Trace amounts of sporadically reappearing HCV RNA can cause infection

Naga Suresh Veerapu,1 Su-Hyung Park,1 Damien C. Tully,2 Todd M. Allen,2 and Barbara Rehermann1

1Immunology Section, Liver Diseases Branch, National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), NIH, Department of Health and Human Services (DHHS), Bethesda, Maryland, USA.

2Ragon Institute of MGH, MIT, and Harvard, Boston, Massachusetts, USA.

Introduction

At least 170 million people worldwide are persistently infected with hepatitis C virus (HCV), a leading cause of chronic inflammatory liver disease, cirrhosis, and cancer. The vast majority of patients who have been treated for chronic HCV infection received IFN-based treatment regimens. Pegylated interferon (PegIFN) in combination with ribavirin (RBV) has been the standard of care until the recent addition of direct-acting antivirals (1). A sustained virologic response (SVR) is defined as undetectable HCV RNA 6 months after completing pegylated IFN-α/ribavirin therapy. A fourth chimpanzee received HCV RNA-negative plasma and PBMCs from healthy blood donors. The 3 experimental chimpanzees, but not the control chimpanzee, generated HCV-specific T cell responses against nonstructural and structural HCV sequences 6–10 weeks after the first infusion of patient plasma and during subsequent infusions. In 1 chimpanzee, T cell responses declined, and this animal developed high-level viremia at week 27. Deep sequencing of HCV demonstrated transmission of a minor HCV variant from the first infusion donor that persisted in the chimpanzee for more than 6 months despite undetectable systemic viremia. Collectively, these results demonstrate that trace amounts of HCV RNA, which appear sporadically in successfully treated patients, can be infectious; furthermore, transmission can be masked in the recipient by an extended eclipse phase prior to establishing high-level viremia.

Successful hepatitis C virus (HCV) treatment is defined as the absence of viremia 6 months after therapy cessation. We previously reported that trace amounts of HCV RNA, below the sensitivity of the standard clinical assay, can appear sporadically in treatment responders. Here, we assessed the infectivity of this RNA and infused 3 chimpanzees sequentially at 9-week intervals with plasma or PBMCs from patients who tested positive for trace amounts of HCV RNA more than 6 months after completing pegylated IFN-α/ribavirin therapy. A fourth chimpanzee received HCV RNA-negative plasma and PBMCs from healthy blood donors. The 3 experimental chimpanzees, but not the control chimpanzee, generated HCV-specific T cell responses against nonstructural and structural HCV sequences 6–10 weeks after the first infusion of patient plasma and during subsequent infusions. In 1 chimpanzee, T cell responses declined, and this animal developed high-level viremia at week 27. Deep sequencing of HCV demonstrated transmission of a minor HCV variant from the first infusion donor that persisted in the chimpanzee for more than 6 months despite undetectable systemic viremia. Collectively, these results demonstrate that trace amounts of HCV RNA, which appear sporadically in successfully treated patients, can be infectious; furthermore, transmission can be masked in the recipient by an extended eclipse phase prior to establishing high-level viremia.

Results

Trace amounts of HCV RNA that sporadically reappear in patients after successful antiviral therapy can transmit HCV infection. Three HCV-naive chimpanzees, A3A013, A3A015, and A3A017, were intravenously infused at 9-week intervals with human plasma or PBMCs (Table 1 and Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI73104DS1). These samples were derived from previously described anti-HCV–positive patients who had experienced an SVR to IFN-based therapy by qualitative COBAS Amplicor HCV Test 2.0 (the standard clinical test used at the NIH) but sporadically tested positive for trace amounts of HCV in plasma or PBMCs using a nested RT-PCR specific for the 5′-UTR of the virus (Table 1 and ref. 8). A fourth HCV-naive chimpan-
ze, A3A025, served as a control and was infused at the same time intervals with HCV RNA-negative plasma and PBMCs from blood donors without any history of HCV infection.

As shown in Figure 1, the control chimpanzee (A3A025) and 2 of the 3 experimental chimpanzees (A3A015 and A3A017) remained HCV RNA negative in the blood and liver throughout the entire study period, as determined by nested RT-PCR. Consistent with this finding, they did not display any significant increase in ALT activity, a marker of liver injury, remained within the normal range throughout the study (Figure 1).

In contrast, the third experimental chimpanzee, A3A013, tested positive for trace amounts of HCV RNA by nested RT-PCR in the liver at weeks 9 and 20 (Figure 2A), and intrahepatic expression of the IFN-stimulated genes (ISGs) OAS1, IFIT1, MX1, CXCL10, CXCL11, CDBB, and IFNG (data not shown). Alanine aminotransferase (ALT) activity, a marker of liver injury, remained within normal range throughout the study (Figure 1).

To determine the source of the high-level viremia in chimpanzee A3A013, tested positive for trace amounts of HCV RNA by nested RT-PCR in the liver at weeks 9 and 20 (Figure 2A), and intrahepatic expression of the IFN-stimulated genes (ISGs) OAS1, IFIT1, MX1, CXCL10, and CXCL11 was increased at multiple time points (Figure 2). Systemic viremia (2 × 10^6 HCV RNA copies/ml) and increased ALT levels (96 U/l) developed at week 27, the day of the fourth infusion (Figure 2A). Viral titers remained between 10^4 and 10^6 HCV RNA for at least 6 months, indicating chronic HCV infection.

The transmitted HCV remains undetectable in the circulation for 27 weeks prior to causing high-level viremia and chronic infection. To determine the source of the high-level viremia in chimpanzee A3A013, we determined the genotype of the infecting virus from a week-20 liver biopsy and a week-29 serum sample from that chimpanzee and compared it with the HCV genotype in the source patients whose plasma and PBMC samples were infused. Based on the sequence of a 1.4-kb HCV 5'-UTR-core-E1 fragment, the infecting virus was genotype 1b. This excluded the second plasma infusion and the PBMC infusion as potential sources of infection, because these were derived from genotype 5- and 2b–infected patients, respectively (Table 1). Phylogenetic analysis of the HCV sequences from chimpanzee A3A013 at weeks 20 and 29 and the HCV sequences of the remaining 2 source patients revealed that the infecting virus was most closely related to and thus likely transmitted by the first infusion sample (Figure 3, A and B). This was consistent with the detection of HCV RNA in the week-9 liver biopsy, which was obtained after the first and prior to the second plasma infusion (Figure 2A). The extended persistence of this variant in the liver in the absence of systemic viremia was also evidenced by the close sequence homology between the intrahepatic HCV sequence at week 20 and the HCV sequence in the circulation at week 29 (Figure 3).

Next, we performed quasispecies analysis by 454 pyrosequencing of the HCV E2-to-NS5B region. As shown in Figure 4A, we observed a greater HCV sequence diversity in the source patient (at the last time point during PegIFN/RBV therapy with an available serum sample and sufficient viremia for sequencing, i.e., less than 6 weeks prior to the first negative quantitative assay) than in the infected chimpanzee A3A013 (week 27 after infection, P < 0.0001). The dominant HCV E2-to-NS5B sequence in the chimpanzee at week 27 was most closely related to a minor quasispecies that represented 15.20% of the HCV sequences in the source patient (Figure 4B). Overall, 156 differences were identified among 7,800 nucleotides analyzed in the E2-to-NS5B region, translating into 38 amino acid differences between chimpanzee quasispecies Q1 and source patient quasispecies Q2. While the HCV nonstructural sequences were the most conserved between
chimpanzee and patient, most of the sequence divergence was observed in the HCV HVR1 region located at the N terminus of E2 (Figure 4A). Consistent with the results for the entire E2-to-NS5B region, the chimpanzee HVR1 sequence was most closely related to a minor HVR1 sequence in the source patient’s serum (3.83% of all HVR1 sequences; Figure 4C), with only 9 amino acid differences between the 2 populations. This HVR1 variant was already observed in the HCV HVR1 region located at the N terminus of E2 chimpanzee and patient, most of the sequence divergence was observed in the HCV HVR1 region located at the N terminus of E2 (Figure 4A). Consistent with the results for the entire E2-to-NS5B region, the chimpanzee HVR1 sequence was most closely related to a minor HVR1 sequence in the source patient’s serum (3.83% of all HVR1 sequences; Figure 4C), with only 9 amino acid differences between the 2 populations. This HVR1 variant was already detectable in the liver biopsy from chimpanzee A3A013 at week 20 after exposure (not shown), when there was no detectable systemic viremia, and it remained the dominant HVR1 variant when high titer viremia developed.

Taken together, these results demonstrate that trace amounts of HCV that sporadically reappear in the circulation of sustained virological responders to IFN-based therapy can be replication competent and transmit infection. Interestingly, the transmitted HCV demonstrated the same phenotype of low-level persistence and temic viremia, because induction of T cell responses against non-structural and nonstructural HCV sequences (Figure 6B). These results indicate that HCV replication occurred despite the absence of systemic viremia, because induction of T cell responses against non-structural HCV antigens, which are not part of the viral particle, requires the translation of viral RNA in infected cells.

The HCV-specific T cell responses of chimpanzees A3A017, A3A017, and A3A013, but not in control chimpanzee A3A025, after some of the plasma infusions. These responses waned prior to each subsequent infusion (Figure 5A), suggesting that the antibodies were passively transferred with the infused plasma. Antibodies against HCV E2 proteins (of genotype 1a and 1b sequences) were not detected at any time point during the study (Figure 5A).

Next, we examined T cell responses by assessing cytokine production by PBMCs in response to in vitro stimulation with overlapping HCV genotype 1a peptides. As shown in Figure 5B, the 3 experimental chimpanzees, but not the control chimpanzee, mounted HCV-specific T cell responses as early as week 6 after the first infusion (TNF-α expression was quantitated by real-time RT-PCR. Intrahepatic expression of the ISG IFIT1, MX1, CXCL10, CXCL11, CDA8, and IFNG mRNA levels were also quantitated by real-time PCR and did not increase over time (not shown). The 4 arrows in each graph indicate the 4 time points at which chimpanzees were infused with the biospecimens. The dotted blue line indicates the upper limit of normal of ALT levels.

The HCV-specific T cells correlated with control of trace amounts of HCV. We performed a detailed analysis of humoral and cellular immune responses to understand (a) why only 1 of 3 experimental chimpanzees developed systemic viremia and (b) why there was an extended eclipse phase of 27 weeks prior to development of systemic viremia.

As shown in Figure 5A, HCV core-, NS3-, NS4+, and NS5-specific antibodies were transiently detectable in experimental chimpanzees A3A015, A3A017, and A3A013, but not in control chimpanzee A3A025, after some of the plasma infusions. These responses waned prior to each subsequent infusion (Figure 5A), suggesting that the antibodies were passively transferred with the infused plasma. Antibodies against HCV E2 proteins (of genotype 1a and 1b sequences) were not detected at any time point during the study (Figure 5A).

Next, we examined T cell responses by assessing cytokine production by PBMCs in response to in vitro stimulation with overlapping HCV genotype 1a peptides. As shown in Figure 5B, the 3 experimental chimpanzees, but not the control chimpanzee, mounted HCV-specific T cell responses as early as week 6 after the first infusion (TNF-α expression was quantitated by real-time RT-PCR. Intrahepatic expression of the ISG IFIT1, MX1, CXCL10, CXCL11, CDA8, and IFNG mRNA levels were also quantitated by real-time PCR and did not increase over time (not shown). The 4 arrows in each graph indicate the 4 time points at which chimpanzees were infused with the biospecimens. The dotted blue line indicates the upper limit of normal of ALT levels.

The HCV-specific T cell responses of chimpanzees A3A015 and A3A017 that remained aviremic throughout the study differed in 2 aspects from the HCV-specific T cell response of chimpanzee A3A013 that developed chronic, high-level HCV infection.
Discussion

We previously described a window of time toward the end of HCV infection in which most of the HCV has been cleared, but traces of virus sporadically reappear in the circulation. These findings were made in a cohort of patients who sporadically tested positive for HCV RNA by nested RT-PCR within the first years after an SVR to IFN-based therapy. The results are consistent with reports showing residual virus in approximately 6% of SVRs by highly sensitive transcription-mediated amplification assays or nested RT-PCR, even though a relapse with high levels of viremia is exceedingly rare.

Our study now provides proof-of-principle that these PCR signals do indeed reflect replication-competent infectious virus. Indeed, our study may have underestimated the transmission rate, because we had to re-use each chimpanzee for 4 sequential infusions. Thus, HCV-specific T cell responses that were induced by the first infusion may have conferred protective immunity against subsequent infusions with human plasma and PBMCs.

Taken together, these results suggest that HCV-specific T cells play a critical role in preventing the establishment of high-level systemic viremia after exposure to trace amounts of HCV.
The delayed appearance of systemic viremia may be due to several factors. First, the fact that HCV persisted in the absence of systemic viremia in both the source patient (8) and the infused chimpanzee in this study suggests that the unusual course of infection is due to the specific viral isolate rather than to host factors. While we excluded IFN resistance as described in a Japanese population due to mutations in the N-terminal NS5A region (18), it is possible that HCV persists in hepatocytes that become refractory to IFN signaling (19, 20). Notably, the source patient experienced a very slow second-phase virological response to IFN-based therapy (not shown). Second, the low viral titer in the injected plasma may have delayed viremia. Recently, Asabe et al. showed delayed systemic viremia in chimpanzees that had been inoculated with 10^1 genomic equivalents (GE) of HBV per milliliter as compared with those inoculated with 10^7 and 10^4 HBV GE per milliliter (21). As in our study, injection of the low-dose inoculum resulted in chronic infection. Finally, our results support the interesting hypothesis that HCV persists in a form that is refractory to eradication by IFN-based — and possibly even direct-acting antiviral — therapy, as recently proposed by Ralston et al. (22). Consistent with this notion, Bauhofer et al. demonstrated in an in vitro study that long-term exposure of differentiated quiescent hepatoma cells to IFN-α reduced HCV replication 1,000-fold, but did not eliminate HCV, and that viral replication rebounded after IFN-α withdrawal (23).

A final interesting aspect of this study is the immune response that the infected chimpanzees mounted. The passively transferred antibodies likely did not contribute much to the control of HCV infection, because they were unable to eliminate the autologous virus in the source patients, and because their titer decreased rapidly after each infusion in the chimpanzees. While the presence of strain-specific neutralizing antibodies cannot be formally excluded, the current data point to a role of the cellular immune response in the control of low-level HCV infection. Specifically, the induction of T cell responses against nonstructural HCV antigens that are not part of the HCV particle suggests that translation of HCV RNA occurred in infected cells. This was consistent with the detection of intrahepatic HCV RNA and ISG induction in chimpanzee A3A013. Chimpanzees A3A015 and A3A017, which also mounted T cell responses, either may have rapidly controlled A3A013 developed systemic viremia only when HCV-specific T cell responses declined.

Although this study documents that sporadically detected HCV RNA can represent infectious virus, it should not be used to justify virological testing beyond 24 weeks after treatment in patients with an SVR. However, the observed delayed viremia after low-level HCV infection may warrant a longer follow-up of health care workers after HCV exposure. Consistent with the results of our study, a case report described 2 health care workers who developed viremia 5 months and 9 months after needlestick injuries, respectively (16). HCV-specific T cell responses were analyzed in 1 of these individuals and, as in our study, were found to decline just prior to the emergence of systemic viremia (16). Thus, the final testing for HCV RNA and HCV antibodies should occur more than 7 months after exposure, which is a longer follow-up than currently recommended by the Centers for Disease Control and Prevention (CDC) (17).
Three naive chimpanzees, A3A013, A3A015, and A3A017, were naive to HCV infection at any time point during the study.

The presence of T cell responses in the absence of viremia and seroconversion in the 3 experimental chimpanzees is reminiscent of the immune status of subgroups of injection drug users, health care workers, and family members of chronic HCV patients who are frequently exposed to low-level HCV but test negative for HCV RNA and antibodies (24–30). Of note, however, there was no substantial increase in the breadth or strength of the immune response after each exposure, which is consistent with attrition of memory T cell subpopulations after heterologous exposures (31, 32). Starting with each inoculation, they were separated from each other until it was confirmed that they tested negative for HCV at the subsequent bleed date. Chimpanzee serum samples and snap-frozen liver biopsies were collected at the indicated time points (Figure 1, A and B, and Figure 2A) and stored at −80°C. Acid citrate dextrose–anticoagulated blood tubes were shipped overnight to the NIH for isolation of PBMCs and plasma.

Methods

Chimpanzees and experimental design

Three naive chimpanzees, A3A013, A3A015, and A3A017, were intravenously infused at New Iberia Research Center (Lafayette, Louisiana, USA) with 15 to 31 ml plasma from anti-HCV–positive patients who had tested negative for HCV RNA by the standard clinical assay used at the NIH (qualitative COBAS Amplicor HCV Test 2.0; Roche Molecular Diagnostics) but tested positive by nested RT-PCR specific for the HCV 5′-UTR (8). The infused chimpanzees remained negative for HCV RNA in the blood, as determined by RT-nested PCR at weeks 1, 2, and 6 after infusion and were subsequently infused at 9-week intervals with 2 plasma samples and 1 PBMC sample from 3 additional patients (Table 1). A control chimpanzee (A3A025) received, at the same time intervals, plasma and PBMCs from blood donors without any history of HCV. The 4 chimpanzees were not exposed to other chimpanzees with HCV infection at any time point during the study.

Virological assays

Qualitative RT-PCR. RNA was extracted from 1 ml whole blood and 0.2 ml plasma using the Roche High Pure Viral Nucleic Acid Large Volume Kit (Roche Diagnostics) and the QIAamp Viral RNA Mini Kit (QIAGEN), respectively. RT and qualitative nested PCR (detection limit, <40 HCV copies/ml) were performed as previously described (8), except that Superscript III (Invitrogen) and a primer amount of 2.5 pmol were used in the RT reaction. Standard precautions were taken to avoid contamination (34). In particular, samples from HCV-negative donors were included in extraction and in reverse and amplification steps, and RNA extraction and RT were performed in a different building than were the nested PCRs.

Quantification of HCV RNA. Real-time PCR assays (detection limit, 200 copies/ml) were performed as previously described (35) using RNA that was extracted from 150 μl serum with the QIAamp Viral RNA Mini Kit.

HCV sequence analysis using PCR products. HCV RNA was extracted from serum or liver biopsy samples using the High Pure Viral Nucleic Acid Large Volume Kit or the Arcturus PicoPure RNA Isolation Kit (Life Technologies), respectively. To sequence (a) full-length HCV from serum of the source patient and chimpanzee A3A013 at 29 weeks after the first HCV exposure and (b) HCV core-to-E1 from serum of the donor of the third infusion and from a liver biopsy of chimpanzee A3A013 at 20 weeks after the first HCV exposure, a 5.2-kb region encoding...
The HCV 5′-UTR to NS3/NS4A junction was reverse transcribed and amplified using nested PCR as described (36). For full-length HCV sequencing, an additional 4.5-kb region encoding HCV NS4 and NS5 was reverse transcribed using Superscript III (Invitrogen) with primer 5′-CTCAGGCTTATGGGCGTGGAG-3′ and amplified by a nested PCR using Platinum Taq DNA Polymerase High Fidelity (Invitrogen), first-round PCR primers 5′-GCATMTACAGGTTTGTGACTCC-3′ and 5′-ATTGGCCCTGGAGTGTTTAGC-3′, and second-round PCR primers 5′-CATCGTGGGATCAATGTGG-3′ and 5′-GCTGTGATATAGTCTCC-3′. Thermal cycling parameters for first- and second-round
PCR were 95°C for 2 minutes, followed by 35 cycles of 94°C for 30 seconds, 52°C for 35 seconds, and 68°C for 5 minutes, with a final extension step at 68°C for 5 minutes. Purified PCR products were directly sequenced with the ABI Prism BigDye Terminator Cycle Sequencing Reaction kit (Applied Biosystems) using reverse primers (listed in Supplemental Table 1). Sequence contigs were assembled with CodonCode Aligner (version 3.7.1.1; CodonCode Corporation), analyzed, and aligned using CLC Workbench 4, version 4.5.1 (CLC bio, QIAGEN).

**HCV quasispecies analysis by 454 pyrosequencing**

RNA was isolated from 140 μl serum using the QIAamp Viral RNA Mini Kit (QIAGEN). Four overlapping amplicons covering HCV E2 to NS5B were generated from RNA using the SuperScript III One-Step RT-PCR System with Platinum Taq DNA Polymerase High Fidelity (Invitrogen) according to the manufacturer’s protocol (primers are listed in Supplemental Table 1). Thermal cycling parameters were as follows: 55°C for 30 minutes, 94°C for 2 minutes, followed by 40 cycles of 94°C for 15 seconds, 58°C for 30 seconds, and 68°C for 4 minutes, with a final extension step at 68°C for 10 minutes, and then held at 10°C. Purified PCR products from each sample were pooled in equimolar ratios, fragmented using the transposon-mediated Nextera DNA Sample Prep Kit (Illumina) following the manufacturer’s protocol, and purified with a DNA Clean and Concentrator Kit (Zymo Research). Adapters and barcodes were added by limited-cycle PCR (Nextera). Small fragments were removed following Roche’s recommended size selection protocol and quantified using a Promega Quantiflor-ST fluorometer. After quantification, barcoded samples were pooled at a final concentration of 10 μl to create the library for sequencing on the GS Junior 454 Genome Sequencer (Roche Diagnostics). Emulsion PCR, breaking, and DNA sequencing were performed according to the manufacturer’s protocols for Lib-L (Roche Diagnostics). Resulting sequence reads were then assembled into a de novo consensus using AV454 and VICUNA (37, 38). Alignments were generated using Mosaik (version 2.1.73), and reads were cleaned of carry-forward and incomplete extension (CAFIE) and homopolymer/frameshift errors using RC454. After cleaning, reads were passed to V Phaser for variant calling. Briefly, V Phaser uses phase and quality filtering with a probability model that recalibrates quality scores for individual bases to iteratively refine probabilities and to define the threshold required to statistically define a true variant from a sequencing artifact (39). Analyses were further subjected to manual inspection to identify and discard any sequencing artifacts. Global haplotype reconstruction was performed with PredictHaplo, version 5, using the default parameter settings. All consensus genome assemblies and annotations generated as part of this study were submitted to NCBI’s GenBank database (KJ679443 and KJ679444).

**Phylogenetic analysis**

A phylogenetic tree was constructed using the neighbor-joining method from the Kimura 2-parameter distance matrix, and bootstrap values were determined from 1,000 bootstrap resamplings using MEGA software, version 5.05 (Center for Evolutionary Medicine and Informatics). Genotype 1a (HCV-1 [M62321], H77 [AF009606], HCV-H [M67463]), genotype 1b (BK [MS8353], Con1 [AJ238799], CG1b [AF333324], HCV-J [D90208]), genotype 2 (HCV-J8 [D10988]), genotype 5A (HCV-SA13 [AF064490]) reference sequences (Figure 3A), and 27 genotype 1b reference sequences that were arbitrarily chosen from Los Alamos HCV Sequence Data (http://hcv.lanl.gov) (Figure 3B) were included, respectively.

**Intrahepatic gene expression**

Snap-frozen liver biopsies were homogenized with a 0.5-ml pestle and tube (Kimble Chase) in 300 μl extraction buffer, and RNA was isolated using the PicoPure RNA Isolation Kit according to the manufacturer’s instructions. Complementary DNA was synthesized using the MonsterScript 1-Strand cDNA Synthesis Kit (Epiconcent Biotechnologies). TaqMan Gene Expression Assays (Applied Biosystems) were performed in duplicate to determine OAS1, IFIT1, MX1, CXCL10, CXCL11, CDB8, and IFNG mRNA levels. The amount of specific mRNA was calculated using comparative cycle threshold values and standard curves (40), normalized to GAPDH and β internal controls, and expressed as fold induction compared with week-0 data.

**HCV-specific T cell responses**

Freshly isolated PBMCs (2 × 10^6/well) were stimulated in RPMI1640 containing 5% FBS, 100 IU/ml penicillin, 100 μg/ml streptomycin, and 2 mM L-glutamine (Mediatech), with 18 pools of overlapping 15-mer peptides of the HCV genotype 1a (H77) sequence (1 μg/ml per peptide, 600 peptides total), DMSO, or 25 μg/ml phytohemagglutinin (PHA-M) in 96-well round-bottom plates. Culture supernatants were harvested after 42 hours for quantitation of TNF-α, CCL4, CXCL9, and CXCL10 using cytometric bead arrays (BD Biosciences) according to the manufacturer’s protocol.

For IFN-γ ELISPOT assays, CD4^+ and CD8^+ T cells were purified to greater than 95% from PBMCs by positive selection with magnetic beads (Miltenyi Biotec). ELISPOT assays were performed with 10^5
CD4+ or CD8+ T cells per well in the presence of 2 × 10^5 irradiated (30 Gy) autologous CD4 CD8+ cells and 18 pools of overlapping HCV genotype 1a peptides (1 μg/ml per peptide, 600 peptides total), DMSO, or 1 μg/ml phytohemagglutinin (PHA-M) in RPMI1640 containing 5% FBS, penicillin, and glutamine, as described (8). In other IFN-γ ELISPOT assays, 2.5 × 10^5 PBMCs were stimulated with 7 pools of HCV NS3 peptides. Each pool contained 14 overlapping 18-mer peptides of the respective genotype 1a, 2b, and 3 sequence (42 peptides per pool). After a 24-hour culture, plates were processed as described (8). Spots were counted using an AID ELISPOT Reader (Autoimmunagnostik), and the HCV-specific response was calculated by subtracting the mean number of spots in the negative control wells from the mean number of spots in the experimental wells.

**HCV-specific antibody responses**

Plasma samples were tested for HCV core, NS3, NS4, and NS5 antibody levels using the Ortho EGI Vitros system (Ortho-Diagnostics). In addition, an anti-E2 enzyme immunoassay (EIA) was performed as previously described using genotype 1a and genotype 1b HCV E2 (41). An anti-E2 antibody response was considered positive if it was more than 2 times higher than the response at week 0.

**Statistics**

Comparison of the sequence diversity within the source patient and chimpanzee A3A013 was performed using the Mann-Whitney U test. A P value of less than 0.05 was considered statistically significant.

**Study approval**

Chimpanzees were studied under protocols approved by the IACUC of the University of Louisiana at Lafayette (Lafayette, Louisiana, USA). Patients were studied under a protocol approved by the NIDDK/NIAIMS institutional review board and provided written informed consent.

**Acknowledgments**

We thank T.J. Rowell, J. Fontenot, and the staff at New Iberia Research Center for the care of the chimpanzees and technical support; T. Jake Liang, Marc Ghany, and Theo Heller at the Liver Diseases Branch, NIDDK, NIH for patient samples and clinical information; and Colin Ogilvie and Karen Power at the Ragon Institute for technical support with 454 pyrosequencing. This work was supported by the intramural research program of the NIDDK, NIH (to B. Rehermann) and NIAID grant U19 AI082630 (to T.M. Allen).

Address correspondence to: Barbara Rehermann, Immunology Section, Liver Diseases Branch, NIDDK, National Institutes of Health, 10 Center Drive, Bldg. 10, Room 9B16C, Bethesda, Maryland 20892, USA. Phone: 301.402.7144; E-mail: Rehermann@nih.gov.

Naga Suresh Veerapu’s present address is: Department of Life Sciences, Shiv Nadar University, Village Chitera, District Gautam Budh Nagar, Uttar Pradesh, India.

---


