER as the primary site for genomic replication and protein synthesis (Jordan et al., 2002; Su et al., 2002; Tardif et al., 2004). It has been reported that apoptotic cell death mediated by virus-induced ER stress contributes to the cytotoxicity of JEV, BVDV, and DEN-2

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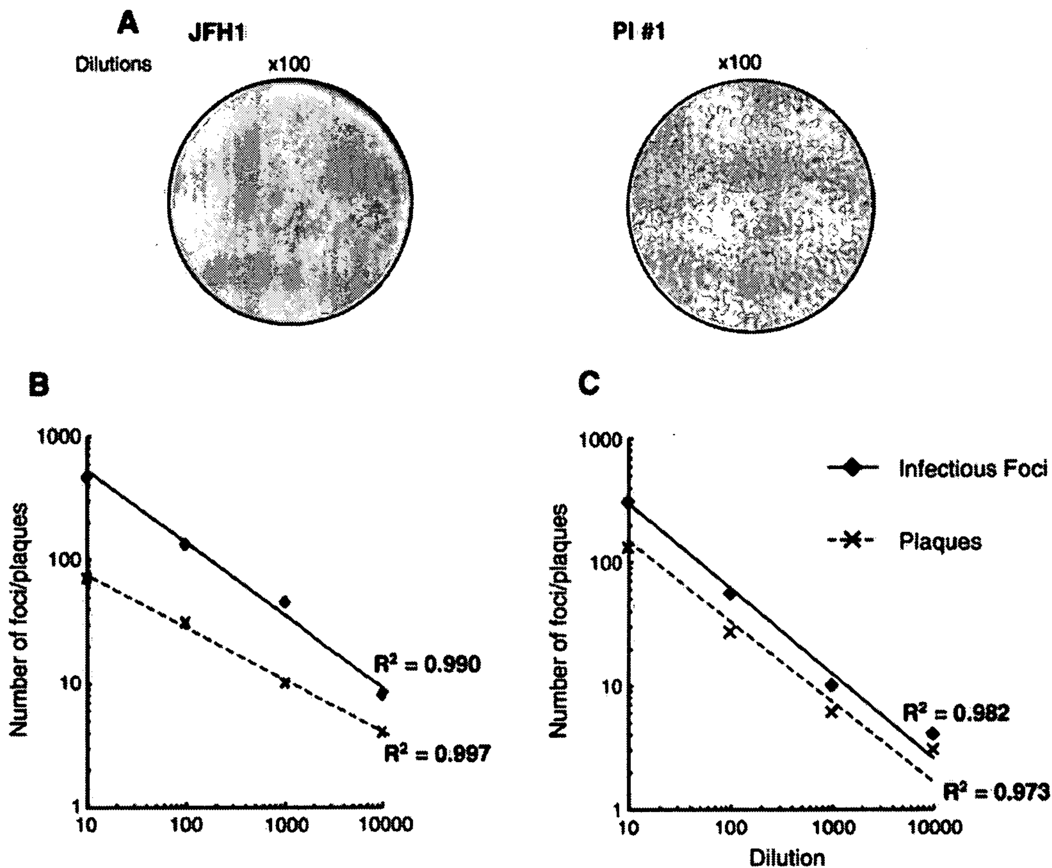

Fig. 7. Correlation of infectious foci or plaques with dilution of an inoculum. (A) Plaque assay. Huh-7.5.1 cells were seeded in collagen-coated 60-mm-diameter plates at density of 4×10^5 cells per plates and were incubated at 37 °C under 5.0% CO_2. After overnight incubation, HCV-JFH1 (left panel) or plaque-purified clone (PI #1) (right panel) 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 containing 0.8% methylcellulose. After 7 days of culture under normal conditions, formation of cytopathic plaque was visualized by staining with 0.08% crystal violet. (B and C) The PFU-adjusted culture supernatant of parental HCV-JFH1 (B) or plaque-purified clone (PI #1) (C) was transferred at various dilutions onto uninfected Huh-7.5.1 cells, and the plaque assay and immunocytochemistry were performed (described above). The infectivity and cytotoxicity were quantified by counting HCV-positive foci and cytopathic plaque respectively. The horizontal axis showed dilutions of the viral supernatant and the vertical axis showed the number of infectious foci or plaques.

(Jordan et al., 2002; Su et al., 2002; Yu et al., 2006). In DEN-2-infected cells, the NS2B-3 protein causes XBP1 splicing and induces ER stress (Yu et al., 2006). These findings are consistent with our results for HCV in that the JFH1 infection induced ER stress and unfolded protein responses and led to apoptotic cell death and formation of plaques.

The ER is closely associated with viral replication and assembly. Most of the HCV structural and nonstructural proteins accumulate in the ER membrane and form a membranous web that is characterized by a convoluted ER structure (Gosert et al., 2003). Moreover, the folding and assembly of HCV proteins require interaction with ER chaperone proteins such as calreticulin, BiP/GRP78, and heat shock protein-90 (HSP90) (Choukhi et al., 1998; Waxman et al., 2001). The ER stress, which is induced by virus replication, involves three different mechanisms (Tardif et al., 2002): transcriptional induction, translational attenuation, and protein degradation. In our study, both GRP78 and phosphorylated eIF2-alpha proteins were induced as viral proteins increased in concentration in HCV-JFH1 infected cells, and the GRP78 or annexin V and HCV core proteins co-localize in cytopathic plaques, showing that HCV infection and replication induce UPR and that ER stress-mediated apoptosis causes the viral cytopathic effects on host cells.

Table 1
Cytopathogenicity and infectivity of JFH1 clones

	PFU/ml [a]	FFU/ml [b]	PFU/FFU
JFH1	$9.7\pm3.8\times10^2$ [c]	$5.6\pm0.9\times10^3$	0.17±0.05
PI #1	$3.0\pm1.9\times10^3$	$4.9\pm1.6\times10^3$	0.58±0.21

[a] PFU, plaque-forming unit.
[b] FFU, focus-forming unit.
[c] Values are displayed as mean±S.D.

Several HCV structural and nonstructural proteins are involved in the ER stress. The structural glycoproteins, E1 and E2, interact with ER chaperones (Choukhi et al., 1998; Liberman et al., 1999), HCV NS4B induces UPR through ATF6 or the IRE1-XBP1 pathway (Zheng et al., 2005), and HCV core triggers apoptosis by inducing ER stress and ER calcium depletion both *in vitro* and *in vivo* (Benali-Furet et al., 2005).

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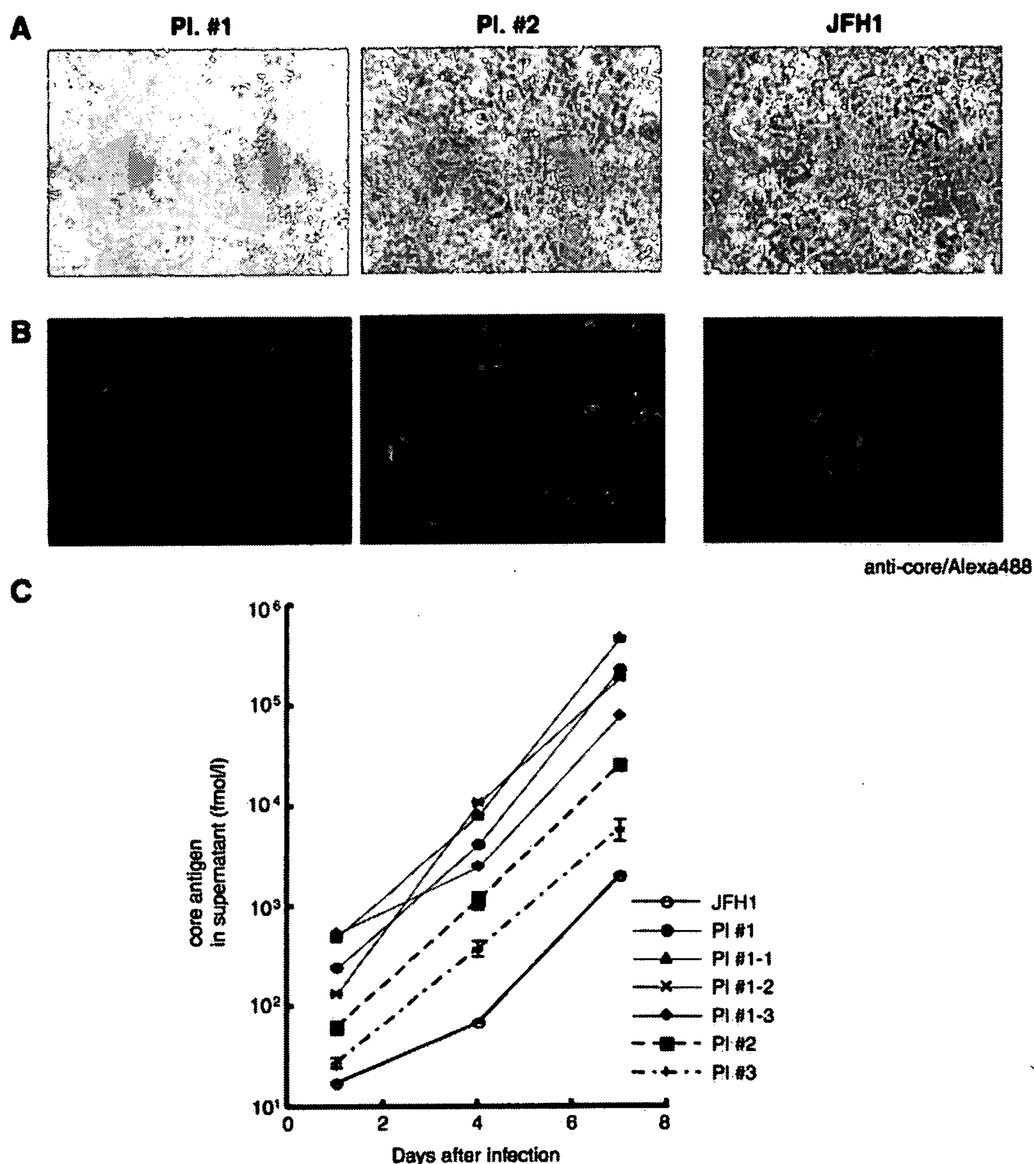

Fig. 8. The isolation of cytopathic plaques. The HCV-JFH1 culture supernatant was transferred at various dilutions onto uninfected Huh-7.5.1 cells. After ~5 h incubation, the supernatant was removed then infected cells were cultured in 0.8% methylcellulose-containing medium in 60-mm-diameter plates. 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

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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).

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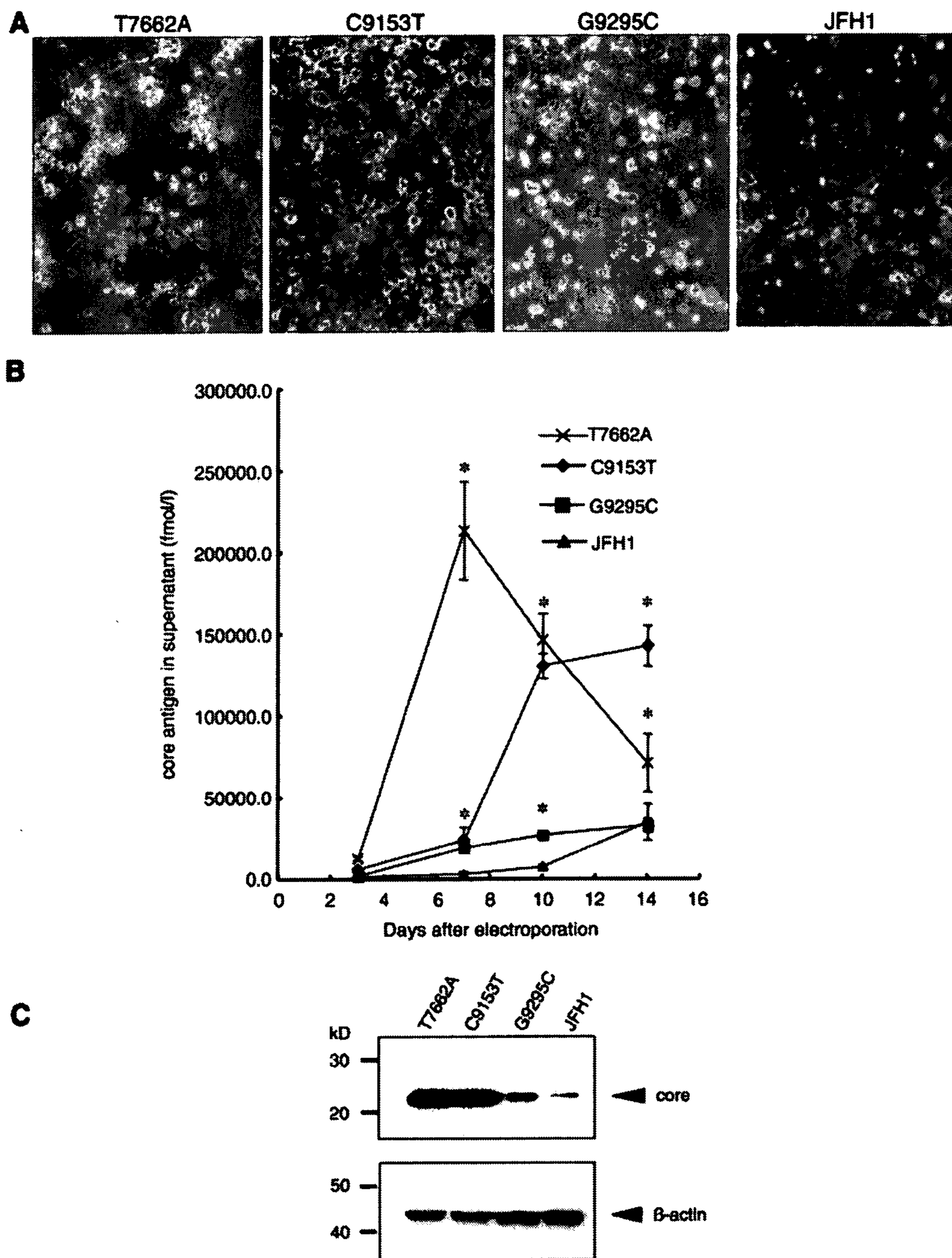

Fig. 9. Introduction of various mutations into the NS5B region of JFH1. The mutations identified in the cytopathic plaque Pl #1; T7662A, C9153T, and G9295C were introduced individually into the parental JFH1. Each JFH1 mutant, T7662A, C9153T, and G9295C, RNA was transfected into Huh-7.5.1 cells by electroporation. 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

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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.

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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.

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C型肝炎ウイルス感染における インターフェロン応答抑制機構

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KEY WORDS

C型肝炎ウイルス, RIG-I, MDA5, IPS-1/Cardif, NS4B

SUMMARY

細胞へのウイルス侵入により，インターフェロン（IFN）の産生誘導が起こり，ウイルス蛋白発現・ウイルス増殖を抑制，さらにアポトーシスによる感染細胞の排除をもたらす．近年細胞内外でのウイルスセンサーとして，Toll様レセプター（Toll-like receptor：TLR），RIG-I，およびMDA5が新たに同定された．一方種々のウイルスはこれらのIFN産生応答系を抑制し，持続増殖状態を引き起こすことが明らかとなっており，IFN系と相互作用するウイルス・宿主蛋白が同定されつつある．今後これらの自然免疫関連分子を標的とした抗ウイルス治療開発へ期待がもたれる．

はじめに

われわれの体を感染症から守る免疫系は，自然免疫系と獲得免疫の2つからなり立っている．これまで獲得免疫系の機構の解析が先行しておこなわれ，T細胞，B細胞による非自己の認識，また認識レセプターとしての抗原レセプターの存在が明らかにされてきた．一方，獲得免疫系をもたない無脊椎動物や植物などにおいても自然免疫系による防御機構が備わっている．このことから，獲得免疫以外にも非自己を認識するレセプターが存在する可能性が考えられ，Toll様レセプター（Toll-like receptor：TLR）の発見を機に自然免疫系の解明が進んだ．近年，TLRを介したIFN遺伝子の誘導機構が明らかにされ[1]，さらに細胞内ウイルスセンサーも報告された[2]．いずれもウイルス存在下での抑制が示唆されており，さらにそれぞれの経路についてウイルス側，宿主側双方の因子についての知見が蓄積しつつある．

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