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Ⅳ. 研究成果の刊行物・別刷

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Identification of the Niemann-Pick C1–like 1 cholesterol absorption receptor as a new hepatitis C virus entry factor

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Hepatitis C virus (HCV) is a leading cause of liver disease worldwide. With ~170 million individuals infected and current interferon-based treatment having toxic side effects and marginal efficacy, more effective antivirals are crucially needed[1]. Although HCV protease inhibitors were just approved by the US Food and Drug Administration (FDA), optimal HCV therapy, analogous to HIV therapy, will probably require a combination of antivirals targeting multiple aspects of the viral lifecycle. Viral entry represents a potential multifaceted target for antiviral intervention; however, to date, FDA-approved inhibitors of HCV cell entry are unavailable. Here we show that the cellular Niemann-Pick C1–like 1 (NPC1L1) cholesterol uptake receptor is an HCV entry factor amendable to therapeutic intervention. Specifically, NPC1L1 expression is necessary for HCV infection, as silencing or antibody-mediated blocking of NPC1L1 impairs cell culture–derived HCV (HCVcc) infection initiation. In addition, the clinically available FDA-approved NPC1L1 antagonist ezetimibe[2,3] potently blocks HCV uptake *in vitro* via a virion cholesterol–dependent step before virion-cell membrane fusion. Moreover, ezetimibe inhibits infection by all major HCV genotypes *in vitro* and *in vivo* delays the establishment of HCV genotype 1b infection in mice with human liver grafts. Thus, we have not only identified NPC1L1 as an HCV cell entry factor but also discovered a new antiviral target and potential therapeutic agent.

HCV is thought to enter cells via receptor-mediated endocytosis beginning with interaction of the viral particle with a series of cell surface receptors, including the tetraspanin CD81 protein[4], scavenger receptor class B member I (SR-BI, also known as SCARB1)[5] and the tight-junction proteins claudin-1 (CLDN1)[6] and occludin (OCLN)[7,8], followed by clathrin-mediated endocytosis and fusion between the virion envelope and the endosomal membrane[9,10]. Although the specifics of each interaction are not fully understood, it is now recognized that multiple cellular factors, as well as many components of the viral particle, not just the viral glycoproteins, participate in the entry process. For example, the HCVcc particle is associated with cellular lipoproteins (for example, low-density lipoprotein and very-low-density lipoprotein)[11,12] and is enriched in cholesterol[13], the latter of which has been shown to be necessary for HCV cell entry[13,14]. Apart from the likely function of cholesterol in viral membrane stabilization and organization, the dependence of HCV infectivity on cholesterol led us to reason that other cholesterol-uptake receptors (apart from SR-BI and LDLR), such as NPC1L1, might also have a role in HCV cell entry.

NPC1L1, a 13-transmembrane-domain cell surface cholesterol-sensing receptor (**Fig. 1a**) expressed on the apical surface of intestinal enterocytes and human hepatocytes, including Huh7 cells (**Supplementary Fig. 1**), is responsible for cellular cholesterol absorption and whole-body cholesterol homeostasis[15,16]. Similar to what has been observed for other HCV entry factors[8], we observed downregulation of NPC1L1 in HCVcc-infected Huh7 cultures. Specifically, as early as day 4 after infection NPC1L1 protein levels were markedly reduced and remained downregulated until the end of the experiment at day 12 after infection (**Fig. 1b**). Having observed a correlation between NPC1L1 expression and HCV infection, we next determined whether NPC1L1 expression levels affect HCV infection by transfecting Huh7 cells with siRNAs targeting NPC1L1 or the known HCV entry factors CD81 or SR-BI. Compared to cells transfected with an irrelevant control siRNA, CD81-, SR-BI- and NPC1L1-silenced cells were significantly less susceptible to HCVcc infection (**Fig. 1c**). The inhibition was HCV specific, as silencing of these proteins had no effect on vesicular stomatitis virus G protein–pseudotyped particle (VSVGpp) infection (**Supplementary Fig. 2a**). Inhibition of HCV also correlated with a reduction in NPC1L1 mRNA and protein and was NPC1L1 specific and not the result of off-target effects (**Fig. 1d,e**, **Supplementary Figs. 3** and **4a,b**). Although protein amounts were only marginally lowered by siRNA knockdown, the effect on HCV was considerable, highlighting the sensitivity of HCV to small changes in NPC1L1 levels. Notably, SR-BI mRNA expression has been shown to be reduced by NPC1L1 knockdown in nonhepatic cells[17] and SR-BI is an HCV entry factor[5], but we found that SR-BI expression was not adversely affected by NPC1L1 silencing in Huh7 cells (**Supplementary Fig. 4c,d**). Finally, NPC1L1 silencing had no effect on HCV subgenomic RNA replication, full-length infectious HCVcc RNA replication or secretion of *de novo* HCVcc (**Supplementary Fig. 5**).

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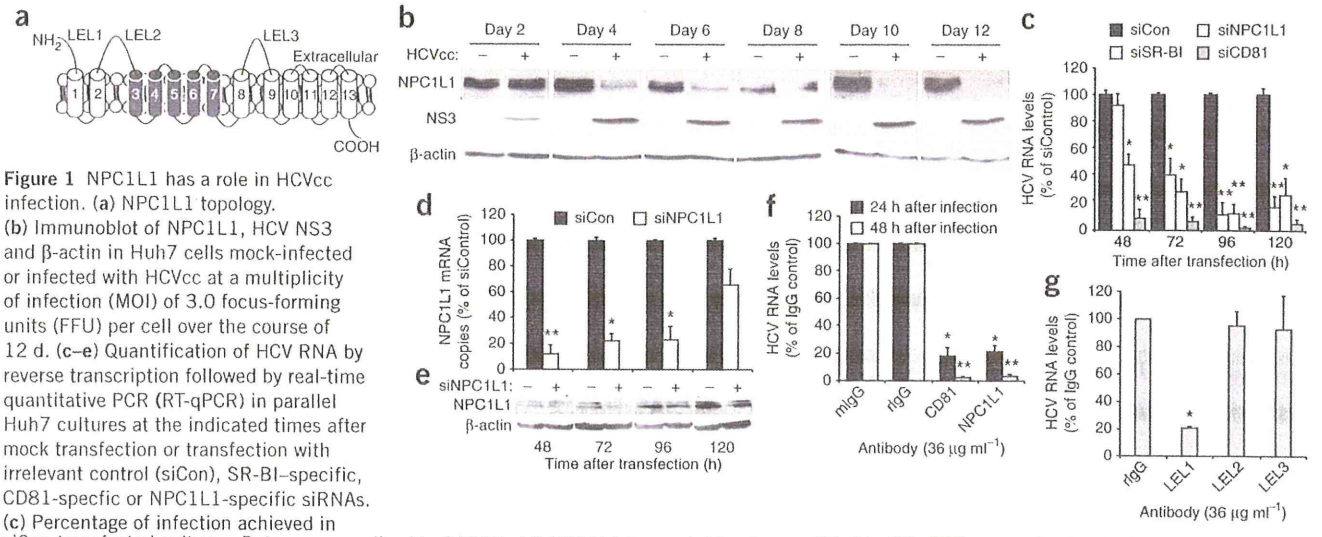

Figure 1 NPC1L1 has a role in HCVcc infection. (**a**) NPC1L1 topology. (**b**) Immunoblot of NPC1L1, HCV NS3 and β-actin in Huh7 cells mock-infected or infected with HCVcc at a multiplicity of infection (MOI) of 3.0 focus-forming units (FFU) per cell over the course of 12 d. (**c–e**) Quantification of HCV RNA by reverse transcription followed by real-time quantitative PCR (RT-qPCR) in parallel Huh7 cultures at the indicated times after mock transfection or transfection with irrelevant control (siCon), SR-BI–specific, CD81-specfic or NPC1L1-specific siRNAs. (**c**) Percentage of infection achieved in siCon-transfected cultures. Data are normalized to GAPDH. (**d**) NPC1L1 transcript levels quantified by RT-qPCR, normalized to GAPDH and graphed as a percentage of the maximum number of copies determined in siCon-transfected cultures at each time point examined. (**e**) Immunoblot of NPC1L1 and β-actin protein in siCon-transfected (–) and siNPC1L1-transfected cultures (+). (**f,g**) Intracellular HCV RNA levels detected in parallel Huh7 cell cultures treated with 36 μg ml^{-1} of a mouse (mIgG) or rabbit (rIgG) isotype control antibody, a CD81-specific antibody or antibodies specific for each of the three LELs of NPC1L1 for 1 h before and during HCVcc infection. Shown are HCV RNA levels, determined by RT-qPCR and normalized to GAPDH levels, 24 h (**f**) or 48 h (**f,g**) after infection. Results are graphed as a percentage of infection achieved in the respective IgG control-treated cultures. In all cases, significant differences relative to controls (one-way analysis of variance (ANOVA) and Tukey's post-hoc *t* test) are denoted as $^{*}P < 0.05$ or $^{**}P < 0.01$. All results are graphed as means ± s.d. for triplicate samples. The data presented are representative of three independent experiments.

Because siRNA-mediated knockdown of NPC1L1 suggested that HCV infection is inhibited at a step before RNA replication or secretion, we next assessed whether HCV infection was susceptible to inhibition by antibody-mediated blocking of cell surface NPC1L1. Compared to cells treated with irrelevant IgG control antibodies, HCVcc infection, as measured by intracellular HCV RNA levels, was significantly reduced in cells treated with an antibody specific for the known HCV cell entry factor CD81 (**Fig. 1f**). When we incubated cells with an NPC1L1-specific antibody, HCVcc infection was similarly reduced (**Fig. 1f**), and the inhibition was HCV specific, as antibody-mediated blocking had no effect on VSVGpp entry (**Supplementary Fig. 2b,c**). To determine the NPC1L1 domains necessary for HCV entry, we treated cells with antibodies targeting each of the three large extracellular loops (LELs) of NPC1L1 and observed that HCV infection was reduced only when NPC1L1 LEL1, but not LEL2 or LEL3, was blocked (**Fig. 1g**). Thus, NPC1L1 silencing and antibody-mediated blocking of NPC1L1 LEL1 reduced HCV infection as effectively as targeting other known HCV cell entry factors.

Ezetimibe is a 2-azetidinone–class drug that has been approved by the FDA as a cholesterol-lowering medication[18]. As ezetimibe has been shown to be a direct inhibitor of NPC1L1 internalization[19,20], we next used this high-affinity, specific pharmacological agent as an alternate means of targeting NPC1L1 before, during or after viral inoculation while additionally evaluating its anti-HCV potential. Specifically, we performed HCVcc foci-reduction assays and quantified foci (that is, clusters of ≥5 HCV E2–positive cells) after ezetimibe treatment. Ezetimibe reduced HCVcc foci formation in a dose-dependent manner when present before infection and then removed (**Fig. 2a**) or only during virus inoculation (**Fig. 2b**). However, when we added ezetimibe to cells after inoculation (**Fig. 2c**), the initiation of HCV-positive foci was unaffected, as would be expected for a viral entry inhibitor. Notably, the highest dose of ezetimibe (25 μM) reduced the size of the HCV-positive foci observed from the typical ≥5 HCV E2–positive cells to only 1–3 HCV E2–positive cells per focus, which accounts for the lower number of foci with ≥5 HCV E2-positive cells being counted in those cultures, suggesting that NPC1L1 may also affect HCV cell-to-cell spread (data not shown). Dose-responsive, time-of-addition–dependent inhibition of HCV infection was also evident when HCV RNA levels were measured (**Supplementary Fig. 6**). We additionally observed ezetimibe sensitivity across a panel of HCVcc intergenotypic clones containing the structural regions of diverse HCV genotypes (1 – 7)[21] (**Fig. 2d**). Finally, because NPC1L1 and SR-BI are both involved in cellular cholesterol uptake and SR-BI has been reported to be a rate-limiting HCV cell entry factor[22], we overexpressed SR-BI before ezetimibe treatment and found that this overexpression did not overcome the dependence of HCV entry on NPC1L1 (**Supplementary Fig. 7**). Likewise, we confirmed that the potent antiviral effect of ezetimibe was not due to drug-mediated cytotoxicity (**Supplementary Figs. 2d,e** and **8a**), changes in cell proliferation (**Supplementary Fig. 8b**), reduced expression of the other known HCV cell surface receptors (**Supplementary Fig. 8c–g**), inhibition of HCV RNA replication (**Supplementary Fig. 9a–c**) or inhibition of virus secretion (**Supplementary Fig. 9d**). Hence, the data support the conclusion that direct pharmacological inhibition of NPC1L1 reduces HCV infection by directly inhibiting viral cell entry.

We next assessed whether ezetimibe inhibits HCVcc binding or a post-binding step by examining cell-associated HCV RNA and protein expression from internalized RNA in vehicle- and ezetimibe-treated HCVcc-infected cultures. At 10 h after infection, a time before detectable HCV RNA replication occurs (**Supplementary Fig. 10**), ezetimibe did not affect cell-bound HCV RNA levels (**Fig. 2e**). In contrast, at later time points, HCV RNA levels (**Fig. 2e**) and *de novo* NS5A protein expression (**Fig. 2f,g**) were reduced in ezetimibe-treated cultures, suggesting HCV can efficiently bind ezetimibe-treated cells, but a post-binding step is prevented. To further test this hypothesis

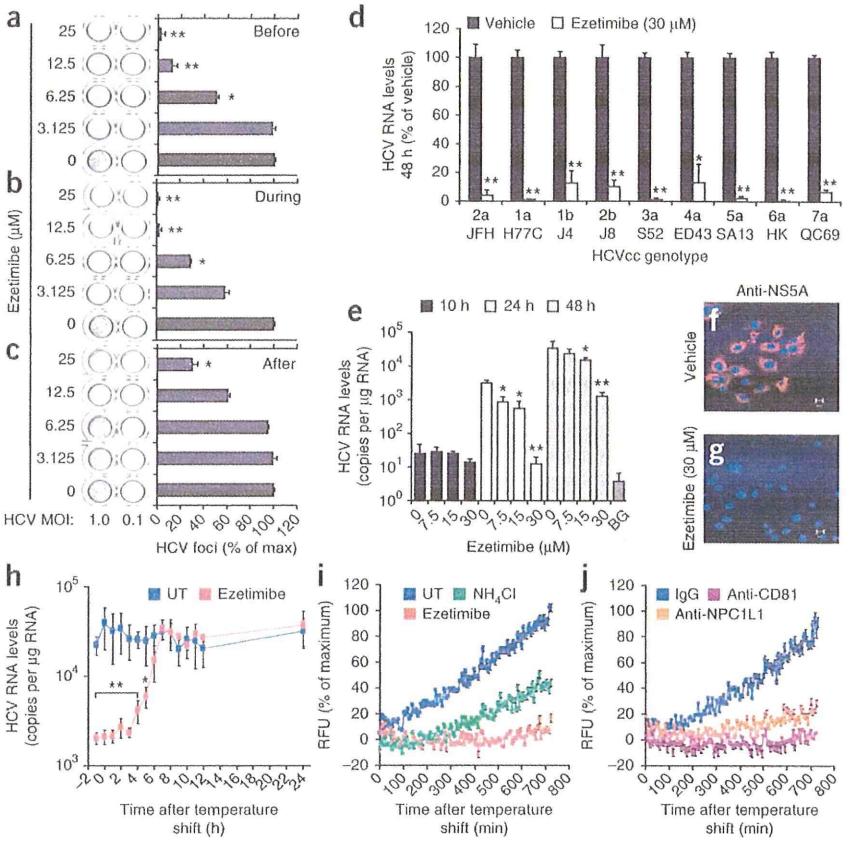

Figure 2 Ezetimibe-mediated inhibition of NPC1L1 reduces HCV entry at a post-binding, prefusion step. (**a**–**c**) Quantification of HCV foci observed in Huh7 cultures treated with vehicle or increasing concentrations of ezetimibe for 6 h before infection and then removed (Before) (**a**), for 12 h coincident with viral inoculation and then removed (During) (**b**) or after viral inoculation (After) (**c**). HCV foci are expressed as a percentage of the foci obtained in vehicle-treated (0 μM) cultures ± s.d. ($n = 3$). MOI, multiplicity of infection. (**d**,**e**) Intracellular HCV RNA levels detected in parallel Huh7 cultures treated with vehicle or the indicated concentrations of ezetimibe beginning 1 h before and during infection with HCVcc containing the structural region of the indicated genotypes (**d**) or HCVcc JFH-1 (**e**). Shown are HCV RNA levels, determined by RT-qPCR and normalized to GAPDH, at the indicated times after infection. Results are graphed as a percentage of infection in vehicle-treated cultures or as mean HCV RNA copies per μg total cellular RNA ± s.d. ($n = 3$). Assay background (BG) is the HCV RNA level detected in uninfected samples. (**f**,**g**) Indirect immunofluorescence analysis of HCV NS5A in vehicle-treated (**f**) and ezetimibe-treated (30 μM) (**g**) cultures 24 h after infection with HCVcc JFH-1. Scale bars, 20 μm. (**h**) Intracellular HCV RNA levels detected in synchronized infections performed in parallel Huh7 cultures treated with vehicle or ezetimibe (30 μM) at the indicated times. Shown are HCV RNA levels, determined by RT-qPCR and normalized to GAPDH, 30 h after infection. Results are graphed as mean HCV RNA copies per μg total cellular RNA ± s.d. ($n = 3$). $^*P < 0.05$ or $^{**}P < 0.01$ for HCV relative to vehicle-treated cultures (one-way ANOVA and Tukey's post-hoc t test). (**i**,**j**) HCV fusion, as measured by DiD fluorescence dequenching in Huh7 cells treated with vehicle (UT), NH_4Cl (10 mM), ezetimibe (30 μM), IgG control antibody (36 μg ml^{-1}), CD81-specific antibody (anti-CD81, 36 μg ml^{-1}), or an antibody to NPC1L1 LEL1 (anti-NPC1L1, 36 μg ml^{-1}). Results are graphed as a percentage of maximum background-corrected relative fluorescence units (RFU) achieved in vehicle-treated or IgG control-treated cultures. All data presented are representative of three independent experiments.

and determine when during the entry process NPC1L1 functions, we assessed the ability of ezetimibe to block HCVcc infection when added at various times after virus binding at 4 °C. Ezetimibe retained inhibitory activity after temperature shift to 37 °C for up to 5 h (half-maximal inhibition at 4 h), confirming that NPC1L1 functions after binding, probably late in viral entry (**Fig. 2h**).

To determine whether ezetimibe acts before fusion, we developed a fluorescence-based HCVcc fusion assay. Specifically, we labeled HCVcc with the hydrophobic fluorophore DiD[23], which incorporates into biological membranes and, at high concentrations, is self-quenching. Upon fusion of viral and target membranes, the DiD fluorophores diffuse away from each other, causing dequenching and allowing for the progression or inhibition of fusion to be measured in real time (**Supplementary Fig. 11**). Compared to NH_4Cl, an inhibitor of endosomal acidification[9], ezetimibe more potently inhibited $HCVcc^{DiD}$ fusion, such that by 12 h after binding we measured only ~10% $HCVcc^{DiD}$ dequenching in ezetimibe-treated cultures as compared to vehicle-treated controls (**Fig. 2i**). Analogously, antibody-mediated inhibition of both CD81 and NPC1L1 also reduced $HCVcc^{DiD}$ fusion (**Fig. 2j**), indicating that the inhibition observed in ezetimibe-treated wells (**Fig. 2i**) was not drug specific. We also observed similar results using $HCVcc^{DiD}$ alternatively purified by iodixanol density gradient centrifugation (**Supplementary Fig. 12a,b**).

As not all viral membrane–incorporated DiD is self-quenched, DiD can also serve as a fluorescent tag to monitor virions during cell entry[24]. Taking advantage of this, we performed fluorescence microscopy analysis of $HCVcc^{DiD}$-infected cultures and noted that although we observed little DiD on the surface of vehicle-treated cells, indicative of successful viral entry and fusion, we observed markedly more DiD on the surface of ezetimibe-treated cells (**Supplementary Fig. 12c,d**). Together with the DiD-fusion data, this indicates that inhibition of NPC1L1 prevents HCVcc cell entry at or before virion–host cell fusion.

Given that antibody-mediated blocking of only NPC1L1 LEL1 (**Fig. 1g**) reduced HCVcc infection, LEL1 has been shown to bind cholesterol[20,25] and infectious HCV particles are enriched in cholesterol[13,26], we next investigated whether the dependence of HCV cell entry on NPC1L1 might be related to the cholesterol contained within the HCV virions[13]. To address this hypothesis, we used viruses containing the E1/E2 glycoproteins derived from the HCV JFH-1 consensus clone but that differ in their virion-associated cholesterol content and assessed their relative dependence on NPC1L1. Specifically, we found that lentivirus particles pseudotyped with the JFH-1 HCV glycoproteins (HCVpp) contained 94% less cholesterol than the authentic JFH-1 HCVcc particles ($HCVcc^{WT}$). In contrast, cell culture–adapted $HCVcc^{G451R}$ produced from a JFH-1 viral clone with a G451R point mutation in the viral E2 glycoprotein ($HCVcc^{G451R}$) contained ~50% more cholesterol than $HCVcc^{WT}$ (**Fig. 3a**). These cholesterol profiles are consistent with

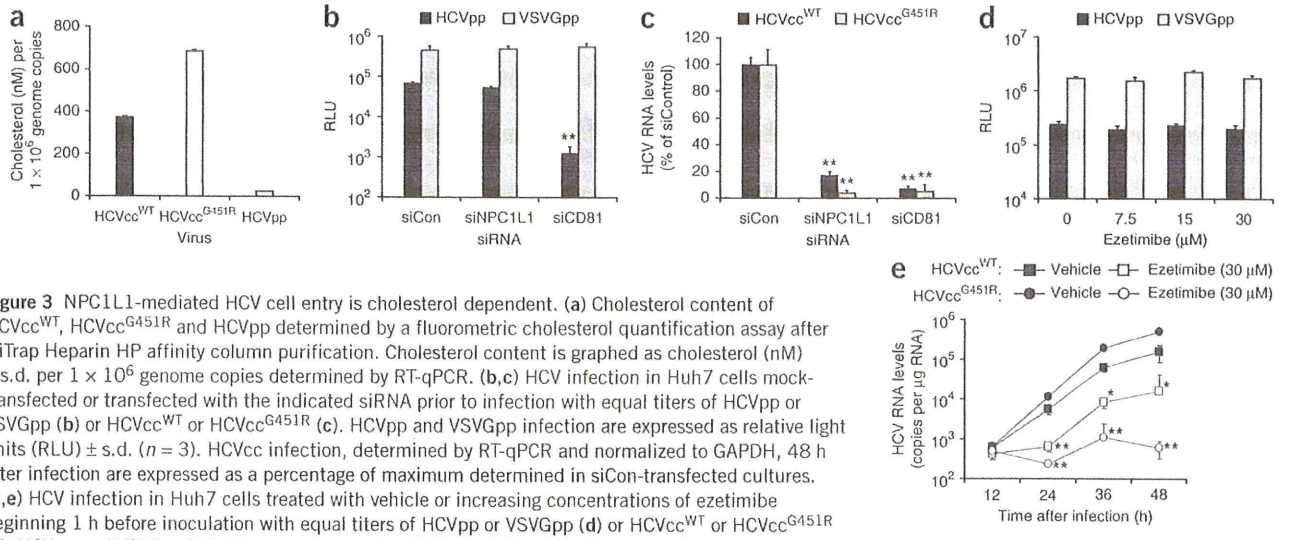

Figure 3 NPC1L1-mediated HCV cell entry is cholesterol dependent. (**a**) Cholesterol content of $HCVcc^{WT}$, $HCVcc^{G451R}$ and HCVpp determined by a fluorometric cholesterol quantification assay after HiTrap Heparin HP affinity column purification. Cholesterol content is graphed as cholesterol (nM) ± s.d. per 1×10^6 genome copies determined by RT-qPCR. (**b**,**c**) HCV infection in Huh7 cells mock-transfected or transfected with the indicated siRNA prior to infection with equal titers of HCVpp or VSVGpp (**b**) or $HCVcc^{WT}$ or $HCVcc^{G451R}$ (**c**). HCVpp and VSVGpp infection are expressed as relative light units (RLU) ± s.d. ($n = 3$). HCVcc infection, determined by RT-qPCR and normalized to GAPDH, 48 h after infection are expressed as a percentage of maximum determined in siCon-transfected cultures. (**d**,**e**) HCV infection in Huh7 cells treated with vehicle or increasing concentrations of ezetimibe beginning 1 h before inoculation with equal titers of HCVpp or VSVGpp (**d**) or $HCVcc^{WT}$ or $HCVcc^{G451R}$ (**e**). HCVpp and VSVGpp infection are expressed as RLU ± s.d. ($n = 3$). HCVcc infection, determined by RT-qPCR and normalized to GAPDH, at the indicated times (h) after infection are expressed as mean HCV RNA copies per μg total cellular RNA ± s.d. $^*P < 0.05$ and $^{**}P < 0.01$ for RNA or RLU values relative to siCon-transfected or vehicle-treated cultures (one-way ANOVA and Tukey's post-hoc *t* test).

the fact that HCVpp is produced from 293T embryonal kidney cells, which do not produce cholesterol-associated lipoproteins[27], and are therefore compositionally distinct from HCVcc, whereas $HCVcc^{G451R}$ has a narrower density range with a higher average mean density than the original JFH-1–derived $HCVcc^{WT}$ (ref. 28). As expected, when CD81 was silenced, both HCVpp (**Fig. 3b**) and $HCVcc^{G451R}$ (**Fig. 3c**) cell entry was reduced; however, when NPC1L1 was silenced or inhibited by ezetimibe, the cholesterol-scarce HCVpp showed NPC1L1-independent cell entry and insensitivity to ezetimibe inhibition (**Fig. 3b**,**d**). In contrast, the cholesterol-abundant $HCVcc^{G451R}$ showed enhanced NPC1L1-dependent cell entry and hypersensitivity to ezetimibe-mediated inhibition (**Fig. 3c**,**e**). Together, these data reveal a correlation between the amount of virion-associated cholesterol and dependence on NPC1L1 for HCV cell entry.

Finally, to assess the involvement of NPC1L1 in HCV cell entry *in vivo*, we evaluated the ability of ezetimibe to inhibit infection of a genotype 1 clinical isolate in a hepatic xenorepopulation model of acute HCV infection[29]. Specifically, we repopulated urokinase-type plasminogen activator–severe combined immunodeficiency (uPA-SCID) mice with human hepatocytes and treated them via oral gavage with ezetimibe (10 mg per kg body weight per day) or diluent alone for a total of 3 weeks, with treatment beginning 2 weeks, 1 week or 2 d before challenge with HCV genotype 1b positive serum (**Fig. 4a**). Ezetimibe treatment delayed the establishment of HCV infection in mice pretreated for 2 weeks before infection (**Fig. 4b**, $P = 0.0192$), confirming the ability of this drug to inhibit HCV infection *in vivo*. However, when mice were pretreated for only 1 week before infection, ezetimibe was less effective at delaying infection ($P = 0.062$), and it was completely ineffective when treatment was initiated only 2 d before challenge or after infection had been established (data not shown). Specifically, 100% of the nine control diluent–treated mice were serum positive for HCV 1 week after challenge, whereas 71% (five out of seven) and 43% (three out of seven) of mice treated with ezetimibe for 2 weeks and 1 week before infection were HCV negative, respectively (**Fig. 4b**,**c**). Although the majority of ezetimibe-treated mice eventually became HCV positive, of the five mice in the 2-week ezetimibe pretreatment group that were HCV negative at week 1, two were completely protected, remaining HCV negative at weeks 2 and 3 after infection (and one mouse died during gavage) (**Supplementary Fig. 13**). Thus, similar to what was recently reported for another potential HCV entry inhibitor, erlotinib[30], ezetimibe was able to delay initial infection *in vivo*. Notably, since NPC1L1 is highly expressed on the apical surface of intestinal enterocytes[15,16], a considerable amount of orally administered ezetimibe initially binds to these cells following oral administration[31]. Thus it is plausible that development of alternate non-oral delivery or drug-targeting methods

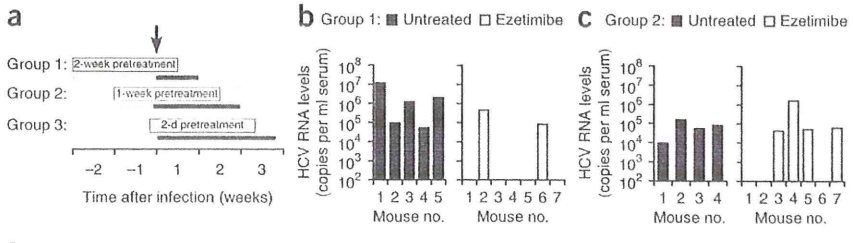

Figure 4 Ezetimibe delays the establishment of HCV infection in hepatic xenorepopulated mice. (**a**) Schematic diagram of an experiment in which uPA-SCID mice transplanted with human hepatocytes[35] were pretreated with diluent alone ($n = 4$ or 5) or ezetimibe (10 mg per kg body weight per day) ($n = 7$), via oral gavage, starting 2 weeks, 1 week or 2 d before infection (indicated by gray bars). The arrow indicates when the mice were intravenously inoculated on day 0 with HCV human serum containing 1.0×10^5 genome copies of HCV genotype 1b and the black bars indicate the time period post-HCV inoculation that treatments were continued. (**b**,**c**) HCV RNA levels (genome copies per milliliter of serum) 1 week after infection from mice pretreated for 2 weeks (**b**) or 1 week (**c**). The lower limit of HCV RNA detection is equal to 100 genomic copies per milliliter of serum. A two-tailed Fisher's exact test was performed to compare categorical variables. In all cases, $P < 0.05$ was used to reject the null hypothesis that the distribution of HCV-positive and HCV-negative mice between ezetimibe-treated and nine diluent-treated mice at specific weeks after infection were the same.

might improve transport of ezetimibe to hepatocytes and increase its anti-HCV efficacy. Nevertheless, our finding that ezetimibe can delay the establishment of HCV genotype 1 infection in mice confirms the involvement of NPC1L1 in HCV infection *in vivo* and highlights the therapeutic potential of further pursuing the refinement or development of anti-NPC1L1 therapies[32] for the treatment of HCV.

Here we have shown that NPC1L1 is an HCV cell entry factor that functions after binding, at or before fusion. These findings, together with the facts that NPC1L1 is a cellular cholesterol receptor, the HCV particle is enriched in cholesterol, and relative dependence on NPC1L1 is correlated with HCV particle cholesterol levels, support and expand upon previous reports suggesting that virion cholesterol is involved in HCV cell entry[13,14,26]. Whether NPC1L1 directly interacts with HCV or indirectly participates in HCV entry by removing virion-associated cholesterol to perhaps reveal protected viral glycoprotein binding sites or confer a required conformational change remains to be determined. Lastly, as NPC1L1 is expressed only on human and primate hepatocytes[33,34], this discovery additionally highlights NPC1L1 as a potential HCV tropism determinant, which may facilitate the future development of a small-animal model of HCV infection.

METHODS

Methods and any associated references are available in the online version of the paper at http://www.nature.com/naturemedicine/.

Note: Supplementary information is available on the Nature Medicine website.

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AUTHOR CONTRIBUTIONS

B.S. made the initial discovery. B.S. and S.L.U. designed the project, analyzed the results and wrote the manuscript. B.S., N.B., D.N.M., S.H., K.A.M. and X.Y. performed experimental work. B.S., S.L.U., M.I. and K.C. designed the hepatic xenorepopulation mouse experiments, and N.H. performed the *in vivo* studies. W.A.A. was involved in the initial conception of the project and provided valuable expertise.

COMPETING FINANCIAL INTERESTS

The authors declare competing financial interests: details accompany the full-text HTML version of the paper at http://www.nature.com/naturemedicine/.

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ONLINE METHODS

HCVcc. Plasmids containing the full-length HCV JFH-1 genome (pJFH1)[36], full-length HCV JFH-1 genome with a G451R mutation in the E2 glycoprotein (pJFH-1^{G451R})[37] and the eight intergenotypic clones (described in ref. 21) were XbaI linearized and transcribed using MEGAscript T7 (Ambion), and 10 μg *in vitro*–transcribed RNA was electroporated (BioRad) into Huh7 cells[38]. We generated HCVcc viral stocks by infecting naive Huh7 cells at an MOI of 0.01 FFU per cell with medium from Huh7 cells electroporated with *in vitro*–transcribed RNA from pJFH-1–based vectors, as previously described[38].

Treatments and analysis. Huh7 cultures were established as previously described[38]. We performed RNA silencing experiments by reverse transfection (Lipofectamine RNAiMAX, Invitrogen) of siRNAs into Huh7 cells. Transfected cells were infected with equal titers of HCVpp or VSVGpp or HCVcc at an MOI of 0.05 FFU per cell) at the indicated times after transfection (**Fig. 1c–e**). For antibody experiments, we treated cells with 36 μg ml^{-1} of antibody before and during infection with HCVcc at an MOI of 0.05 FFU per cell. For ezetimibe inhibition experiments, cells were vehicle-treated or treated with increasing concentrations of ezetimibe (Sequoia Research Products) before infection, during the time of virus inoculation and/or after virus inoculation with HCVcc at an MOI of 0.1–1.0 FFU per cell. The ezetimibe concentrations of 3.125–30 μM (that is, 1.5–12.28 μg per ml culture medium) used in this study are consistent with previously published reports[19,20,39] and are additionally in line with patient daily intake concentrations of 10 mg d^{-1} (that is, 2.0–3.3 μg per ml of serum). For RT-qPCR analysis, we isolated total cellular RNA from triplicate culture wells after infection or transfection. For HCV E2–positive foci analysis, we fixed infected cells with 4% (wt/vol) paraformaldehyde 72 h after infection, and immunocytochemical staining for HCV E2 was performed. See **Supplementary Methods** for further details.

HCV infection in chimeric mice. All mouse studies were conducted with protocols approved by the Ethics Review Committee for Animal Experimentation of the Graduate School of Biomedical Sciences, Hiroshima University. Male uPA-SCID mice transplanted with human hepatocytes (BD Biosciences[35]) were purchased from PhenixBio[40]. Mice were treated daily with 10 mg per kg body weight ezetimibe via oral gavage of a 0.02 mg ml^{-1} solution of ezetimibe resuspended in corn oil (100 μl 20g^{-1}) for a total of 3 weeks, with treatment initiation beginning 2 weeks, 1 week or 2 d before infection[16]. Control mice were treated via oral gavage with corn oil alone (100 μl per 20 g body weight). A total of four to seven mice were included in each group. On day 0, we intravenously inoculated mice with serum from HCV-infected humans containing 1.0×10^5 copies of HCV genotype 1b. Mouse serum samples were obtained for HCV RNA or human albumin determination by RT-qPCR and Alb-II Kit (Eiken Chemical), respectively.

Statistical analyses. Data are presented as the means ± s.d. We determined significant differences by one-way ANOVA followed by Tukey's post-hoc *t* test (GraphPad Prism software). To compare categorical variables we used a two-tailed Fisher's exact test (SPSS). In all cases, a P value <0.05 was considered statistically significant.

Additional methods. Detailed methodology is described in the **Supplementary Methods**.

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Impact of Viral Amino Acid Substitutions and Host Interleukin-28B Polymorphism on Replication and Susceptibility to Interferon of Hepatitis C Virus

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Amino acid (aa) substitutions of core 70 and 91 and in the NS5A (nonstructural protein 5A) interferon sensitivity determining region (ISDR) as well as genetic polymorphisms in the host interleukin-28B (IL28B) locus affect the outcome of interferon (IFN)-based therapies for patients with chronic hepatitis C. The combination of these factors and the quasispecies nature of the virus complicate understanding of the underlying mechanism. Using infectious hepatitis C virus (HCV) genotype 1b clone HCV-KT9, we introduced substitutions at both core aa70 (Arg to Gln) and aa91 (Leu to Met). We also introduced four and nine ISDR aa substitutions into core mutant HCV-KT9. Using human hepatocyte chimeric mice with different IL28B genotypes, we examined the infectivity, replication ability, and susceptibility to IFN of these clones. Although aa substitutions in the ISDR significantly impaired infectivity and replication ability of the virus, core aa70 and 91 substitutions did not. The effect of IFN treatment was similar in core wild-type and mutant viruses. Interestingly, virus titer was significantly higher in mice with the favorable IL28B allele (rs8099917 TT and rs12979860 CC) in the transplanted hepatocytes than in mice with hepatocytes from rs8099917 TG and rs12979860 TT donors ($P < 0.001$). However, the effect of IFN was significantly greater, and intrahepatic expression levels of IFN-stimulated genes were significantly higher in mice with the favorable IL28B allele. *Conclusion:* Our data suggest that HCV replication levels and response to IFN are affected by human hepatocyte IL28B single-nucleotide polymorphism genotype and mutations in the ISDR. The mechanism underlying the clinically observed association of wild-type core protein in eradication-favorable host cells should be investigated further. (HEPATOLOGY 2011;54:764-771)

Chronic hepatitis C virus (HCV) infection is the leading cause of cirrhosis, liver failure, and hepatocellular carcinoma.[1,2] Interferon (IFN) is an essential component of therapy for patients with chronic HCV infection, and the most effective currently available therapy is combination therapy with pegylated (PEG)-IFN and ribavirin (RBV).[3-5] Among HCV genotypes, genotype 1 is the most resistant to

Abbreviations: aa, amino acid; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; HCV, hepatitis C virus; HSA, human serum albumin; IFN, interferon; IL28B, interleukin-28B; ISDR, interferon-sensitivity–determining region; ISG, interferon-stimulated gene; MxA, myxovirus resistance protein A; NVR, nonvirological response; OAS, oligoadenylate synthetase; PBS, phosphate-buffered saline; PEG, pegylated; PKR, RNA-dependent protein kinase; RBV, ribavirin; RT-PCR, reverse-transcription polymerase chain reaction; SCID, severe combined immunodeficiency; SNP, single-nucleotide polymorphism; SVR, sustained virological response; uPA, urokinase-type plasminogen activator.

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IFN therapy.[6] The limited success of combination therapy for genotype 1 HCV infection is because of the low response rate during therapy and high relapse rate after therapy.[7]

Recent studies have identified both viral and host factors predictive of IFN therapy. Among the viral factors, amino acid (aa) substitutions in the IFN-sensitivity–determining region (ISDR) (nucleotides 2209-2248 or aa positions 237-276 within the NS5A region) are associated with sustained virological response (SVR) after IFN treatment in HCV genotype 1b patients.[8,9] Akuta et al. reported that substitution of aa70 or 91 in the HCV core region are independent predictors of SVR and nonvirological response (NVR).[10-12] Recently, we[13] and another group[14] also reported that wild-type HCV core aa70 and two or more aa substitutions in the ISDR are effective predictors of SVR in patients with HCV genotype 1b.

Among host factors associated with SVR, many common genetic polymorphisms in the human genome have been identified, including single-nucleotide polymorphisms (SNPs).[15-19] More recently, an association between several linked SNPs in the interleukin-28B (IL28B) locus and the effect of combination therapy has been reported.[20-22]

We recently reported that the core aa wild type is significantly more likely to be found in patients with the eradication-favorable IL28B SNP genotype.[23-25] The underlying mechanism of this association as well as the reason for the differential response to therapy by viruses with core aa substitutions are unknown. This is partly because of the presence of HCV quasispecies in human serum samples and the difficulty of performing infection experiments in a small animal model.

The severe combined immunodeficient (SCID) urokinase-type plasminogen activator (uPA) mouse permits repopulation of the liver with human hepatocytes, resulting in human hepatocyte chimeric mice able to develop HCV viremia after injection of serum samples positive for the virus.[26] We and other groups have reported that the human hepatocyte chimeric mouse is useful for evaluating anti-HCV drugs, such as IFN-alpha and NS3-4A protease inhibitor.[27,28] We have further improved the replacement levels of the human hepatocytes in this mouse model,[29] which enabled us to perform infection experiments more easily because highly repopulated mice (defined as human serum albumin [HSA] levels well above 1 mg/mL) successfully develop viremia more often than poorly repopulated mice.[30] Using this mouse model, we developed a reverse genetics system for HCV.[31,32] This system is useful for studying characteristics of HCV strains with various substitutions of interest, because the effects of quasispecies can be minimized. Furthermore, as there is no adaptive immune system in this mouse model, we are able to examine the replication of HCV and the effect of therapy while avoiding the influence of the immunological response. In the present study, we investigated effects of viral and host factors on HCV infectivity, replication ability, and IFN susceptibility using genetically engineered genotype 1b HCV-infected mice that underwent transplantation with hepatocytes having eradication-favorable or eradication-unfavorable IL28B SNP genotypes.

Table 1. Characteristics of Donors for Transplanted Human Hepatocytes

Donor	A	B	C	D
Sex	Female	Male	Female	Male
Age	10	2	5	2
Ethnic group	Caucasian	Caucasian	African American	Hispanic
rs8099917	TG	TT	TG	TT
rs8109886	AA	CC	AA	CC
rs12979860	TT	CC	TT	CC
rs11882871	GG	AA	GG	AA
rs73930703	TT	CC	TT	CC
rs8107030	AG	AA	AG	AA
rs28416813	GG	CC	GG	CC
rs8103142	CC	TT	CC	TT
rs11881222	GG	AA	GG	AA
rs4803217	AA	CC	AA	CC

Materials and Methods

Animal Treatment. Generation of the $uPA^{+/+}$/$SCID^{+/+}$ mice and transplantation of human hepatocytes were performed as described previously.[29] All animal protocols described in this study were performed in accord with the guidelines of the local committee for animal experiments, and all animals received humane care. Infection, extraction of serum samples, and sacrifice were performed under ether anesthesia. Mouse serum concentrations of HSA, which serve as useful markers of the extent of repopulation, were measured as previously described.[29] Mice underwent transplantation with frozen human hepatocytes obtained from four different human donors (Table 1). Genotyping of IL28B SNPs of human hepatocytes was performed using the Invader assay as described previously.[33,34] We used 1000 IU/g/day of IFN-alpha (Dainippon Sumitomo Pharma Co., Tokyo, Japan) for 2 weeks. This dosage was selected based on a previous report showing that this regimen reduced mouse serum

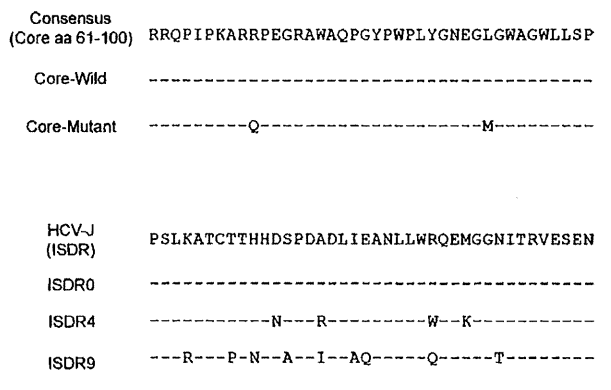

Fig. 1. The aa sequences of infectious genotype 1b HCV clones, Core-Wild, Core-Mutant (substitutions at aa70 and aa91), and ISDR variants (with 0, 4, and 9 substitutions).

HCV RNA levels by 0.5-2 log copies/mL during therapy.[31]

HCV RNA Transcription and Inoculation into Mice. We previously established an infectious genotype 1b HCV clone, HCV-KT9, that was obtained from a Japanese patient with severe acute hepatitis (GenBank accession no. AB435162).[32] Ten micrograms of plasmid DNA, linearized by digestion with *Xba*I (Promega, Madison, WI), was transcribed in a 100-μL reaction volume with T7 RNA polymerase (Promega) at 37°C for 2 hours and then analyzed by agarose gel electrophoresis. Each transcription mixture was diluted with 400 μL of phosphate-buffered saline (PBS) and injected into the livers of chimeric mice.[32] The HCV-KT9 clone has aa substitutions at aa70 and 91 (arginine to glutamine and leucine to methionine, respectively) in the core region (Core-Mutant), compared to the consensus sequence,[10-12] and no aa substitutions in the ISDR (ISDR0),[8] relative to the prototype sequence (HCV-J).[35] Using the original HCV-KT9 clone, we created two additional HCV clones having wild-type core aa70 and 91 (Core-Wild) and four (ISDR4) and nine (ISDR9) aa substitutions in the ISDR, respectively (Fig. 1). To introduce the aa substitutions, site-directed mutagenesis was performed with a QuikChange site-directed mutagenesis kit (Stratagene, La Jolla, CA).

Human Serum Samples. Human serum samples containing a high titer of genotype 1b HCV (2.2×10^6 copies/mL) were obtained from a patient with chronic hepatitis after obtaining written informed consent. Aliquots of serum were stored in liquid nitrogen until use. Core 70 and 91 aas were Gln and Leu, respectively, and only one aa substitution was present in the ISDR. The study protocol involving human subjects conformed to the ethical guidelines of the 1975 Declaration of Helsinki and was approved by the institutional review committee.

Quantitation of HCV RNA and IFN-stimulated gene-expression levels. RNA was extracted from mice serum and liver samples by Sepa Gene RV-R (Sankojunyaku, Tokyo, Japan), dissolved in 8.8 μL of ribonuclease-free H_2O, and reverse transcribed using random primer (Takara Bio Inc., Shiga, Japan) and M-MLV reverse transcriptase (ReverTra Ace, TOYOBO Co., Osaka, Japan) in 20 μL of reaction mixture according to the instructions provided by the manufacturer. Nested polymerase chain reaction (PCR) and quantitation of HCV by Light Cycler (Roche Diagnostics, Tokyo, Japan) were performed as previously described.[32] Quantitation of IFN-stimulated genes (ISGs) (myxovirus resistance protein A [MxA], oligoadenylate synthetase [OAS], and RNA-dependent protein kinase [PKR]) was performed using real-time PCR Master Mix (Toyobo, Kyoto, Japan) and TaqMan Gene Expression Assay primer and probe sets (PE Applied Biosystems, Foster City, CA). Thermal cycling conditions were as follows: a precycling period of 1 minute at 95°C, followed by 40 cycles of denaturation at 95°C for 15 seconds and annealing/extension at 60°C for 1 minute. ISG messenger RNA expression levels were expressed relative to the endogenous RNA levels of the housekeeping reference gene, glyceraldehyde-3-phosphate dehydrogenase (GAPDH).

Statistical Analysis. The HCV infectious ratio of chimeric mice was assessed using the chi-square test. Mice serum HCV RNA titers, HSA concentrations, and ISG expression levels were compared using the Mann-Whitney U test. A P value less than 0.05 was considered statistically significant.

Results

Influence of aa Substitutions in the HCV Core Region and ISDR on HCV Infectivity and Replication Ability. We investigated the influence of aa substitutions in the core region and ISDR on HCV infectivity and replication ability in mice that underwent transplantation with human hepatocytes obtained from donor A (Table 1). Each 30 μg of *in vitro*–transcribed RNA was inoculated into the livers of mice. Six weeks after inoculation, serum HCV RNA titers increased above the detectable limit (1000 copies/mL) in 11 of 12 (92%) mice infected with Core-Wild-ISDR0 and in 14 of 16 (88%) mice with Core-Mutant-ISDR0 (Fig. 2A). HCV RNA titers in Core-Wild-ISDR0– and Core-Mutant-ISDR0–infected mice increased to the same levels (Fig. 2B). In contrast, serum HCV

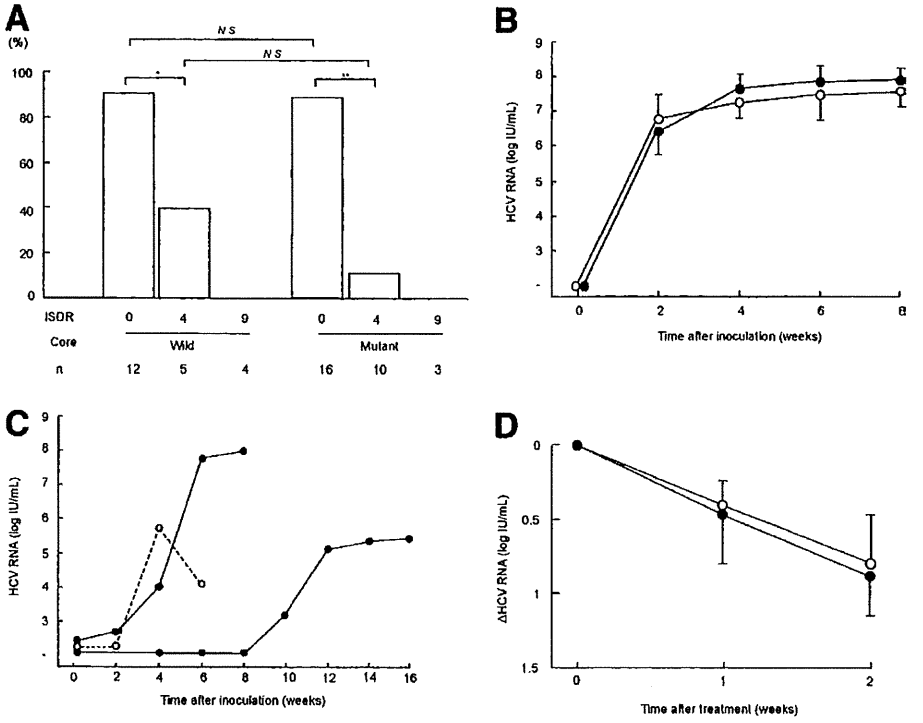

Fig. 2. Infectivity and replication ability of HCV clones. Mice that underwent transplantation with hepatocytes obtained from donor A were inoculated with 30 μg of *in vitro*-transcribed RNAs of indicated clones. (A) Proportion of HCV-infected mice. Infection was defined as serum HCV RNA titer above the detection limit (1000 copies/mL) 6 weeks after inoculation. aa sequences of the core (Wild or Mutant) and number of substitutions in the ISDR are noted below the graph. (B) Time course of serum HCV RNA levels in mice inoculated with either Core-Wild-ISDR0 (closed circles, n = 11) or Core-Mutant-ISDR0 (open circles, n = 14) HCV clones. Data are represented as mean ± standard deviation. (C) Time course of serum HCV RNA levels in two Core-Wild-ISDR4-infected mice (closed circles) and a Core-Mutant-ISDR4-infected mouse (open circles). Serum HCV RNA levels were measured until the mice died. (D) Core-Wild-ISDR0- (closed circles, n = 8) and Core-Mutant-ISDR0 (open circles, n = 4)-infected mice were treated daily with 1000 IU/g/day of IFN-alpha for 2 weeks. Mice serum HCV RNA titers were measured at the indicated times. $*P < 0.05$, $**P < 0.01$; NS, not significant.

RNA titer increased above the detection limit in only two of five (40%) Core-Wild-ISDR4 mice and in only 1 of 10 (10%) Core-Mutant-ISDR4 mice, and the titers in these mice were lower than in mice with ISDR0 (Fig. 2C). HCV RNA titers failed to increase above the detection limit in mice with Core-Wild-ISDR9 and Core-Mutant-ISDR9 (Fig. 2A).

Influence of Core aa Substitutions on the Effect of IFN. To investigate the influence of aa substitutions in the core region on the effect of IFN, Core-Wild-ISDR0– and Core-Mutant-ISDR0–infected mice were treated with 1000 IU/g of human IFN-alpha daily for 2 weeks. The treatment resulted in a 0.84 ± 0.3 log IU/mL reduction of HCV RNA titer in Core-Wild-ISDR0–infected mice and a 0.79 ± 0.34 log IU/mL reduction in Core-Mutant-ISDR0–infected mice (Fig. 2D).

We also investigated the influence of aa substitutions in the core region on the effect of IFN plus RBV combination therapy. Core-Wild-ISDR0– and Core-Mutant-ISDR0–infected mice were treated with 1000 IU/g of human IFN-alpha and 20 mg/kg of RBV daily for 2 weeks. The treatment resulted in similar HCV RNA reductions in all treated mice. However, as with IFN monotherapy, there were no significant differences in HCV reductions among mice with different aa substitutions in the core region (data not shown). The dose of ribavirin used was relatively small, however, because of the drug's toxicity in mice.

HCV Infectivity, Replication Levels, and IFN Susceptibility by Core aa Substitutions and Genetic Variation in the IL28B Locus. We investigated the influence of IL28B genotypes on HCV infectivity, replication ability, and IFN susceptibility. *In vitro*–transcribed RNA (30 μg) was inoculated into the livers of mice with hepatocytes from donor A (rs8099917 TG and rs12979860 TT) or donor B (rs8099917 TT and rs12979860 CC). Eight weeks after inoculation, serum HCV RNA titers increased above the detection limit in 22 of 25 (88%) mice with hepatocytes from donor A and in 20 of 23 (87%) mice with hepatocytes from donor B (Fig. 3A). Serum HCV RNA levels were

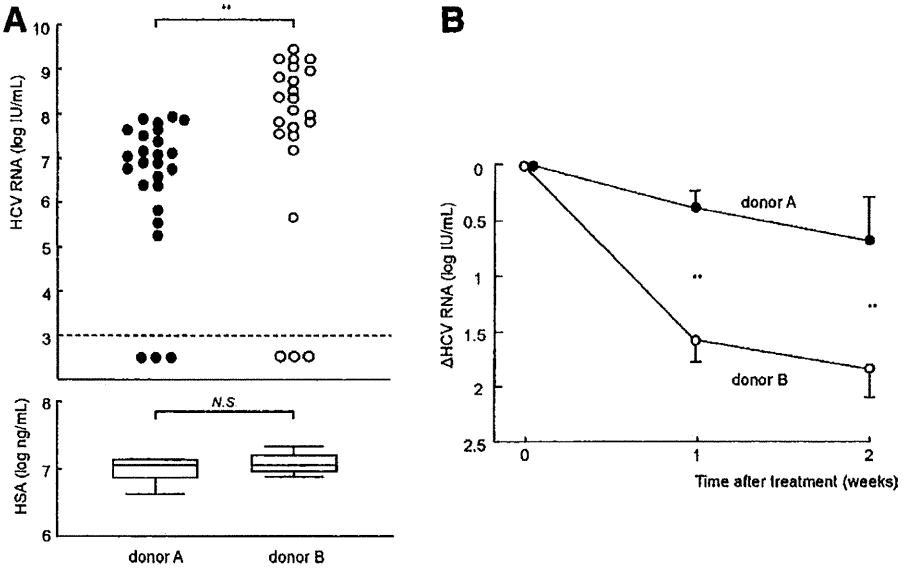

Fig. 3. HCV infectivity, replication ability, and IFN susceptibility in HCV-KT9-injected mice. Mice that underwent transplantation with hepatocytes from donor A (rs8099917 TG and rs12979860 TT) (closed circles, n = 25) or B (rs8099917 TT and rs12979860 CC) (open circles, n = 23) were intrahepatically inoculated with RNA transcribed from either Core-Wild-ISDR0 or Core-Mutant-ISDR0 clones. (A) Eight weeks after infection, serum HCV RNA titers (upper panel) and HSA concentrations (lower panel) were measured. The horizontal dotted line indicates the HCV RNA titer detection limit (1000 copies/mL). In these box-and-whisker plots, lines within the boxes represent median values; the upper and lower lines of the boxes represent the 75th and 25th percentiles, respectively; the upper and lower bars outside the boxes represent the 90th and 10th percentiles, respectively. (B) HCV-infected mice with hepatocytes from donor A (closed circles, n = 12) or B (open circles, n = 8) were treated daily with 1000 IU/g/day of IFN-alpha for 2 weeks. Changes in mice serum HCV RNA titers measured after 1 and 2 weeks are shown. Data are represented as mean ± standard deviation. $*P < 0.05$, $**P < 0.01$; NS, not significant.

significantly higher in mice with hepatocytes from donor B than from donor A ($P < 0.001$). HCV-infected mice were treated with 1000 IU/g of human IFN-alpha daily for 2 weeks. The treatment resulted in 0.65 ± 0.38 and 1.84 ± 0.23 log IU/mL reductions in HCV RNA titer in mice with hepatocytes from donors A and B, respectively ($P < 0.01$) (Fig. 3B). Interestingly, despite the higher serum HCV RNA levels, reduction levels of HCV were higher in mice that underwent transplantation with hepatocytes obtained from donor B than in mice that underwent transplantation with hepatocytes obtained from donor A.

To confirm an association between IL28B SNP genotype and HCV RNA titer, we compared HCV RNA titers using mice with hepatocytes from an additional pair of donors with the favorable (donor C) and unfavorable (donor D) SNP genotypes. To determine whether results obtained by clonal infection would be comparable to results obtained using the more natural serum injection, which should have contained more complex viral species, mice were injected with genotype 1b HCV obtained from a human patient with core and ISDR substitutions, as described above. Mice with hepatocytes from donor C (rs8099917 TG and rs12979860 TT) or donor D (rs8099917 TT and rs12979860 CC) were inoculated intravenously with 10^5 copies of HCV. Eight weeks after inoculation, serum HCV RNA titer increased above the detection limit in 13 of 14 (93%) mice with hepatocytes from donor C (rs8099917 TG and rs12979860 TT) and in 12 of 12 (100%) mice with hepatocytes from donor D (rs8099917 TT and rs12979860 CC) (Fig. 4A). With results similar to those found for the mice inoculated with transcribed HCV RNA, serum HCV RNA levels were significantly higher in mice with hepatocytes from donor D than from donor C ($P < 0.001$), and the effect of IFN was also greater in donor D mice than in donor C mice (Fig. 4B); however, statistical significance using these donors was only achieved at week 1, probably resulting from fluctuation of HCV RNA titers and the small number of animals analyzed.

Expression Levels of ISGs in Mouse Livers. ISG expression levels in mice livers were measured after 2 weeks of IFN treatment (Fig. 4B). MxA, OAS, and PKR levels were significantly higher in mice with human hepatocytes from donor D than from donor C (Fig. 4C).

Discussion

In this study, we investigated the effect of substitutions at core protein aa70 and 91 and within the

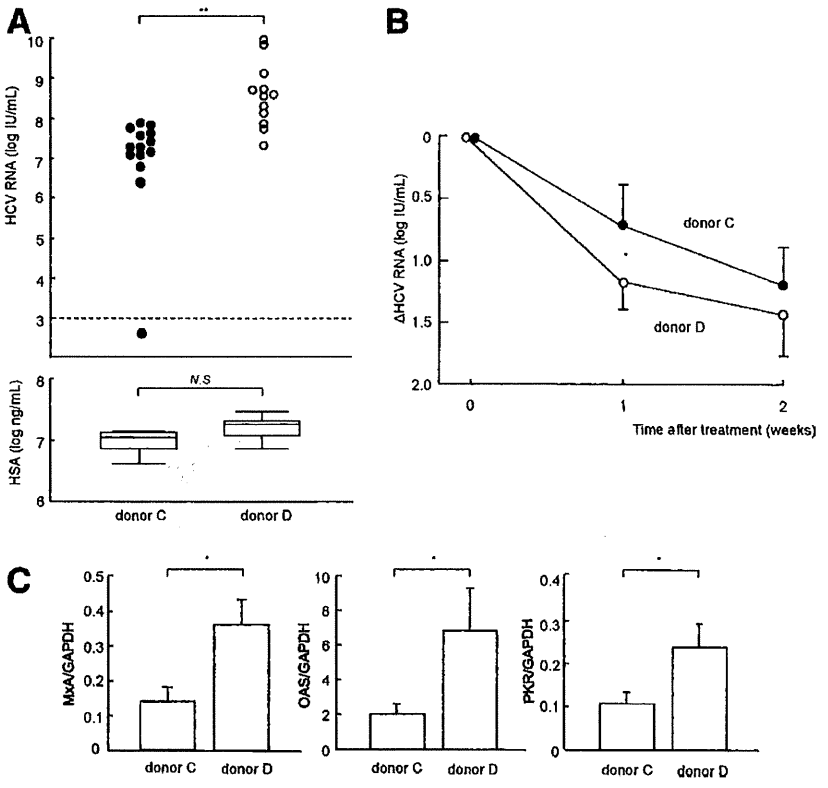

Fig. 4. HCV infectivity, replication ability, and IFN susceptibility in HCV-infected mice. Mice that underwent transplantation with hepatocytes from donor C (rs8099917 TG and rs12979860 TT) (closes circles, n = 14) or D (rs8099917 TT and rs12979860 CC) (open circles, n = 12) were intravenously injected with HCV-infected patient serum samples. (A) Eight weeks after infection, serum HCV RNA titers (upper panel) and HSA concentrations (lower panel) were measured. The horizontal dotted line indicates the HCV RNA titer detection limit (1000 copies/mL). In these box-and-whisker plots, lines within the boxes represent median values; the upper and lower lines of the boxes represent the 75th and 25th percentiles, respectively; the upper and lower bars outside the boxes represent the 90th and 10th percentiles, respectively. HCV-infected mice with hepatocytes from donor C (closed circles, n = 5) or D (open circles, n = 4) were treated daily with 1000 IU/g/day of IFN-alpha for 2 weeks. (B) Changes in mice serum HCV RNA titers measured after 1 and 2 weeks are shown. (C) Intrahepatic ISG expression levels in the IFN-treated mice with donor C (n = 4) or D (n = 3) were measured and expressed relative to GAPDH messenger RNA. Data are reported as mean ± standard deviation. $*P < 0.05$, $**P < 0.01$; NS, not significant.

ISDR, which have been reported to be associated with the outcome of IFN plus ribavirin combination therapy.[8-14] Clones with core aa70 and 91 substitutions showed comparable infection and replication abilities, whereas clones with substitutions in the ISDR showed reduced infectivity and replication rates. It has been reported that patients infected with HCV strains with multiple substitutions in the ISDR have lower viral titers than those with wild-type ISDR, and that these patients respond well to IFN therapy.[8,9] We showed, in this study, that infectivity and replication ability of HCV are apparently impaired in ISDR mutants (Fig. 2A,C). This may explain, at least partially, the better effect of IFN therapy in patients with multiple ISDR mutations. However, why aa substitutions in this particular region are associated with the effect of IFN still remains to be elucidated. In contrast, aa substitutions in the core, which more profoundly affect the outcome of combination therapy,[10-13] did not influence the infectivity and replication ability of the virus (Fig. 2A,B). This suggests that aa substitutions in this region affect response to therapy in a way that is independent of the replication level of the virus. A recent report by Eng et al.[36] showed that a mutation in core aa91 results in the production of minicore protein, which might alter the effect of IFN. The presence of minicore protein and its effect on IFN therapy should be further investigated using the chimeric mouse model.

In contrast to these viral substitutions, host IL28B genotype significantly affected viral replication levels (Figs. 3A and 4A). Curiously, replication levels of the virus are higher in mice with human hepatocytes from donors with rs8099917 TT and rs12979860 CC genotypes, even though these genotypes are associated with successful response to the therapy.[20-22] This result is consistent with clinical observation of higher viral loads in patients with the rs12979860 CC genotype.[20] The favorable IL28B genotype is associated not only with successful response to IFN treatment, but also to spontaneous clearance of the virus.[37,38] However, the incidence of HCV infection was similar in mice with hepatocytes from donors with rs8099917 TT and rs8099917 TG (Figs. 3A and 4A), suggesting that spontaneous clearance was rare. The fact that our animal model was immunodeficient suggests that spontaneous clearance of HCV might require the involvement of the adaptive immune system. The wild-type core protein, aa70, is reported to be found more often in patients with the rs8099917 TT genotype,[23,24] even though patients with this genotype are more likely to be able to eradicate the virus without therapy during

the natural course of infection.[37,38] These data suggest that core aa70 wild-type virus can be eradicated more easily in the natural course of infection, especially in patients with rs8099917 TT or rs12979860 CC genotypes; but once the infection is established, core aa70 wild type replicates more effectively than core aa70 mutant strains.

The effect of IFN on reduction of the virus did not differ between core aa70 wild-type and mutant strains, which showed similar replication levels (Fig. 2D). This is in contrast to clinical observations that the effect of therapy on viral reduction is more prominent in patients with wild-type core protein.[13,25] One of the differences between the mouse model and human patients is term of infection. Long-term HCV infection results in alteration of lipid metabolism and accumulation of lipids in hepatocytes.[39] Patients with fatty change of the liver often fail to respond to therapy.[40] We observed no severe fatty change in mouse livers, suggesting that such long-term change might be absent in this mouse model (data not shown).

On the other hand, the effect of IFN was significantly greater in mice with hepatocytes with the eradication-favorable IL28B genotype (rs8099917 TT and rs12979860 CC) (Figs. 3B and 4B), despite the higher replication rate of the virus. This suggests that the IL28B genotype affects the outcome of therapy based on a different mechanism than viral replication. Because of strong linkage disequilibrium, genotypes of the SNPs around the two IL28B landmark SNPs (rs8099917 and rs12979860) were identical between donors A and C as well as between B and D (data not shown). Further study using human hepatocytes with various IL28B SNP genotypes will identify a primary SNP that directly affects the outcome of therapy. Response to IFN was associated with higher expression levels of ISGs, including MxA, OAS, and PKR (Fig. 4C). This is in agreement with previous studies showing that SVR is associated with stronger induction of ISG expression.[41] However, we observed no statistically significant differences in ISG expression levels from the IL28B SNP genotype before therapy (data not shown). This may result from lower ISG expression levels before therapy and the relatively small number of mice examined. Because there is no adaptive immune system in this mouse model, such differences primarily involve individual hepatocytes, although whether the presence of immune cells enhances this difference should be investigated further.

In summary, we demonstrated that viral infectivity and replication ability are associated with hepatocyte IL28B genotype and are not associated with viral substitutions in the core protein or ISDR. Understanding the mechanism underlying the higher, more prolonged expression of antiviral genes in response-favorable hepatocytes will help us to develop improved therapeutic regimens to eradicate HCV more effectively.

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Rapid Emergence of Telaprevir Resistant Hepatitis C Virus Strain from Wildtype Clone *In Vivo*

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Telaprevir is a potent inhibitor of hepatitis C virus (HCV) NS3-4A protease. However, the emergence of drug-resistant strains during therapy is a serious problem, and the susceptibility of resistant strains to interferon (IFN), as well as the details of the emergence of mutant strains *in vivo*, is not known. We previously established an infectious model of HCV using human hepatocyte chimeric mice. Using this system we investigated the biological properties and mode of emergence of mutants by ultra-deep sequencing technology. Chimeric mice were injected with serum samples obtained from a patient who had developed viral breakthrough during telaprevir monotherapy with strong selection for resistance mutations (A156F [92.6%]). Mice infected with the resistant strain (A156F [99.9%]) developed only low-level viremia and the virus was successfully eliminated with interferon therapy. As observed in patients, telaprevir monotherapy in viremic mice resulted in breakthrough, with selection for mutations that confer resistance to telaprevir (e.g., a high frequency of V36A [52.2%]). Mice were injected intrahepatically with HCV genotype 1b clone KT-9 with or without an introduced resistance mutation, A156S, in the NS3 region, and treated with telaprevir. Mice infected with the A156S strain developed lower-level viremia compared to the wildtype strain but showed strong resistance to telaprevir treatment. Although mice injected with wildtype HCV showed a rapid decline in viremia at the beginning of therapy, a high frequency (11%) of telaprevir-resistant NS3 V36A variants emerged 2 weeks after the start of treatment. *Conclusion:* Using deep sequencing technology and a genetically engineered HCV infection system, we showed that the rapid emergence of telaprevir-resistant HCV was induced by mutation from the wildtype strain of HCV *in vivo*. (HEPATOLOGY 2011;54:781-788)

Chronic hepatitis C virus (HCV) infection is a leading cause of cirrhosis, liver failure, and hepatocellular carcinoma.[1,2] The current standard treatment for patients chronically infected with HCV is the combination of peg-interferon (PEG-IFN) and ribavirin (RBV).[3-5] However, this treatment results in sustained viral response (SVR), defined as negative for HCV RNA 24 weeks after cessation of the therapy, in only about 50% of patients with genotype 1 HCV infection with high viral loads.[3-5] Given the low

Abbreviations: HCV, hepatitis C virus; HSA, human serum albumin; PEG-IFN, peg-interferon; RBV, ribavirin; RT-PCR, reverse transcript-polymerase chain reaction; SCID, severe combined immunodeficiency; SVR, sustained viral response; uPA, urokinase-type plasminogen activator.

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effectiveness of the current therapy, many molecules have been screened for antiviral activity against HCV for use in development of novel anti-HCV therapies. A number of new selective inhibitors of HCV proteins, the so-called STAT-C (specifically targeted antiviral therapy for HCV) inhibitors, are currently under development. Telaprevir is a reversible, selective, specific inhibitor of the HCV NS3-4A protease that has shown potent antiviral activity in HCV replicon assays.[6] Although the antiviral effect of telaprevir is quite potent, monotherapy using these drugs results in rapid emergence of drug-resistant strains.[7,8] Accordingly, these drugs are used in combination with pegylated-IFN and ribavirin for chronic hepatitis C patients. Because the HCV virus replicates rapidly and RNA polymerase lacks a proofreading system, HCV viral quasispecies can emerge *de novo*, and some of these variants may confer resistance. Although a resistant variant is initially present at low frequency, it may quickly emerge as the dominant species during antiviral treatment.[9,10] Resistant clones against HCV NS3-4A protease inhibitors have reportedly been induced in replicon systems.

The immunodeficient urokinase-type plasminogen activator (uPA) mouse permits repopulation of the liver with human hepatocytes, resulting in human hepatocyte chimeric mice that are able to develop HCV viremia after injection of serum samples positive for the virus.[11] We and other groups have reported that the human hepatocyte chimeric mouse is useful for evaluating the effect of NS3-4A protease inhibitor.[12,13] Using this mouse model, we developed a reverse genetics systems for HCV.[14,15] This system is useful to study characteristics of HCV strains with various substitutions of interest because the confounding effects of quasispecies can be minimized. Using ultra-deep sequencing technology, we demonstrate the rapid emergence of telaprevir resistance in HCV as a result of mutation from wildtype strain using genetically engineered HCV-infected human hepatocyte chimeric mice.

Materials and Methods

Animal Treatment. Generation of the $uPA^{+/+}$/$SCID^{+/+}$ mice and transplantation of human hepatocytes were performed as described recently by our group.[16] All mice were transplanted with frozen human hepatocytes obtained from the same donor. Mice received humane care and all animal protocols were performed in accordance with the guidelines of the local committee for animal experiments. Infection, extraction of serum samples, and sacrifice were performed under ether anesthesia. Mice were injected either intravenously with HCV-positive human serum samples or intrahepatically with *in vitro*-transcribed genotype 1b HCV RNA. HCV-infected mice were administered either perorally with 200-300 mg/kg of telaprevir (VX950; MP424; Mitsubishi Tanabe Pharma, Osaka, Japan) twice a day or intramuscularly with 1,500 IU/g of IFN-alpha (Dainippon Sumitomo Pharma, Tokyo). The telaprevir dose was determined in a previous study in which this dosage range was found to yield serum concentrations equivalent to treated human patients.[13]

Human Serum Samples. After obtaining written informed consent, human serum samples containing genotype 1b HCV were obtained from two patients with chronic hepatitis. The individual serum samples were divided into aliquots and stored separately in liquid nitrogen until use. The study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki and was approved *a priori* by the Institutional Review Committee.

HCV RNA Transcription and Inoculation into Chimeric Mice. We have previously established an infectious genotype 1b HCV clone HCV-KT9 derived from a Japanese patient with severe acute hepatitis (GenBank access. no. AB435162).[15] We cloned this HCV complementary DNA (cDNA) into plasmid pBR322 under a T7 RNA promoter to create the plasmid pHCV-KT9. Ten μg of plasmid DNA, linearized by *Xba*I (Promega, Madison, WI) digestion, were transcribed in a 100 μL reaction volume with T7 RNA polymerase (Promega) at 37°C for 2 hours and analyzed by agarose gel electrophoresis. Each transcription mixture was diluted with 400 μL of phosphate-buffered saline (PBS) and injected into the livers of chimeric mice.[15] The QuikChange site-directed mutagenesis kit (Stratagene, Foster City, CA) was used to introduce a substitution at amino acid 156 of the NS3 region (A156S).

RNA Extraction and Amplification. RNA was extracted from serum samples by Sepa Gene RV-R (Sankojunyaku, Tokyo), dissolved in 8.8 μL RNase-free H_2O, and reverse transcribed using a random primer (Takara Bio, Shiga, Japan) and M-MLV reverse transcriptase (ReverTra Ace, Toyobo, Osaka, Japan) in a 20-μL reaction mixture according to the instructions provided by the manufacturer. Nested polymerase chain reaction (PCR) and quantitation of HCV by Light Cycler (Roche Diagnostic, Japan, Tokyo) were performed as reported.[15]

Ultra-Deep Sequencing. We adapted multiplex sequencing-by-synthesis to simultaneously sequence

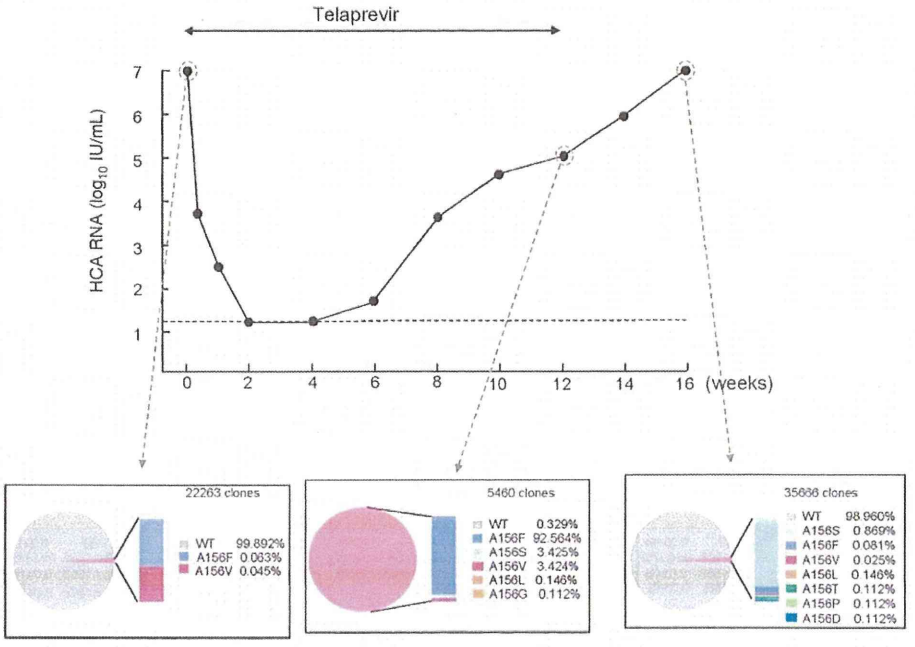

Fig. 1. Changes in serum HCV RNA levels in a telaprevir-treated chronic hepatitis C patient. A 55-year-old woman infected with genotype 1b HCV was treated with 750 mg of telaprevir every 8 hours for 12 weeks. Serum HCV RNA (upper panel) and the amino acid (aa) frequencies at aa156 in the HCV NS3 region by ultra-deep sequencing at the indicated times are shown. The horizontal dotted line indicates the detectable limit (1.2 log copy/mL).

multiple genomes using the Illumina Genome Analyzer. Briefly, cDNA was fragmented using sonication and the resultant fragment distribution was assessed using the Agilent BioAnalyzer 2100 platform. A library was prepared using the Multiplexing Sample Preparation Kit (Illumina, CA). Imaging analysis and base calling were performed using Illumina Pipeline software with default settings.[17-23] The N-terminal 543 nucleotides of NS3 protease were analyzed. This technique revealed an average coverage depth of over 1,000 sequence reads per basepair in the unique regions of the genome. Read mapping to a reference sequence was performed using Bowtie.[24] Because of the short 36 nucleotide read length, mapping hypervariable regions with multiple closely spaced variants against a reference sequence yields poor coverage. Therefore, common variants were identified by relaxing the mismatch settings as well as using *de novo* assembly using ABySS.[25] Multiple alternative reference sequences were included to improve coverage in variable regions. Codon counts were merged and analyzed using R v. 2.12.

Results

Emergence of a Telaprevir-Resistant Variant in a Hepatitis C Patient Treated with Telaprevir and Analysis of the A156F Mutation. A 55-year-old woman infected with genotype 1b HCV was treated with 750 mg of telaprevir every 8 hours for 12 weeks (Fig. 1). After 1 weeks of treatment, serum HCV RNA titer decreased below the detectable limit (1.2 log copy/mL). However, HCV RNA titer became positive by week 4. By week 12, HCV RNA titer had increased to 4.8 log copy/mL and telaprevir treatment was discontinued. Because direct sequence analysis showed an A156F mutation in the NS3 region in the serum samples at 12 weeks, we performed ultra-deep sequence analysis and confirmed the high frequency (92.5%) of A156F mutation. Four weeks after cessation of treatment (at 16 weeks), sequence analysis revealed that the major strain had reverted to wildtype (99%). To analyze the replication ability and the susceptibility of the A156F mutation to telaprevir, 100 μL serum samples containing 10^4 copies of HCV obtained at week 12 were injected into human hepatocyte chimeric mice. Two wildtype HCV-inoculated mice became positive for HCV RNA 2 weeks after inoculation and serum HCV RNA titer increased to high levels (7.6 and 7.8 log copy/mL, respectively) at 6 weeks after inoculation (Fig. 2). In contrast to wildtype HCV-infected mice, a mouse inoculated with serum containing the A156F mutant developed measurable viremia at 4 weeks postinoculation, although serum HCV RNA titer remained low at 6 weeks (5.2 log copy/mL). Eight weeks after inoculation ultra-deep sequence analysis showed a high frequency (99.9%) of A156F mutation. From this point the mouse was administrated 200 mg/kg of telaprevir perorally twice a day for 4 weeks. However, this treatment resulted in no reduction in serum HCV RNA level. During the observation period the A156F mutation remained at

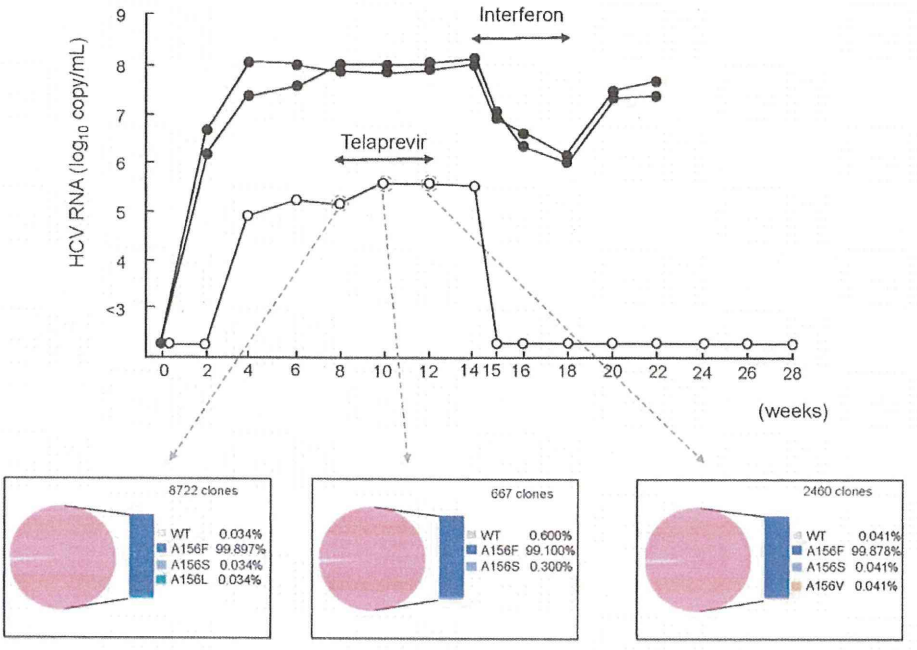

Fig. 2. Changes in serum virus titers in HCV-infected mice. Mice were injected with either wildtype (closed circles) or A156F-mutated HCV serum samples (obtained from an HCV-infected patient who received telaprevir monotherapy for 12 weeks; see Fig. 1) (open circles). Six weeks after injection the A156F mutant mouse was treated with 200 mg/kg of telaprevir orally twice a day for 4 weeks and injected intramuscularly with 1,500 IU/g/day of interferon-alpha for 4 weeks. Serum HCV RNA (upper panel) and amino acid (aa) frequencies at aa156 in the HCV NS3 region by ultra-deep sequencing at the indicated times are shown.

high frequency (>99%). To analyze the susceptibility of the A156F mutation to IFN, wildtype or A156F-mutated HCV-infected mice were treated with 1,500 IU/g/day of IFN-alpha for 4 weeks. Treatment resulted in only a two log reduction in HCV RNA level in wildtype HCV-infected mice. In contrast, serum HCV RNA titer decreased below the detectable limit 1 week after treatment in an A156F-infected mouse. Ten weeks after cessation of IFN-treatment (at week 28), HCV RNA in the mouse serum remained undetectable, suggesting that HCV RNA was eliminated. These results demonstrate that the A156F variant is associated with telaprevir-resistance, but the mutant has low replication ability and a high susceptibility to IFN.

Effect of Telaprevir on HCV-Infected Mice and Sequence Analysis of NS3 Region. Next we investigated the effect of telaprevir on wildtype HCV-infected mice. Two chimeric mice were inoculated intravenously with serum samples containing 10^5 copies of HCV obtained from an HCV-positive patient (Fig. 3). Six weeks after inoculation both mice were administered 200 mg/kg of telaprevir perorally twice a day for 4 weeks. Serum HCV RNA titer in both mice rapidly decreased; however, in one of the mice HCV RNA titer increased again 3 weeks after the start of treatment. Ultra-deep sequence analysis of the NS3 region showed that following the start of telaprevir administration the frequency of the V36A mutation increased from 18% at 2 weeks to 52% at 4 weeks, at which point it was accompanied by an increase in the HCV RNA titer. Two weeks after cessation of telaprevir treatment (at week 12), ultra-deep sequence analysis revealed that the frequency of the V36A mutant had decreased to 13% and the frequency of the wildtype HCV had increased to 84%, although the HCV RNA titer increased only slightly.

Intrahepatic Injection of HCV-KT9-Wild RNA and KT9-NS3-A156S RNA into Human Hepatocyte Chimeric Mice. We previously established an infectious genotype 1b HCV clone, HCV-KT9 (HCV-KT9-wild).[15] We created a telaprevir-resistant HCV clone by introducing an A156S amino acid substitution in the NS3 region of HCV-KT9 (KT9-NS3-A156S) (Fig. 4A). Using wildtype and telaprevir-resistant clones we investigated the replication ability *in vivo*. Mice were injected intrahepatically with 30 μg of *in vitro*-transcribed HCV-KT9-wild RNA or KT9-NS3-A156S RNA. Mice injected with HCV-KT9-wild developed measurable viremia at 2 weeks postinoculation and by 4 weeks postinoculation HCV RNA had reached 10^7 copy/mL (Fig. 4B). On the other hand, mice injected with KT9-NS3-A156S developed measurable viremia at 4 weeks postinoculation but maintained only low levels of viremia. These results suggest that the telaprevir-resistant HCV clone has a lowered replication ability compared to the wildtype HCV clone *in vivo*.

Treatment with Telaprevir and Analysis of Mutagenesis in Mice. Two mice infected with HCV-KT9-wild and one mouse infected with KT9-NS3-A156S were treated with 200 mg/kg of telaprevir twice a day for 2 weeks (Fig. 5A), resulting in 1.4 and 2.7 log