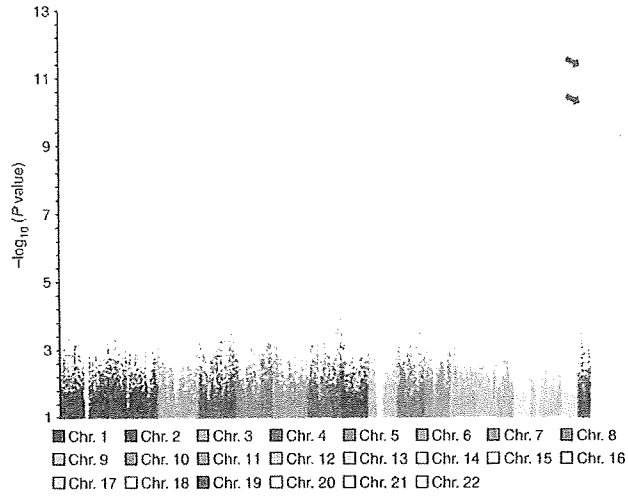

Figure 1 Genome-wide association results with PEG-IFN-α/RBV treatment in 142 Japanese patients with HCV (78 NVR and 64 VR samples). *P* values were calculated by using a χ^2 test for allele frequencies. The dots with arrows for chromosome 19 denote SNPs that showed significant genome-wide associations ($P < 8.05 \times 10^{-8}$) with response to PEG-IFN-α/RBV treatment.

kinetics during treatment, and amino acid pattern in the interferon sensitivity–determining region, have been reported to be significantly associated with the treatment outcome in a number of independent studies[8–10]. Studies have also provided strong evidence that ~20% of patients with HCV genotype 1 and 5% of patients with genotype 2 or 3 have a null response to PEG-IFN-α/RBV. No definite predictor of this resistance is currently available that make it possible to bypass the initial 12–24 weeks' treatment before deciding whether treatment should be continued. If a reliable predictor of non-response were identified for use in patients before treatment initiation, then an estimated 20%, including those who have little or no chance to achieve SVR, could be spared the side effects and cost of treatment.

Host factors, including age, sex, race, liver fibrosis and obesity, have also been reported to be associated with PEG-IFN-α/RBV therapy outcome[11,12]. However, little is known about the host genetic factors that might be associated with the response to therapy: thus far only a few candidate genes, including those encoding type I interferon receptor-1 (*IFNAR1*) and mitogen-activated protein kinase–activated protein kinase 3 (*MAPKAPK3*), have been reported to be associated with treatment response[13,14]. We describe here a GWAS for response to PEG-IFN-α/RBV treatment.

We conducted this GWAS to identify host genes associated with response to PEG-IFN-α/RBV treatment in 154 Japanese patients with HCV genotype 1 (82 with NVR and 72 with virologic response (VR), based on the selection criteria as described in Online Methods). We used the Affymetrix SNP 6.0 genome-wide SNP typing array for 900,000 SNPs. A total of 621,220 SNPs met the following criteria: (i) SNP call rate ≥95%, (ii) minor allele frequency (MAF) ≥1% and (iii) deviation from Hardy-Weinberg equilibrium (HWE) $P \geq 0.001$ in VR samples. After excluding 4 NVR and 8 VR samples that showed quality control (QC) call rates of <95%, 78 NVR and 64 VR samples were included in the association analysis. **Figure 1** shows a genome-wide view of the single-point association data based on allele frequencies. Two SNPs located close to *IL28B* on chromosome 19 showed strong associations, with a minor allele dominant model (rs12980275, $P = 1.93 \times 10^{-13}$, and rs8099917, $P = 3.11 \times 10^{-15}$, respectively), with NVR to PEG-IFN-α/RBV treatment (**Table 1**). The rs8099917 lies between *IL28B* and *IL28A*, ~8 kb downstream from *IL28B* and ~16 kb upstream from *IL28A*. These associations reached genome-wide levels of significance for both SNPs in this initial GWAS cohort (Bonferroni criterion $P < 8.05 \times 10^{-8}$ (0.05/621,220)). The frequencies of minor allele–positive patients were much higher in the NVR group than in the VR group for both SNPs (74.3% in NVR, 12.5% in VR for rs12980275; 75.6% in NVR, 9.4% in VR for rs8099917). Notably, individuals homozygous for the minor allele were observed only in the NVR group. The VR group, as compared to the NVR group, showed genotype frequencies closer to those in the healthy Japanese population[15], yet the minor allele frequencies were slightly higher in the transient virologic response (TVR) group (23.1%, 15.4%) than in the SVR group (9.8%, 7.8%) (**Table 1**). We applied the Cochrane-Armitage test on all the SNPs and found a genetic inflation factor, λ, of 1.029 for the GWAS stage (**Supplementary Fig. 1**). We also carried out principal component analysis in 142 samples for the GWAS stage together with the HapMap samples (CEU, YRI, CHB and JPT) (**Supplementary Fig. 2**); this suggested that the effect of population stratification was negligible.

Table 1 Significant association of two SNPs (rs12980275 and rs8099917) with response to PEG-IFN-α/RBV treatment

					Null responder (NVR[a], *n* = 128)			Responder (VR[a], *n* = 186)			Responder (SVR[a], *n* = 140)			NVR vs. VR		NVR vs. SVR	
dbSNP rsID	Nearest gene	MAF[b] (allele)	Allele (1/2)	Stage	11	12	22	11	12	22	11	12	22	OR (95% CI)[c]	*P* value[d]	OR (95% CI)[c]	*P* value[d]
rs12980275	*IL28B*	0.15 (G)	A/G	GWAS	20 (25.6)	54 (69.2)	4 (5.1)	56 (87.5)	8 (12.5)	0 (0.0)	46 (90.2)	5 (9.8)	0 (0.0)	20.3 (8.3–49.9)	1.93×10^{-13}	26.7 (9.3–76.5)	7.41×10^{-13}
				Replication	10 (20.0)	37 (74.0)	3 (6.0)	101 (82.8)	21 (17.2)	0 (0.0)	73 (82.0)	16 (18.0)	0 (0.0)	19.2 (8.3–44.4)	5.46×10^{-15}	18.3 (7.6–44.0)	8.37×10^{-13}
				Combined	30 (23.4)	91 (71.1)	7 (5.5)	157 (84.4)	29 (15.6)	0 (0.0)	119 (85.0)	21 (15.0)	0 (0.0)	17.7 (10.0–31.3)	2.84×10^{-27}	18.5 (10.0–34.4)	3.99×10^{-24}
rs8099917	*IL28B*	0.12 (G)	T/G	GWAS	19 (24.4)	56 (71.8)	3 (3.8)	58 (90.6)	6 (9.4)	0 (0.0)	47 (92.2)	4 (7.8)	0 (0.0)	30.0 (11.2–80.5)	3.11×10^{-15}	36.5 (11.6–114.6)	5.00×10^{-14}
				Replication	11 (22.0)	37 (74.0)	2 (4.0)	108 (88.5)	14 (11.5)	0 (0.0)	78 (87.6)	11 (12.4)	0 (0.0)	27.4 (11.5–65.3)	9.47×10^{-18}	25.1 (10.0–63.1)	1.00×10^{-14}
				Combined	30 (23.4)	93 (72.7)	5 (3.9)	166 (89.2)	20 (10.8)	0 (0.0)	125 (89.3)	15 (10.7)	0 (0.0)	27.1 (14.6–50.3)	2.68×10^{-32}	27.2 (13.9–53.4)	1.11×10^{-27}

[a]NVR, null virologic response; VR, virologic response; SVR, sustained virologic response. The 186 VRs consisted of 46 transient virologic response (TVRs) and 140 SVRs. [b]Minor allele frequency and minor allele in 184 healthy Japanese individuals[15]. The MAF of the SNPs in SVR is similar to that of TVR group, whereas that of NVR is much higher (76.6%). [c]Odds ratio for the minor allele in a dominant model. [d]*P* value by χ^2 test for the minor allele dominant model.

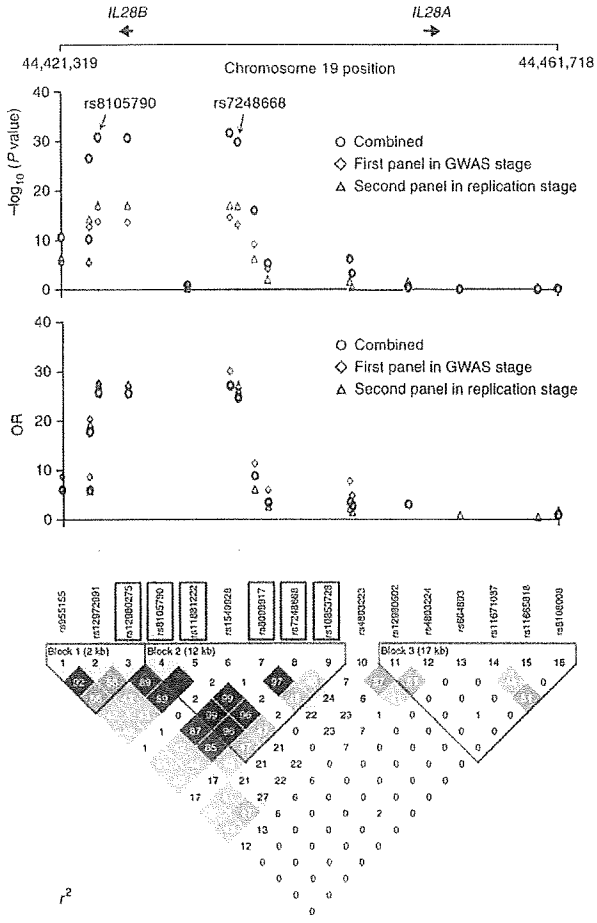

Figure 2 Genomic structure, *P* value and OR plots in association analysis and LD map around *IL28B* and *IL28A* (chr.19, nucleotide positions 44421319–44461718; build 35). *P* values by the χ^2 test for minor allele dominant effect model are shown for the first panel of 142 samples in the GWAS stage, the second panel of 172 samples in the replication stage, and the combined analysis. Below are estimates of pairwise r^2 for 16 SNPs selected in the replication study using a total of 314 Japanese patients with HCV treated with PEG-IFN-α/RBV. Boxes indicate the significantly associated SNPs with response to PEG-IFN-α/RBV treatment both in the GWAS stage and in the replication stage. Dotted lines indicate the region with the strongest associations from the positions of rs8105790 to rs7248668.

We analyzed the region of ~40 kb (chr. 19, nucleotide positions 44421319–44461718; build 35) containing the significantly associated SNPs (rs12980275 and rs8099917) using Haploview software for linkage disequilibrium (LD) and haplotype structure based on the HapMap data for individuals of Japanese ancestry. The LD blocks were analyzed using the four-gamete rule, and four blocks were observed (**Supplementary Fig. 3**). We selected 16 SNPs for both replication study and high-density association mapping, including tagging SNPs estimated on the basis of the haplotype blocks, one SNP located within *IL28B* (rs11881222) and the significantly associated SNPs from the GWAS stage (rs12980275 and rs8099917) (**Supplementary Table 1**).

To validate the results of the GWAS stage, 16 SNPs selected for the replication stage, including the original SNPs, were genotyped using the DigiTag2 assay in an independent set of 172 Japanese patients with HCV treated with PEG-IFN-α/RBV treatment (50 NVR and 122 VR samples), together with the first panel of 142 samples analyzed in the GWAS stage (**Supplementary Table 1**). The associations of the original SNPs were replicated in the replication cohort of 172 patients ($P = 5.46 \times 10^{-15}$, OR = 19.2 for rs12980275; $P = 9.47 \times 10^{-18}$, OR = 27.4 for rs8099917; **Table 1**). The combined *P* values for both stages reached 2.84×10^{-27} (OR = 17.7; 95% CI = 10.0–31.3) and 2.68×10^{-32} (OR = 27.1; 95% CI = 14.6–50.3), respectively (**Table 1**). Notably, when we compared the SVR ($n = 140$) with the NVR group ($n = 128$), the original two SNPs (rs12980275 and rs8099917) again showed strong associations: both *P* values and ORs were similar to those observed in the comparison between VR and NVR, and the combined *P* values for both stages reached 3.99×10^{-24} (OR = 18.5; 95% CI = 10.0–34.4) and 1.11×10^{-27} (OR = 27.2; 95% CI = 13.9–53.4), respectively (**Table 1**). Comparing SVR ($n = 140$) versus NVR plus TVR ($n = 174$), we again found that these SNPs were significantly associated ($P = 1.71 \times 10^{-16}$, OR = 8.8; 95% CI 5.1–15.4 for rs12980275; $P = 1.18 \times 10^{-18}$, OR = 12.1; 95% CI 6.5–22.4 for rs8099917, **Supplementary Table 2**), suggesting that these SNPs would predict NVR as well as SVR before PEG-IFN-α/RBV therapy.

Among the newly analyzed SNPs in the replication study, six (rs12980275, rs8105790, rs11881222, rs8099917, rs7248668 and rs10853728) showed significant associations both in the GWAS stage ($P < 8.05 \times 10^{-8}$) and in the replication stage ($P < 0.0031$ (0.05/16)) after Bonferroni correction. These SNPs are located within a 15.7-kb region that includes *IL28B* (**Fig. 2** and **Supplementary Table 1**). In particular, the strongest associations with NVR were observed for four SNPs, rs8105790, rs11881222, rs8099917 and rs7248668, that are located in the downstream flanking region, the third intron and the upstream flanking region of *IL28B*. The combined *P* values for these polymorphisms were 1.98×10^{-31} (OR = 25.7; 95% CI = 13.9–47.6), 2.84×10^{-31} (OR = 25.6; 95% CI = 13.8–47.3), 2.68×10^{-32} (OR = 27.1; 95% CI = 14.6–50.3) and 1.84×10^{-30} (OR = 24.7; 95% CI = 13.3–45.8), respectively (**Supplementary Table 1**). We then sequenced this region to identify further variants and found three SNPs (rs8103142, rs28416813 and rs4803219) located in the third exon, the first intron and the upstream flanking region of *IL28B*, and a few infrequent variations. These SNPs also showed strong associations in the combined dataset of 128 NVR and 186 VR samples ($P = 1.40 \times 10^{-29}$, OR = 26.6 for rs8103142; $P = 5.52 \times 10^{-28}$, OR = 22.3 for rs28416813; $P = 2.45 \times 10^{-29}$, OR = 23.3 for rs4803219; **Supplementary Table 3**). We also performed LD and haplotype analyses with seven SNPs. These SNPs were in strong LD, and the risk haplotype showed a level of association similar to those of individual SNPs ($P = 1.35 \times 10^{-25}$, OR = 11.1; 95% CI = 6.6–18.6) (**Table 2**). These results suggest that the association with NVR was primarily driven by one of these SNPs.

Table 2 Association analysis of response to treatment by *IL28B* haplotype

SNP							Frequencies			
rs8105790	rs11881222	rs8103142	rs28416813	rs4803219	rs8099917	rs7248668	NVR group	VR group	*P* value	OR (95% CI)
T	**A**	**T**	**C**	**C**	**T**	**G**	0.543	0.942	1.81×10^{-32}	0.1 (0.04–0.12)
C	**G**	**C**	**G**	**T**	**G**	**A**	0.387	0.054	1.35×10^{-25}	11.1 (6.6–18.6)

Association analysis of haplotypes consisting of seven SNPs with response to PEG-IFN-α/RBV treatment in 314 Japanese patients with HCV. Boldface letters: rs11881222 (third intron); rs8103142 (third exon).

Table 3 Factors associated with NVR by logistic regression model

Factors	Odds ratio	95% CI	*P* value
rs8099917 (G allele)	37.68	16.71–83.85	<0.0001
Age	1.02	0.98–1.07	0.292
Gender (Female)	3.32	1.49–7.39	0.003
Re-treatment[a]	1.12	0.55–2.33	0.750
Platelet count	0.93	0.87–1.01	0.080
Aminotransferase level	1.00	0.99–1.00	0.735
Fibrosis stage[20]	1.10	0.73–1.66	0.658
HCV-RNA level	1.01	0.99–1.02	0.139

[a]Re-treatment, non-response to previous treatment with interferon-α (plus RBV).

To examine the relative contribution of factors associated with NVR, we used a logistic regression model. One tagging SNP located within *IL28B* (minor allele of rs8099917) was the most significant factor for predicting NVR, followed by gender (**Table 3**). Clinically, viral factors such as HCV genotype and HCV RNA level are important for the outcome of PEG-IFN-α/RBV therapy. Indeed, mean HCV-RNA level was significantly lower in SVR (SVR versus TVR, $P = 0.002$; SVR versus NVR, $P = 0.016$; **Supplementary Table 4**). Mean platelet count and the proportion of mild fibrosis (F1–F2) were significantly higher in SVR than in NVR.

Real-time quantitative PCR assays in peripheral blood mononuclear cells revealed a significantly lower level of *IL28* mRNA expression in individuals with the minor alleles (**Fig. 3**), suggesting that variant(s) regulating *IL28* expression is associated with a response to PEG-IFN-α/RBV treatment. *IL28B* encodes a cytokine distantly related to type I (α and β) interferons and the interleukin (IL)-10 family. This gene and *IL28A* and *IL29* (encoding IL-28A and IL-29, respectively) are three closely related cytokine genes that encode proteins known as type III IFNs (IFN-λs) and that form a cytokine gene cluster at chromosomal region 19q13 (ref. 16). The three cytokines are induced by viral infection and have antiviral activity[16,17]. All three interact with a heterodimeric class II cytokine receptor that consists of IL-10 receptor beta (IL10Rβ) and IL-28 receptor alpha (IL28Rα, encoded by *IL28RA*)[16,17], and they may serve as an alternative to type I IFNs in providing immunity to viral infection.

Notably, a recent report showed that the strong antiviral activity evoked by treating mice with TLR3 or TLR9 agonists was significantly reduced in both $IL28RA^{-/-}$ and $IFNAR^{-/-}$ mice, indicating that IFN-λ is important in mediating antiviral protection by ligands for TLR3 and TRL9 (ref. 18). IFN-λ induced a steady increase in the expression of a subset of IFN-stimulated genes, whereas IFN-α induced the same genes with more rapid and transient kinetics[19]. Therefore, it is possible that IFN-λ induces a slower but more sustained response that is important for TLR-mediated antiviral protection. This might be one of the ways that a genetic variant regulating *IL28* expression influences the response to PEG-IFN-α/RBV treatment. Further research will be required to fully understand the specific mechanism by which a genotype might affect the response to treatment.

In conclusion, the strongest associations with NVR were observed for seven SNPs, rs8105790, rs11881222, rs8103142, rs28416813, rs4803219, rs8099917 and rs7248668, that are located in the downstream flanking region, the third intron, the third exon, the first intron and the upstream flanking region of *IL28B*. Further studies following our report of this robust genetic association to NVR may make it possible to develop a pre-treatment predictor of which individuals are likely to respond to PEG-IFN-α/RBV treatment. This would remove the need for the initial 12–24 weeks of treatment that is currently used as a basis for a clinical decision about whether treatment should be continued. That would allow better targeting of PEG-IFN-α/RBV treatment, avoiding the unpleasant side effects that commonly accompany the treatment where it is unlikely to be beneficial, and reduce overall treatment costs. Because of the small number of samples in this study, we plan to conduct a further prospective multicenter study to establish these SNPs as a clinically useful marker.

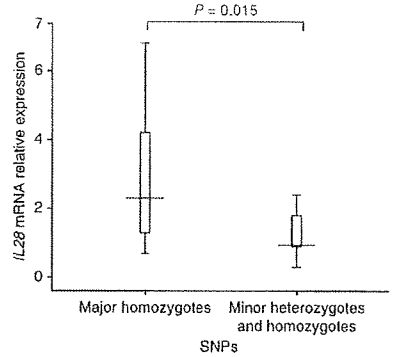

Figure 3 Quantification of *IL28* mRNA expression. The expression level of *IL28* genes was determined by real-time quantitative RT-PCR using RNA purified from peripheral blood mononuclear cells. Distribution of relative gene expression levels was compared between the individuals homozygous for major alleles ($n = 10$) and the heterozygous or homozygous individuals carrying minor alleles ($n = 10$) of rs8099917 by using the Mann-Whitney *U*-test. The bars indicate the median. All samples were obtained from HCV-infected patients before PEG-IFN-α/RBV therapy.

METHODS

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

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

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AUTHOR CONTRIBUTIONS

Study design and discussion: Y.T., N.N., N.M., K.T., M.M.; sample collection: Y.T., M.K., K.M., N.S., M.N., M.K., K.H., S.H., Y.I., E.M., E.T., S.M., Y.M., M.H., A.S., Y.H., S.N., I.S., M.I., K.I., K.Y., F.S., N.I.; genotyping: N.N.; statistical analysis: N.N., A.K., K.I.; quantitative RT-PCR: M.S.; manuscript writing: Y.T., N.N., K.T., M.M.

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1. Ray Kim, W. Global epidemiology and burden of hepatitis C. *Microbes Infect.* 4, 1219–1225 (2002).
2. Manns, M.P. *et al.* Peginterferon alfa-2b plus ribavirin compared with interferon alfa-2b plus ribavirin for initial treatment of chronic hepatitis C: a randomised trial. *Lancet* **358**, 958–965 (2001).

3. Fried, M.W. *et al.* Peginterferon alfa-2a plus ribavirin for chronic hepatitis C virus infection. *N. Engl. J. Med.* **347**, 975–982 (2002).
4. Hadziyannis, S.J. *et al.* Peginterferon-alpha2a and ribavirin combination therapy in chronic hepatitis C: a randomized study of treatment duration and ribavirin dose. *Ann. Intern. Med.* **140**, 346–355 (2004).
5. Bruno, S. *et al.* Peginterferon alfa-2b plus ribavirin for naive patients with genotype 1 chronic hepatitis C: a randomized controlled trial. *J. Hepatol.* **41**, 474–481 (2004).
6. Sezaki, H. *et al.* Poor response to pegylated interferon and ribavirin in older women infected with hepatitis C virus of genotype 1b in high viral loads. *Dig. Dis. Sci.* **54**, 1317–1324 (2009).
7. Fried, M.W. Side effects of therapy of hepatitis C and their management. *Hepatology* **36**, S237–S244 (2002).
8. Pascu, M. *et al.* Sustained virological response in hepatitis C virus type 1b infected patients is predicted by the number of mutations within the NS5A-ISDR: a meta-analysis focused on geographical differences. *Gut* **53**, 1345–1351 (2004).
9. Shirakawa, H. *et al.* Pretreatment prediction of virological response to peginterferon plus ribavirin therapy in chronic hepatitis C patients using viral and host factors. *Hepatology* **48**, 1753–1760 (2008).
10. Akuta, N. *et al.* Predictive factors of early and sustained responses to peginterferon plus ribavirin combination therapy in Japanese patients infected with hepatitis C virus genotype 1b: amino acid substitutions in the core region and low-density lipoprotein cholesterol levels. *J. Hepatol.* **46**, 403–410 (2007).
11. Walsh, M.J. *et al.* Non-response to antiviral therapy is associated with obesity and increased hepatic expression of suppressor of cytokine signalling 3 (SOCS-3) in patients with chronic hepatitis C, viral genotype 1. *Gut* **55**, 529–535 (2006).
12. Gao, B., Hong, F. & Radaeva, S. Host factors and failure of interferon-alpha treatment in hepatitis C virus. *Hepatology* **39**, 880–890 (2004).
13. Matsuyama, N. *et al.* The dinucleotide microsatellite polymorphism of the IFNAR1 gene promoter correlates with responsiveness of hepatitis C patients to interferon. *Hepatol. Res.* **25**, 221–225 (2003).
14. Tsukada, H. *et al.* A polymorphism in MAPKAPK3 affects response to interferon therapy for chronic hepatitis C. *Gastroenterology* **136**, 1796–1805 (2009).
15. Nishida, N. *et al.* Evaluating the performance of Affymetrix SNP Array 6.0 platform with 400 Japanese individuals. *BMC Genomics* **9**, 431 (2008).
16. Kotenko, S.V. *et al.* IFN-λs mediate antiviral protection through a distinct class II cytokine receptor complex. *Nat. Immunol.* **4**, 69–77 (2003).
17. Sheppard, P. *et al.* IL-28, IL-29 and their class II cytokine receptor IL-28R. *Nat. Immunol.* **4**, 63–68 (2003).
18. Ank, N. *et al.* An important role for type III interferon (IFN-lambda/IL-28) in TLR-induced antiviral activity. *J. Immunol.* **180**, 2474–2485 (2008).
19. Marcello, T. *et al.* Interferons alpha and lambda inhibit hepatitis C virus replication with distinct signal transduction and gene regulation kinetics. *Gastroenterology* **131**, 1887–1898 (2006).
20. Desmet, V.J., Gerber, M., Hoofnagle, J.H., Manns, M. & Scheuer, P.J. Classification of chronic hepatitis: diagnosis, grading and staging. *Hepatology* **19**, 1513–1520 (1994).

ONLINE METHODS

Study cohorts. From April 2007 to April 2009, samples were obtained from 314 patients with chronic HCV (genotype 1) infection who were treated at 15 multicenter hospitals (liver units with hepatologists) throughout Japan. Each patient was treated with PEG-IFN-α2b (1.5 μg per kg body weight (μg/kg) subcutaneously once a week) or PEG-IFN-α2a (180 μg/kg once a week) plus RBV (600–1,000 mg daily depending on body weight). As a reduction in the dose of PEG-IFN-α and RBV can contribute to a less sustained virological response[21], only patients with an adherence of >80% dose for both drugs during the first 12 weeks were included in this study. HBsAg-positive and/or anti-HIV–positive individuals were excluded from this study.

NVR (seen in ~20% of total treated patients) was defined as less than a 2-log-unit decline in the serum level of HCV RNA from the pre-treatment baseline value within the first 12 weeks and detectable viremia 24 weeks after treatment. VR was defined as the achievement of SVR or transient TVR in this study; SVR was defined as undetectable HCV RNA in serum 6 months after the end of treatment, whereas TVR was defined as a reappearance of HCV RNA in serum after treatment was discontinued in a patient who had undetectable HCV RNA during the therapy or on completion of the therapy. Of 878 patients with HCV genotype 1 treated by PEG-IFN-α/RBV at 14 hospitals, only 114 (13.0%) met the criteria for NVR in this study. For the GWAS stage of the study, a case-control study was conducted comparing individuals with NVR (82 individuals) and VR (72 individuals). For the replication stage, an independent cohort of samples from 172 Japanese patients with HCV genotype 1, including 50 with NVR and 122 with VR, was obtained from an independent cohort study at Tokyo Medical and Dental University Hospital (Ochanomizu Liver Conference Study Group) and Musashino Red Cross Hospital. Clinical data from the combined cohorts, with a total of 140 SVR, 46 TVR and 128 NVR patients, are shown in **Supplementary Table 4**.

Informed consent was obtained from each patient who participated in the study. The study protocol conforms to the relevant ethical guidelines as reflected in *a priori* approval by the ethics committees of all the participating universities and hospitals.

SNP genotyping and data cleaning. In the GWAS stage, we genotyped 154 Japanese patients with HCV receiving PEG-IFN-α/RBV treatment using the Affymetrix Genome-Wide Human SNP Array 6.0 according to the manufacturer's instructions. After exclusion of 4 NVR samples and 8 SVR samples with QC call rates <95%, the remaining 142 samples were recalled using the Birdseed version 3 software (Affymetrix). The average overall call rate of 78 NVR and 64 VR samples reached 99.46% and 99.46%, respectively. We then applied the following thresholds for QC in data cleaning: SNP call rate ≥95% for all samples, MAF ≥1% for all samples and HWE *P* value ≥0.001 for VR group[22,23]. A total of 621,220 SNPs on autosomal chromosomes passed the QC filters and were used for association analysis. All cluster plots for the SNPs showing $P < 0.001$ in association analyses by comparing allele frequencies in NVR and VR groups were checked by visual inspection. SNPs with ambiguous genotype calls were excluded. **Supplementary Table 5** shows SNPs that might be weakly associated with NVR ($P < 10^{-4}$).

Although the 12 samples noted above were excluded from the GWAS stage by data cleaning, their quality was good enough for the SNP typing in the replication study, and thus they were included in the replication stage. In the subsequent replication stage with high-density association mapping, SNP genotyping in the independent set of 172 patients was completed using the DigiTag2 assay[24] and direct sequencing using the Applied Biosystems 3730 DNA Analyzer (Applied Biosystems). In addition, strongly associated SNPs identified in the GWAS stage were also genotyped for the GWAS samples using the DigiTag2 assay, and the results were 100% concordant to those from the GWAS platform.

Screening for new polymorphisms. To determine possible genomic variants in the region of *IL28B* and its promoter, we sequenced the 3.3-kb region in a total of 48 Japanese patients with HCV (28 NVR and 20 VR). We selected 7 samples from NVR patients who were minor allele homozygotes for 2 SNPs (rs12980275 and rs8099917), 11 samples from NVR and 10 samples from VR heterozygotes, and 10 samples from NVR and 10 samples from VR major allele homozygotes. The sequencing primers were designed using the Visual OMP Nucleic Acid software (**Supplementary Table 6**). PCR was carried using TaKaRa LA *Taq* polymerase (Takara Biochemicals) under the following thermal cycler conditions: stage 1, 94 °C for 1 min; stage 2, 98 °C for 10 s, 68 °C for 15 min, for a total of 30 cycles; stage 3, 72 °C for 10 min. A 50-μl PCR analysis was performed using 2.5 U TaKaRa LA *Taq* with 1× LA PCR buffer II, 0.4 mM dNTP, 10 pmol of each primer and 10 ng of genomic DNA. For sequencing, 7.0 μl of the PCR products were incubated with 3 μl of Exonuclease I/Shrimp Alkali Phosphatase (Takara Biochemicals) first for 90 min at 37 °C and then for another 10 min at 80 °C. Sequencing reactions were performed with the use of a BigDye Terminator Cycle Sequencing FS Ready Reaction Kit (Applied Biosystems). After purification with MultiScreen-HV (Millipore) and Sephadex G-50 Fine (GE Healthcare UK Ltd.), the reaction products were applied to the Applied Biosystems 3730 DNA Analyzer.

In the variation screening, three SNPs (rs8103142, rs28416813 and rs4803219) and a few infrequent variations were detected. We then typed these SNPs in all of the 314 patients.

Statistical analysis. The observed association between a SNP and response to PEG-IFN-α/RBV treatment was assessed by χ^2 test with a two-by-two contingency table in three genetic models: allele frequency model, dominant-effect model and recessive-effect model. SNPs on the X chromosome were removed because gender was not matched between the NVR group and the VR group. A total of 621,220 SNPs passed the QC filters in the GWAS stage; therefore, significance levels after the Bonferroni correction for multiple testing were $P = 8.05 \times 10^{-8}$ (0.05/621,220) in the GWAS stage and $P = 0.0031$(0.05/16) in the replication stage. None of the 16 markers genotyped in the replication stage showed deviations from Hardy-Weinberg equilibrium in the VR group ($P > 0.05$).

The inflation factor λ was estimated based on the median χ^2 and revealed to be 1.029 (median) and 1.011 (mean), suggesting that the population substructure should not have any substantial effect on the statistical analysis (**Supplementary Fig. 1**). In addition, the principal component analysis on the 142 patients (78 NVR samples and 64 VR samples) analyzed in the GWAS stage together with the HapMap samples also revealed that the effect of population stratification was negligible (**Supplementary Fig. 2**).

For the replication study and the high-density association mapping, 16 SNPs were selected from the region of ~40 kb (chr. 9, nucleotide positions 44421319–44461718; build 35) containing the significantly associated SNPs (rs12980275 and rs8099917) in the GWAS stage by analyzing, using Haploview software, LD and haplotype structure based on the HapMap data for individuals of Japanese descent. These SNPs included tagging SNPs estimated on the basis of haplotype blocks, SNPs located within the *IL28B* and *IL28A* genes (rs11881222 and rs576832, respectively) and the significantly associated SNPs identified in the GWAS stage (**Supplementary Table 1**). On the basis of the genotype data from the total of 314 patients in the GWAS stage and replication stages, haplotype blocks were estimated using the four-gamete rule, and three blocks were observed (**Fig. 2**). Association of haplotype with response to PEG-IFN-α/RBV treatment was analyzed using Haploview software.

The logistic regression model was used to assess the factors associated with NVR. STATA 10 (Statacorp LP) was used for all analysis. Age, platelet count, and aminotransferase (ALT) and HCV-RNA levels were applied as continuous variables.

Real-time quantitative RT-PCR for *IL28* gene. A layer of mononuclear cells was collected via Ficoll from peripheral blood. Total RNA was isolated using the RNeasy Mini Kit and the RNase-Free DNase Set (Qiagen) according to the manufacturer's protocol. First-strand cDNA was synthesized using SuperScript II reverse transcriptase with Oligo $(dT)_{12-18}$ primer (Invitrogen). The relative quantification of the target gene was determined using Custom TaqMan Gene Expression Assays, and the expression of glyceraldehyde-3-phosphate dehydrogenase was used to normalize the gene expression level (Applied Biosystems) according to the manufacturer's protocol. The data were analyzed by the $2[-\Delta\Delta C_t]$ method using Sequence Detector version 1.7 software (Applied Biosystems). A standard curve was prepared by serial tenfold dilutions of

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human cDNA. The curve was linear over 7 logs with a correlation coefficient of 0.998. The specific detection of *IL28B* in real-time PCR is hard to establish, because the nucleotide differences between *IL28A* and *IL28B* consist of only 9 nucleotides scattered throughout the gene. Primers and probes are designed for the *IL28* gene (**Supplementary Table 6**).

URLs. The results of the present GWAS have been registered at a public database: https://gwas.lifesciencedb.jp/cgi-bin/gwasdb/gwas_top.cgi.

21. McHutchison, J.G. *et al.* Adherence to combination therapy enhances sustained response in genotype-1-infected patients with chronic hepatitis C. *Gastroenterology* **123**, 1061–1069 (2002).
22. Miyagawa, T. *et al.* Variant between *CPT1B* and *CHKB* associated with susceptibility to narcolepsy. *Nat. Genet.* **40**, 1324–1328 (2008).
23. Miyagawa, T. *et al.* Appropriate data cleaning methods for genome-wide association study. *J. Hum. Genet.* **53**, 886–893 (2008).
24. Nishida, N., Tanabe, T., Takasu, M., Suyama, A. & Tokunaga, K. Interferons alpha and lambda inhibit hepatitis C virus replication with distinct signal transduction and gene regulation kinetics. *Gastroenterology* **131**, 1887–1898 (2006).

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Absence of viral interference and different susceptibility to interferon between hepatitis B virus and hepatitis C virus in human hepatocyte chimeric mice☆

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***Background/Aims*: Both hepatitis B virus (HBV) and hepatitis C virus (HCV) replicate in the liver and show resistance against innate immunity and interferon (IFN) treatment. Whether there is interference between these two viruses is still controversial. We investigated the interference between these two viruses and the mode of resistance against IFN.**

***Methods*: We performed infection experiments with either or both of the two hepatitis viruses in human hepatocyte chimeric mice. Huh7 cell lines with stable production of HBV were also established and transfected with HCV JFH1 clone. Mice and cell lines were treated with IFN. The viral levels in mice sera and culture supernatants and messenger RNA levels of IFN-stimulated genes were measured.**

***Results*: No apparent interference between the two viruses was seen *in vivo*. Only a small (0.3 log) reduction in serum HBV and a rapid reduction in HCV were observed after IFN treatment, regardless of infection with the other virus. In *in vitro* studies, no interference between the two viruses was observed. The effect of IFN on each virus was not affected by the presence of the other virus. IFN-induced reductions of viruses in culture supernatants were similar to those in *in vivo* study.**

***Conclusions*: No interference between the two hepatitis viruses exists in the liver in the absence of hepatitis. The mechanisms of IFN resistance of the two viruses target different areas of the IFN system.**

Keywords: **Superinfection; JFH-1; IFN-stimulated genes**

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Abbreviations: GAPDH, glyceraldehydes-3-phosphate dehydrogenase; HBeAg, hepatitis B e antigen; HBsAg, hepatitis B surface antigen; HBV, hepatitis B virus; HCV, hepatitis C virus; IFN, interferon; OAS, 2′,5′-oligoadenylate synthetase; PCR, polymerase chain reaction; SCID, severe combined immunodeficiency; uPA, urokinase-type plasminogen activator.

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1. Introduction

Both hepatitis B virus (HBV) and hepatitis C virus (HCV) infections are serious health problems worldwide. More than 350 million people are infected with HBV, and more than 170 million people are infected with HCV [1,2]. Both types of hepatitis viruses result in the development of chronic liver infection and lead to death due to liver failure and hepatocellular carcinoma [3]. To date, interferon (IFN) remains one of the most important drugs available for the treatment of both types of hepatitis viral infections. Although it is assumed that IFN suppresses viral replication through the effect of IFN-induced gene products such as mixovirus resistance protein A (MxA), RNA-dependent protein kinase (PKR), and 2′,5′-oligoadenylate synthetase (OAS) [4], the precise mechanism of action of these proteins on both hepatitis viruses are unknown.

Coinfection with both viruses leads to a rapid and severe progression of chronic liver disease [5], with a higher risk of hepatocellular carcinoma [6]. Currently, there is a debate about whether or not there is interference between the two hepatitis viruses, with some favoring such interference [7] and others arguing against such a concept [8]. A number of mechanisms can cause interference between viruses. A major mechanism of interference is induction of IFN by one virus to prevent replication of the second virus; however, viruses develop their own strategies to resist the effect of IFN. In clinical practice, practitioners often perceive that reduction of HBV in serum by IFN therapy is poorer compared with HCV. HCV levels in sera of IFN-treated patients decrease relatively rapidly, and a proportion of patients eventually show complete eradication of the virus. Furthermore, the recent use of pegylated IFN (PEG-IFN) in combination with ribavirin has improved the eradication rate [9]. Eradication of HBV by IFN, however, is usually difficult, even when using IFN combined with ribavirin [10].

The mechanisms developed by viruses to resist host innate immunity, including IFN signaling, are well established in some viruses. Such mechanisms involve interruption of IFN signaling by interacting molecules that transduce the signal from the IFN receptor through the Janus kinase (Jak) signal transducer and activator of transcription (STAT) pathway [4]. Viral proteins of paramixoviruses, for example, inhibit IFN signaling [11]. Several studies have also examined the mechanisms by which HCV resists the host immune system. These include degradation of Cardif adaptor protein by NS3A/4 protease [12]. Generally, expression of HCV protein is associated with inhibition of STAT1 function independent of STAT tyrosine phosphorylation [13]. Additionally, expression of the HCV core protein in cultured cells is associated with increased expression levels of the suppressor of cytokine signaling 3 (SOCS-3) [14]. The NS5A and E2 proteins are both inhibitors of PKR [15]. These strong actions of HCV against innate immunity are consistent with the high chronicity rate of the virus. IFN, however, effectively reduces HCV replicon in Huh7 cells [16], suggesting that the virus has little potential to disturb the actions of IFN.

In contrast to HCV, the mechanisms of IFN resistance by HBV are poorly understood. To date, only a few studies have reported the molecular mechanisms of HBV resistance against the actions of IFN. The HBV-related resistance to IFN, for example, involves upregulation of protein phosphatase 2A (PP2A) as the primary event, which subsequently leads to inhibition of protein arginine methyltransferase 1 (PRMT1) and reduced STAT1 methylation [17]. In addition to these molecular mechanisms, microarray analyses of serial liver biopsies of experimentally infected chimpanzees showed striking differences in the early immune responses to HBV and HCV. HCV, for example, induced early changes in the expression of many intrahepatic genes, including genes involved in type 1 IFN response [18], whereas HBV did not induce any detectable changes in the expression of intrahepatic genes in the first weeks of infection [19].

HBV–HCV double infection is a good model to use for assessment of the mechanism of IFN resistance by these two viruses because one can test the effect of IFN on one virus in the presence of the other virus. Recently, Bellecave et al. [20] established a novel *in vitro* model system in Huh7 cells that allowed the analysis of both viruses in a replicating context and reported the absence of direct viral interference. To this end, we used human hepatocyte chimeric mice and cell culture systems in the present study. The results showed that the presence of HBV does not affect the actions of IFN on HCV and vice versa. These results suggest the lack of interference between the two viruses in liver cells and indicate that the reported interference between the two viruses might be via inflammation including death of infected cells by cytotoxic T cells, cytokines including IFN-α and IFN-β, and interleukins produced by hepatocytes and infiltrating T cells.

2. Materials and methods

2.1. Transfection of Huh7 cells with HBV DNA and HCV RNA

Huh7 cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% (v/v) fetal bovine serum at 37 °C and under 5% CO_2. Cloning of HBV DNA and the plasmid construction were performed as described previously [21]. For production of stably transfected cell lines, Huh7 cells were seeded onto 90-mm-diameter culture dishes. Twenty micrograms of the plasmid pTRE-HB-wt [21] was transfected by the calcium phosphate precipitation method. Twenty-four hours after transfection, the cells were split and cultured in Hygromycin B-DMEM selection medium (300 μg/ml; Invitrogen Japan K.K., Osaka, Japan), while 50 colonies were isolated and cultured for identification of virus-producing cell lines. Clones positive

for both hepatitis B surface antigen (HBsAg) and hepatitis B e antigen (HBeAg) were selected and further analyzed for production of HBV particles. Finally, three cell lines that produced more than 10^5 copies per milliliter of HBV DNA in supernatant were selected and used for further experiments.

For transfection with HCV RNA, we used pJFH1, which contains the complementary DNA of full-length genotype 2a HCV clone JFH1 downstream of the T7 promoter [22]. *In vitro* synthesis of HCV RNA and electroporation into Huh7 cells were performed as described previously [22,23]. Briefly, cells were treated with trypsin, washed twice with ice-cold RNase-free phosphate-buffered saline, and resuspended in Opti-MEM I (Invitrogen, Carlsbad, CA, USA) at a final concentration of 7.5×10^6 cells per milliliter. Then, 10 μg of HCV RNA to be electroporated was mixed with 0.4 mL of cell suspension and subjected to an electric pulse (950 μF and 260 V) using the Gene Pulser II Electroporation System (Bio-Rad, Hercules, CA, USA). After electroporation, the cell suspension was left for 5 min at room temperature and then incubated under normal culture conditions in a 10-cm-diameter cell culture dish.

2.2. Generation of human hepatocyte chimeric mice

Generation of the urokinase-type plasminogen activator $(uPA)^{+/+}$ and severe combined immunodeficiency $(SCID)^{+/+}$ mice and transplantation of human hepatocytes were performed as described recently by our group [21,23,24]. All mice were transplanted with frozen human hepatocytes obtained from the same donor. Infection, extraction of serum samples, and euthanasia were performed under ether anesthesia. The concentration of serum human serum albumin, which correlates with the repopulation index [24], was measured in mice as described previously [21]. All animal protocols described in this study were performed in accordance with the guidelines of the local committee for animal experiments. The experimental protocol was approved by the Ethics Review Committee for Animal Experimentation of Graduate School of Biomedical Sciences, Hiroshima University, Hiroshima, Japan.

2.3. Human serum samples

Human serum samples containing high titers of either HBV DNA (5.3×10^6 copies per milliliter) or genotype 1b HCV (2.2×10^6 copies per milliliter) were obtained from patients with chronic hepatitis with a written informed consent. The individual serum samples were divided into small aliquots and separately stored in liquid nitrogen until use. Chimeric mice were injected intravenously with 50 μL of either HBV- or HCV-positive human serum. Some mice were injected with HBV-positive human serum at 6 weeks after injection of HCV-positive human serum.

2.4. Analysis of HBV and HCV

HBsAg and HBeAg in culture supernatants were measured by commercially available enzyme-linked immunosorbent assay (ELISA) kits (Abbott Japan, Osaka, Japan). DNA was extracted from these samples by SMITEST (Genome Science Laboratories, Tokyo, Japan) and dissolved in 20 μL H_2O [21,25]. 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 random primer (Takara Bio Inc., Shiga, Japan) and M-MLV reverse transcriptase (ReverTra Ace, TOYOBO Co., Osaka, Japan) in a 20-μL reaction mixture according to the instructions provided by the manufacturer [23]. HCV core antigen in the culture medium was detected with HCV Ag assay (Ortho-Clinical Diagnostics, Rochester, NY, USA).

2.5. RNA extraction and measurement of mRNAs of interferon-induced genes by quantitative reverse transcription-polymerase chain reaction

Total RNA was extracted from cell lines using the RNeasy Mini Kit (Qiagen, Valencia, CA, USA). One nanogram of each RNA was reverse transcribed with ReverseTra Ace (TOYOBO Co.) and Random Primer (Takara Bio, Kyoto, Japan). We quantified the transcripts for MxA, OAS, and PKR. Amplification and detection were performed using ABI PRISM 7300 (Applied Biosystems, Foster City, CA, USA). Results were normalized to the transcript levels of glyceraldehydes-3-phosphate dehydrogenase (GAPDH).

2.6. Statistical analysis

Changes in HBV DNA and HCV RNA in mice sera were compared by Mann–Whitney test and unpaired t test. Differences in HBV DNA and HCV core antigen in mice sera and culture supernatants were analyzed by one-way analysis of variance followed by Scheffe's test. A P value of <0.05 was considered statistically significant.

3. Results

3.1. Infection of chimeric mouse with HBV and HCV and susceptibility to interferon

To investigate the interference between HBV and HCV and to examine the effect of IFN on both of these two viruses *in vivo*, we used six human chimeric mice. Each of six mice was inoculated intravenously with 50 μL of serum samples obtained from either HBV- or HCV-positive patients. The median HBV DNA level in HBV-positive serum-inoculated mice was 1.4×10^8 copies per milliliter (range: 5.3×10^6–3.6×10^9 copies per milliliter) at 6 weeks after inoculation (Fig. 1A), similar to our recent observation [21]. Similarly, the median HCV RNA level in HCV-positive human serum-inoculated mice was 1.0×10^7 copies per milliliter (range: 1.2×10^6–0.8×10^7 copies per milliliter) at 4 weeks after inoculation (Fig. 1B), as reported recently by our group [23]. Six weeks after inoculation, three of six HBV- or HCV-infected mice were treated daily with 7000 IU/g per day of intramuscular IFN-α for 2 weeks. Treatment resulted in a decrease of only 0.3 log in mice serum HBV DNA level compared to that in mice without treatment (Fig. 1A). In contrast, the same therapy resulted in a rapid decrease in HCV RNA to undetectable levels, as confirmed by quantitative polymerase chain reaction (PCR; Fig 1B).

To investigate the direct interference of the two viruses, we performed double-infection experiments. Ten chimeric mice were first inoculated intravenously with 50 μL of HCV-positive human serum samples. Six weeks after HCV infection when the mice developed HCV viremia, 50 μL of HBV-positive human serum samples were inoculated intravenously in 5 of 10 HCV-infected mice. All five mice became positive for both HBV and HCV at 2 weeks after HBV infection. No significant decrease in HCV RNA levels was observed in these superinfected mice before or after the development of HBV viremia (Fig. 2A). After HBV infection, there was no apparent decrease in HCV titer (Fig. 2B). Moreover, HBV DNA level in HBV–HCV-coinfected mice was comparable with that of only HBV-infected mice (Fig. 2B). These results sug-

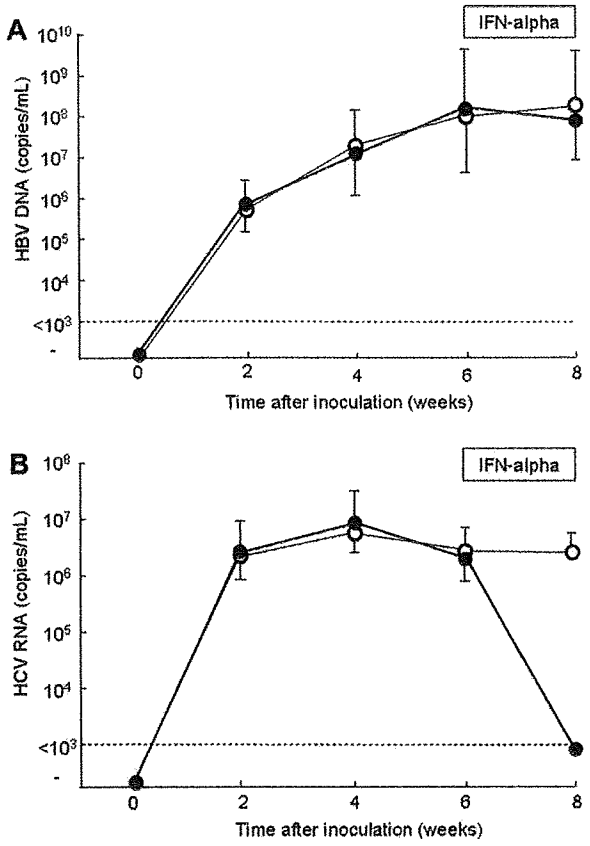

Fig. 1. Changes in serum virus titers in mice inoculated with hepatitis B virus (HBV) – positive or hepatitis C virus (HCV) – positive human serum samples. (A) HBV DNA levels in six mice inoculated with HBV-positive serum samples. (B) HCV RNA levels in six mice inoculated with HCV-positive serum samples. Six weeks after inoculation, three of six mice were treated daily with (closed circles) or without (open circles) 7000 IU/g per day of interferon-alpha intramuscularly for 2 weeks. Mice serum samples were extracted every 2 weeks after inoculation. Data are mean plus or minus standard deviation ($n = 3$). The horizontal dashed line represents the detection limit (10^3 copies per milliliter).

gest no interference between the two viruses in mice, which lack immunocytes known to cause hepatitis.

To further investigate if infection with either of the two hepatitis viruses alters the effect of IFN against the other virus, three HBV–HCV-coinfected mice were treated with IFN-α (Fig. 3A). Such treatment resulted in a rapid decrease in HCV RNA in all mice to undetectable levels as confirmed by quantitative PCR (Fig. 3B). In contrast, no significant decrease in HBV DNA titers was observed in these mice (Fig. 3B). These results are similar to the reduction of HCV RNA and HBV DNA in mice that were infected with either of these hepatitis viruses. These results indicate that HCV is more susceptible to IFN-α than HBV and that each virus does not alter the effect of IFN on the other virus. Because the effect of IFN on HCV was not disturbed by HBV, we assumed that HBV has no effect on the signal from IFN receptor to IFN-stimulated genes. It is possible, however, that HBV and HCV replicated in different cells in these mice. Because it was impossible to detect HCV protein and RNA in HCV-infected mouse liver by histologic examination, we performed *in vitro* experiments.

3.2. Production of both HBV- and HCV-producing cells and the effect of interferon

To investigate the effect of IFN on HBV and HCV *in vitro*, we created cell lines that produce both HBV and HCV. First, we established stable HBV-producing Huh7 cell lines. Three cell lines (Clone-39, -42, and -53) that produced HBsAg, HBeAg, and HBV DNA into the supernatant were selected (Table 1). These cell lines continuously produced HBV for more than 3 months (data not shown). Next, JFH1 RNA was transfected into these HBV-producing cell lines to produce both HBV DNA and HCV proteins into the supernatant. HBV DNA levels in the supernatants of these cell lines decreased in Clone-39, increased in Clone-42, and did not change in Clone-53 after JFH1 transfection (Fig. 4A). In contrast, HCV core antigen levels in the supernatants were higher in two of the three cell lines (Clone-39 and -42) than in Huh7 cells, and the level was not different in the remaining cell line (Clone-53) (Fig. 4B). These results indicate that the production of each of the two viruses does not disturb the replication of the other virus.

3.3. Effects of interferon on HBV and HCV in vitro

The effects of IFN on virus production in both HBV- and HCV-producing cell lines was examined by adding different amounts of IFN-α (0, 50, and 500 IU/mL) into the culture. The mRNA levels of intracellular IFN-stimulated genes such as MxA, OAS, and PKR increased in a dose-dependent manner in all three cell lines as well as in parental Huh7 cells (Fig. 5A). Following the addition of IFN, no apparent reduction of HBV was noted in the supernatant of HBV–HCV-cotransfected cell lines (Fig. 5B). In contrast, the levels of HCV core antigen in the supernatant decreased in all three cell lines treated with IFN, and the decrease was dose-dependent (Fig. 5C).

4. Discussion

Although IFN treatment for chronic HCV infection has improved with the advent of PEG-IFN, the rate of viral eradication remains unsatisfactory [9]. The mechanism responsible for failure of IFN to eradicate the virus completely must be clarified. To study the mechanism of viral resistance against IFN, analysis of viral interference may give us some hints because one of the major mechanisms of interference is through the action of IFN.

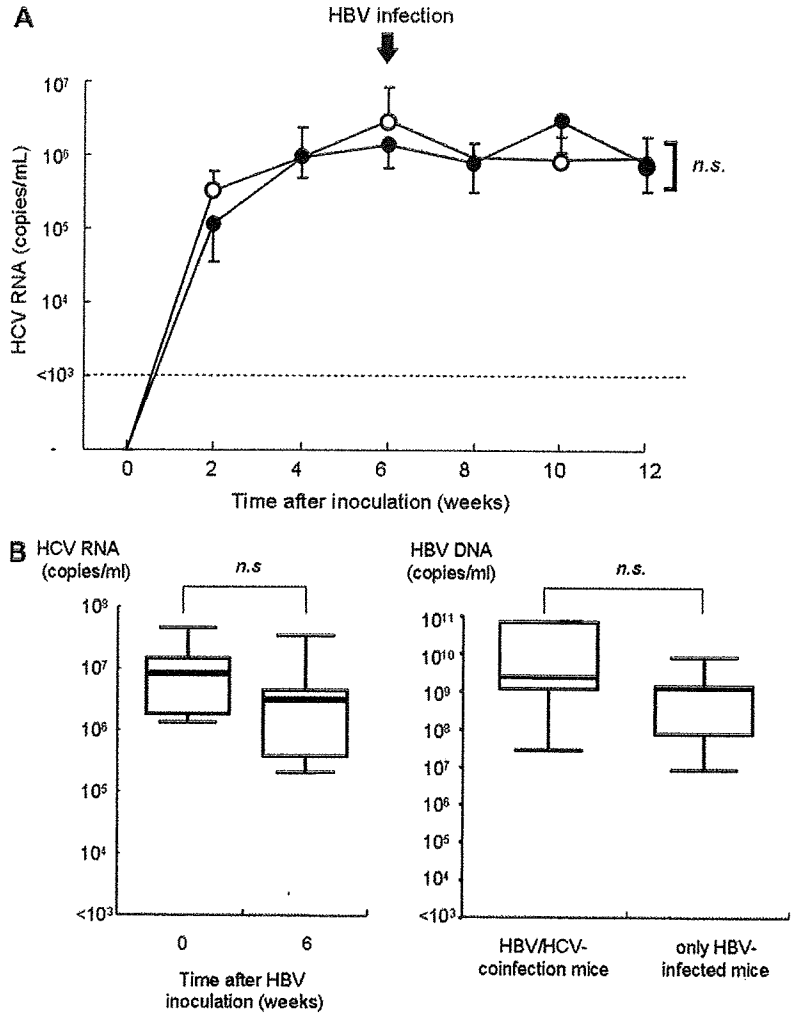

Fig. 2. Comparison of hepatitis C virus (HCV) and hepatitis B virus (HBV) titers in experimentally infected mice. (A) Ten mice were inoculated with HCV-positive serum samples. Six weeks after HCV infection, 5 of the 10 mice were inoculated with HBV-positive human serum samples (closed circles). The remaining five mice (open circles) did not receive HBV inoculation. Data are mean plus or minus standard deviation ($n = 3$). (B) Serum HCV RNA titers in five mice infected with HCV before and at 6 weeks after HBV superinfection (left panel). Serum HBV DNA titers in five mice coinfected with HBV and HCV were compared with those of five mice with HBV infection only (Fig. 1) at 12 weeks after HCV inoculation (right panel). In these box-and-whisker plots, lines within the boxes represent the median values; the upper and lower lines of the boxes represent the 25th and 75th percentiles, respectively.

Accumulation of mononuclear cells is usually seen in the livers of infected individuals, in association with the state of inflammation. It is thus difficult to examine the interference of hepatitis viruses in infection and replication in liver cells without taking into consideration the effect of these immune cells as well as the chemokines and cytokines produced by these cells. Instead, the present study was designed to examine the interference between HBV and HCV in an experimental setup lacking such inflammatory interferences. The SCID-based human hepatocyte chimeric mouse model is ideal for investigating such interaction. We expected either reduction of HCV after inoculation of HBV in HCV-infected mice or failure to develop HBV viremia or low-level HBV viremia in these mice due to viral interference; however, no reduction in HCV titers occurred in these mice, and HBV infection developed in a manner similar to that in naïve mice (Fig. 2). We thus confirmed that there is no interference between the two viruses in the absence of immune reaction via the infiltrating lymphocytes in the liver.

Wieland et al. reported that HBV did not induce any genes during entry or expansion in HBV-infected chimpanzee livers and suggested that HBV was a stealthy virus early in the infection [19]. Because no reduction in HCV was noted during and after the development of high-level HBV viremia, we assume that HBV escapes innate immunity via an excellent mechanism without

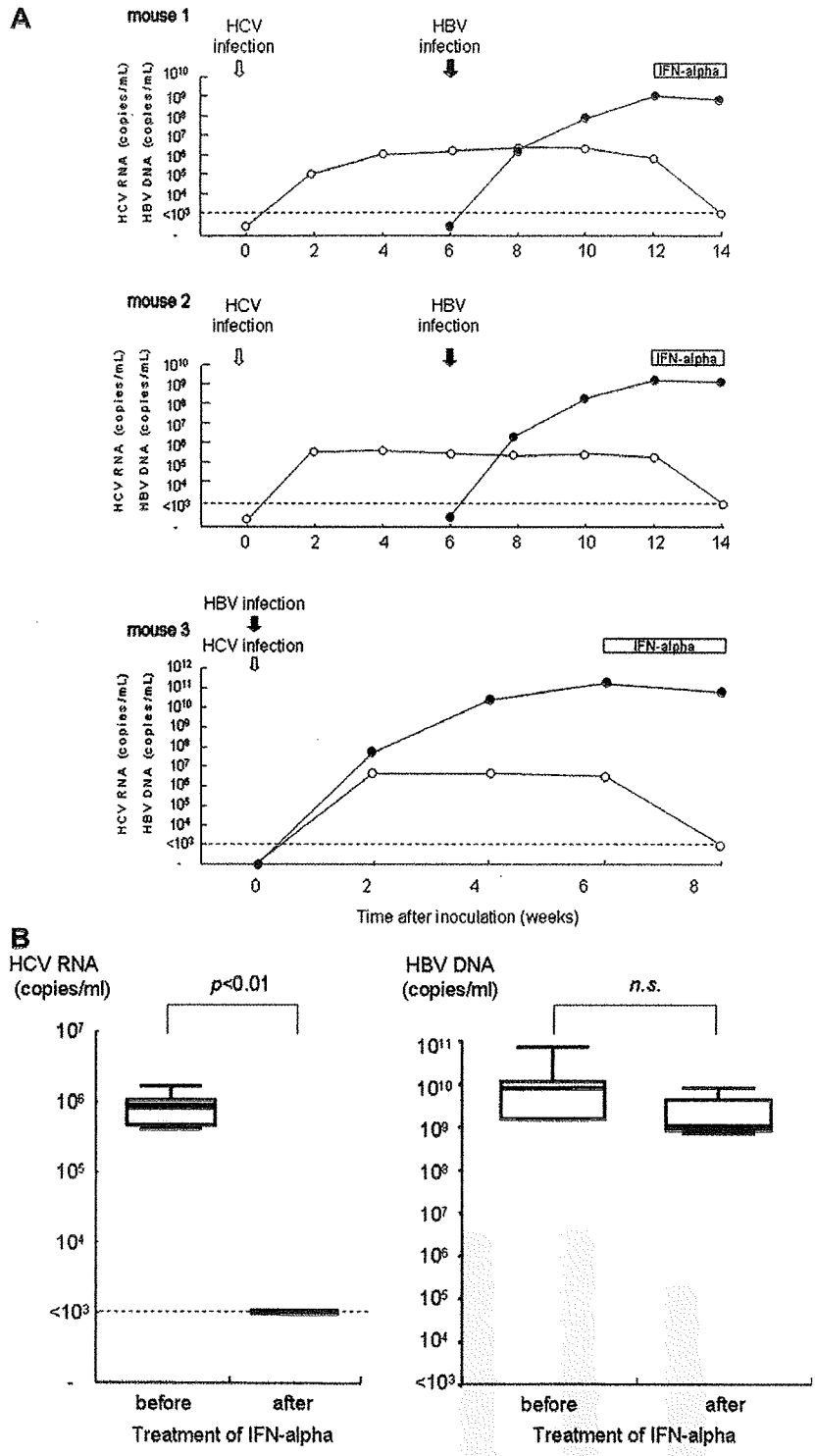

Fig. 3. Changes in serum hepatitis C virus (HCV) RNA and hepatitis B virus (HBV) DNA levels and effects of IFN on HBV–HCV-coinfected mice. Three mice (mouse 1, 2, and 3) were inoculated with both HBV- and HCV-positive human serum samples and treated daily with 7000 IU/g per day of interferon-alpha (IFN-α) intramuscularly for 2 weeks. Mice sera samples were obtained every 2 weeks after injection, and HCV RNA (open circles) and HBV DNA (close circles) were analyzed by quantitative polymerase chain reaction. (A) The horizontal dashed line represents the detectable limit (10^3 copies per milliliter). (B) Serum HCV RNA and HBV DNA titers in mice before and after 2-week IFN-α treatment. In these box-and-whisker plots, lines within the boxes represent median values; the upper and lower lines of the boxes represent the 25th and 75th percentiles, respectively.

Table 1
Hepatitis B virus (HBV) markers in supernatants of stable HBV-transfected cell lines.

Clone	HBsAg (IU/L)	HBeAg (IU/L)	HBV DNA (log copies per milliliter)
39	0.46	4.57	5.2
42	8.16	1.34	5.3
53	0.08	9.29	5.4

Abbreviations: HBsAg, hepatitis B surface antigen; HBeAg, hepatitis B e antigen.

evoking the IFN production system in liver cells. Further study using double-infected mice treated with anti-HBV nucleotide analogs and anti-HCV protease inhibitors should be conducted to confirm the present findings.

With regard to the use of IFN as a treatment, we initially assumed that HBV infection would prevent the effect of IFN on HCV and possibly vice versa in double-infection mice. Unexpectedly, the reduction of HCV by IFN therapy was quite similar in mice infected with HCV only and in those coinfected with HBV and HCV (Figs. 1 and 3). This finding indicated that HBV does not disturb the effect of IFN through signal transduction from the IFN receptor through the Jak-STAT pathway. It was, however, considered possible that HBV and HCV infect different liver cells in mice and replicated without being affected by each other. It has been reported that the same liver cell could be infected with both HBV and HCV [20,26], but it was difficult in the present study to confirm that these two viruses replicate in the same liver cell of mice because it is difficult to visualize HCV antigen and RNA in pathologic sections of the mouse liver. To address this issue, we transfected HCV to stable HBV-producing cell lines (Fig. 4). We thought that both HCV and HBV were produced from successfully HCV RNA transfected cells because transfected cells were stable HBV-producing cells. Presence of the both hepatitis viruses in the same hepatocytes has also been shown by a recent report by Bellecave et al. [20]. We showed in our cell line experiments that only HBV-transfected cell lines produced HBV and that cells cotransfected with HBV and HCV did not show a clear effect of HCV replication on HBV production (Fig. 4A). Similarly, stable production of HBV did not alter the replication of HCV (Fig. 4B). These data are consistent with a recent report [20] that showed that HCV could infect cells producing HBV and suggest a lack of interference between the two viruses in liver cells.

Using HCV-transfected HBV-producing cell lines, we demonstrated that presence of HBV did not disturb the actions of IFN on HCV (Fig. 5C). HCV utilizes certain machinery to disrupt the innate immune system; however, once exposed a large concentration of IFN, the virus shows high sensitivity, as shown in the replicon system [16,27]. Thus, HCV seems to have a relatively weak ability to disturb the antiviral actions of IFN compared with HBV. In contrast, HBV showed strong resistance against IFN in cells with diminished HCV replication [28]. The fact that HBV does not disturb IFN signaling but resists the actions of IFN suggests that HBV counteracts the actions of IFN at IFN-induced antiviral product levels.

Although the culture environment is different from the replicon system, the JFH1 strain seems relatively resistant to IFN [29]. This suggests that the core and envelope proteins, which are absent in the replicon system, might play a role in IFN resistance; however, we could not show any effect for HCV infection on the actions of IFN on HBV replication. This finding sug-

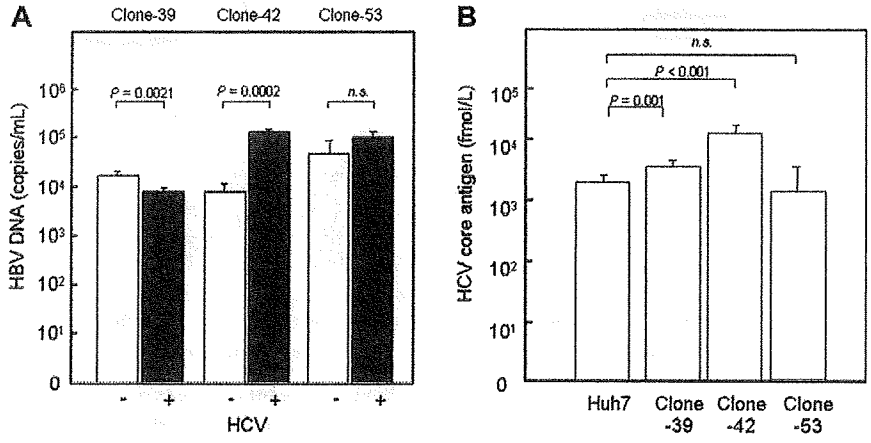

Fig. 4. Virus titers in supernatants of hepatitis B virus (HBV)–transfected or hepatitis C virus (HCV)–transfected cell lines. Huh7 cells were initially stably transfected with 1.4 genome-length HBV DNA. Three cell lines (Clone-39, -42, and -53) producing HBV DNA into the supernatant were selected. (A) HBV DNA levels in supernatants of HBV-producing cell lines 72 hours after transfection with JFH1 RNA (HCV positive) or control plasmid (HCV negative). (B) HCV core antigen levels in the supernatant of parental Huh7 cells and HBV-producing cell lines 72 h after transfection with JFH1 RNA. Data are mean plus or minus standard deviation ($n = 3$).

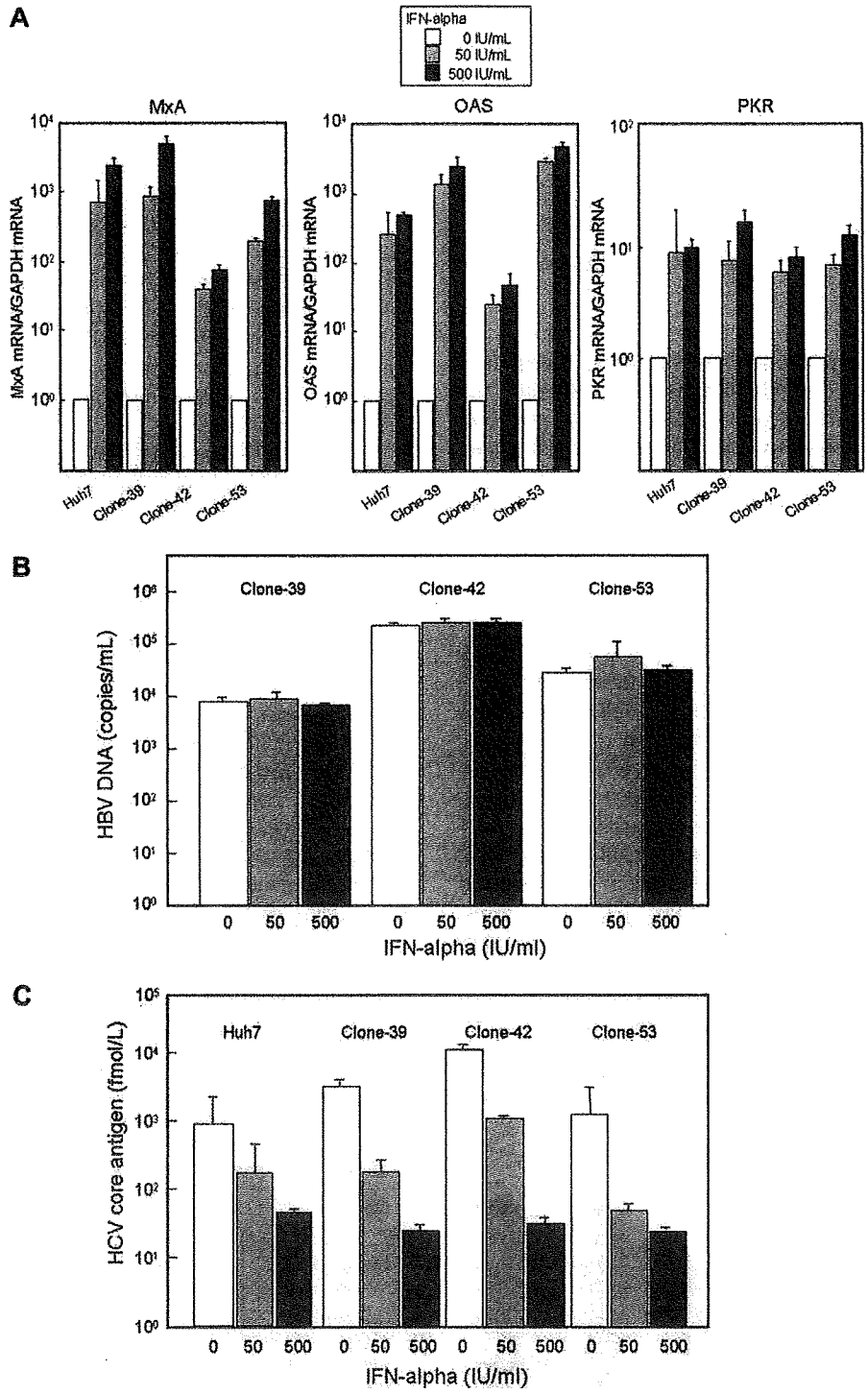

Fig. 5. Effects of interferon (IFN) treatment on hepatitis B virus (HBV) and hepatitis C virus (HCV) *in vitro*. Parental Huh7 cells and three HBV-transfected Huh7 cell lines (Clone-39, -42, and -53) were transfected with JFH1 RNA. Immediately after JFH1 transfection, the cell lines were treated with IFN-α (0, 50, and 500 IU/mL) for 72 h. (A) Intracellular gene expression levels of mixovirus resistance protein A (MxA), 2′,5′-oligoadenylate synthetase (OAS), and RNA-dependent protein kinase (PKR) were measured. RNA levels were expressed relative to glyceraldehydes-3-phosphate dehydrogenase (GAPDH) messenger RNA. (B) HBV DNA and (C) HCV core antigen in supernatants were measured. Data are mean plus or minus standard deviation ($n = 3$).

gests that the core and envelope proteins have only a weak effect on IFN resistance.

In clinical practice, HBV shows high resistance against IFN therapy. This is also the case in the cell culture system, as we showed in this study and has been reported in previous studies [20,28]. The mechanism by which hepatitis viruses resist IFN needs to be clarified in order to develop new and effective therapies for eradication of these viruses.

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References

[1] Maddrey WC. Hepatitis B: an important public health issue. J Med Virol 2000;61:362–366.
[2] Global surveillance and control of hepatitis C. Report of a WHO Consultation organized in collaboration with the Viral Hepatitis Prevention Board, Antwerp, Belgium. J Viral Hepat 1999;6:35–47.
[3] Beasley RP. Hepatitis B virus. The major etiology of hepatocellular carcinoma. Cancer 1988;61:1942–1956.
[4] Samuel CE. Antiviral actions of interferons. Clin Microbiol Rev 2001;14:778–809.
[5] Sagnelli E, Coppola N, Scolastico C, Filippini P, Santantonio T, Stroffolini T, et al. Virologic and clinical expressions of reciprocal inhibitory effect of hepatitis B, C, and delta viruses in patients with chronic hepatitis. Hepatology 2000;32:1106–1110.
[6] Chiaramonte M, Stroffolini T, Vian A, Stazi MA, Floreani A, Lorenzoni U, et al. Rate of incidence of hepatocellular carcinoma in patients with compensated viral cirrhosis. Cancer 1999;85:2132–2137.
[7] Cacciola I, Pollicino T, Squadrito G, Cerenzia G, Orlando ME, Raimondo G. Occult hepatitis B virus infection in patients with chronic hepatitis C liver disease. N Engl J Med 1999;341:22–26.
[8] Raimondo G, Brunetto MR, Pontisso P, Smedile A, Maina AM, Saitta C, et al. Longitudinal evaluation reveals a complex spectrum of virological profiles in hepatitis B virus/hepatitis C virus-coinfected patients. Hepatology 2006;43:100–107.
[9] Fried MW, Shiffman ML, Reddy KR, Smith C, Marinos G, Gonçales Jr FL, et al. Peginterferon alfa-2a plus ribavirin for chronic hepatitis C virus infection. N Engl J Med 2002;347:975–982.
[10] Liu CJ, Lai MY, Chao YC, Liao LY, Yang SS, Hsiao TJ, et al. Interferon alpha-2b with and without ribavirin in the treatment of hepatitis B e antigen-positive chronic hepatitis B: a randomized study. Hepatology 2006;43:742–749.
[11] Gotoh B, Komatsu T, Takeuchi K, Yokoo J. Paramyxovirus strategies for evading the interferon response. Rev Med Virol 2002;12:337–357.
[12] Evans JD, Seeger C. Cardif: a protein central to innate immunity is inactivated by the HCV NS3 serine protease. Hepatology 2006;43:615–617.
[13] Blindenbacher A, Duong FH, Hunziker L, Stutvoet ST, Wang X, Terracciano L, et al. Expression of hepatitis C virus proteins inhibits interferon alpha signaling in the liver of transgenic mice. Gastroenterology 2003;124:1465–1475.
[14] Bode JG, Ludwig S, Ehrhardt C, Albrecht U, Erhardt A, Schaper F, et al. IFN-alpha antagonistic activity of HCV core protein involves induction of suppressor of cytokine signaling-3. FASEB J 2003;17:488–490.
[15] Taylor DR, Shi ST, Romano PR, Barber GN, Lai MM. Inhibition of the interferon-inducible protein kinase PKR by HCV E2 protein. Science 1999;285:107–110.
[16] Frese M, Pietschmann T, Moradpour D, Haller O, Bartenschlager R. Interferon-alpha inhibits hepatitis C virus subgenomic RNA replication by an MxA-independent pathway. J Gen Virol 2001;82:723–733.
[17] Christen V, Duong F, Bernsmeier C, Sun D, Nassal M, Heim MH. Inhibition of alpha interferon signaling by hepatitis B virus. J Virol 2007;81:159–165.
[18] Su AI, Pezacki JP, Wodicka L, Brideau AD, Supekova L, Thimme R, et al. Genomic analysis of the host response to hepatitis C virus infection. Proc Natl Acad Sci USA 2002;99:15669–15674.
[19] Wieland S, Thimme R, Purcell RH, Chisari FV. Genomic analysis of the host response to hepatitis B virus infection. Proc Natl Acad Sci USA 2004;101:6669–6674.
[20] Bellecave P, Gouttenoire J, Gajer M, Brass V, Koutsoudakis G, Blum HE, et al. Hepatitis B and C virus coinfection: a novel model system reveals the absence of direct viral interference. Hepatology 2009;50:46–55.
[21] Tsuge M, Hiraga N, Takaishi H, Noguchi C, Oga H, Imamura M, et al. Infection of human hepatocyte chimeric mouse with genetically engineered hepatitis B virus. Hepatology 2005;42:1046–1054.
[22] Wakita T, Pietschmann T, Kato T, Date T, Miyamoto M, Zhao Z, et al. Production of infectious hepatitis C virus in tissue culture from a cloned viral genome. Nat Med 2005;11:791–796.
[23] Hiraga N, Imamura M, Tsuge M, Noguchi C, Takahashi S, Iwao E, et al. Infection of human hepatocyte chimeric mouse with genetically engineered hepatitis C virus and its susceptibility to interferon. FEBS Lett 2007;581:1983–1987.
[24] Tateno C, Yoshizane Y, Saito N, Kataoka M, Utoh R, Yamasaki C, et al. Near completely humanized liver in mice shows human-type metabolic responses to drugs. Am J Pathol 2004;165:901–912.
[25] Noguchi C, Ishino H, Tsuge M, Fujimoto Y, Imamura M, Takahashi S, et al. G to A hypermutation of hepatitis B virus. Hepatology 2005;41:626–633.
[26] Rodríguez-Iñigo E, Bartolomé J, Ortiz-Movilla N, Platero C, López-Alcorocho JM, Pardo M, et al. Hepatitis C virus (HCV) and hepatitis B virus (HBV) can coinfect the same hepatocyte in the liver of patients with chronic HCV and occult HBV infection. J Virol 2005;79:15578–15581.
[27] Blight KJ, Kolykhalov AA, Rice CM. Efficient initiation of HCV RNA replication in cell culture. Science 2000;290:1972–1974.
[28] Hayashi Y, Koike K. Interferon inhibits hepatitis B virus replication in a stable expression system of transfected viral DNA. J Virol 1989;63:2936–2940.
[29] Miyamoto M, Kato T, Date T, Mizokami M, Wakita T. Comparison between subgenomic replicons of hepatitis C virus genotypes 2a (JFH-1) and 1b (Con1 NK5.1). Intervirology 2006;49:37–43.

Research article

Adoptive immunotherapy with liver allograft–derived lymphocytes induces anti-HCV activity after liver transplantation in humans and humanized mice

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After liver transplantation in HCV-infected patients, the virus load inevitably exceeds pre-transplantation levels. This phenomenon reflects suppression of the host-effector immune responses that control HCV replication by the immunosuppressive drugs used to prevent rejection of the transplanted liver. Here, we describe an adoptive immunotherapy approach, using lymphocytes extracted from liver allograft perfusate (termed herein liver allograft–derived lymphocytes), which includes an abundance of NK/NKT cells that mounted an anti-HCV response in HCV-infected liver transplantation recipients, despite the immunosuppressive environment. This therapy involved intravenously injecting patients 3 days after liver transplantation with liver allograft–derived lymphocytes treated with IL-2 and the CD3-specific mAb OKT3. During the first month after liver transplantation, the HCV RNA titers in the sera of recipients who received immunotherapy were markedly lower than those in the sera of recipients who did not receive immunotherapy. We further explored these observations in human hepatocyte–chimeric mice, in which mouse hepatocytes were replaced by human hepatocytes. These mice unfailingly developed HCV infections after inoculation with HCV-infected human serum. However, injection of human liver–derived lymphocytes treated with IL-2/OKT3 completely prevented HCV infection. Furthermore, an in vitro study using genomic HCV replicon–containing hepatic cells revealed that IFN-γ–secreting cells played a pivotal role in such anti-HCV responses. Thus, our study presents what we believe to be a novel paradigm for the inhibition of HCV replication in HCV-infected liver transplantation recipients.

Introduction

Liver failure and hepatocellular carcinoma (HCC) due to chronic hepatitis C infection are the most common indications for liver transplantation (LT), and the incidences of both have been projected to increase further in the future. Recurrent HCV infection of the allograft is universal, occurs immediately after LT, and is associated with accelerated progression to cirrhosis, graft loss, and death (1, 2). This reflects the suppression of those host-effector immune responses that usually control HCV replication, suggesting that the immunosuppressive environment may play a major role in the rapid progression of recurrent HCV infection after LT (3, 4). Further, the immunosuppressive condition described above is considered to increase the incidence of cancer recurrence after LT in HCC patients. We recently proposed the novel strategy of adjuvant immunotherapy for preventing the recurrence of HCC after LT; this immunotherapy involves intravenously injecting LT recipients with activated liver allograft–derived NK cells (5, 6). Since the immunosuppressive regimen currently used after LT reduces the adaptive immune components but effectively maintains the innate components of cellular immunity (7–9), the augmentation of the NK cell response, which is thought to play a pivotal role in innate immunity, may be a promising immunotherapeutic approach (6). We confirmed that the IL-2/anti-CD3 mAb–treated (IL-2/OKT3–treated) liver allograft–derived NK cells expressed a significantly high level of the tumor necrosis factor–related apoptosis-inducing ligand (TRAIL), which is a critical molecule for tumor cell killing. Further, these cells showed high cytotoxicity against HCC cells, with no such effect on normal cells (5). After obtaining approval from the ethical committee of our institute, we successfully administered adoptive immunotherapy with IL-2/OKT3–treated liver lymphocytes to liver cirrhosis patients with HCC in a phase I trial. Although the long-term benefits of this approach with regard to the control of HCC recurrence after LT remain to be elucidated, this trial provided a unique opportunity to study whether the adoptive administration of IL-2/OKT3–treated liver lymphocytes could also mount an anti-HCV response in HCV-infected LT recipients.

Previous studies have highlighted the important roles of innate lymphocytes in developing immunity against hepatotropic viruses, including HCV (10, 11). In this regard, it is known that patients with chronic HCV infection show diminished NK and NKT cell responses (12–14). In the case of an LT, it has recently been reported that the host CD56$^+$ innate lymphocyte population,

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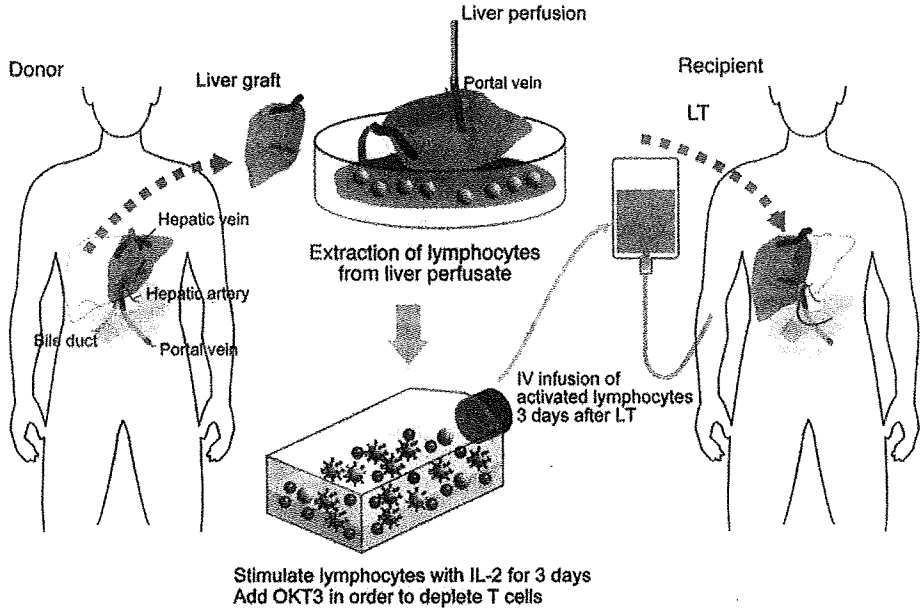

Figure 1
Schematic outline of adoptive immunotherapy with lymphocytes extracted from liver allograft perfusate. The therapy involved giving an intravenous injection of IL-2/OKT3–treated liver lymphocytes to LT recipients. The lymphocytes were extracted from the donor liver graft perfusate. After 3 days of culture with IL-2 (100 JRU/ml), the activated liver NK cell–enriched lymphocytes were administered to the LT recipients through venous circulation. OKT3 (1 μg/ml) was added to the culture medium 1 day before this administration in order to prevent GVHD.

consisting of NK and NKT cells, is appreciably associated with the severity of HCV recurrence after LT (15). These insights into the immunopathogenesis of HCV recurrence indicate that the innate immune components mentioned above are potential targets for therapeutic manipulation. In this study, we have demonstrated for the first time to our knowledge that adoptive immunotherapy with IL-2/OKT3–treated liver lymphocytes, including abundant NK and NKT cells, shows anti-HCV activity after LT, even in an immunosuppressive environment.

Results

Adoptive transfer of IL-2/OKT3–treated liver lymphocytes. The human liver contains a significant number of resident lymphocytes. These cells include abundant $CD56^+$ NK and NKT cells, many of which differ phenotypically and functionally from the circulating cells (14, 16). In our previous study, we performed ex vivo perfusion of the liver through the portal vein, which was necessary in order to flush blood from the liver graft before implantation. Liver-resident lymphocytes were then extracted from the perfusates (number of lymphocytes extracted from normal liver perfusates, 0.5 ± 0.1 cells per gram of liver weight; $n = 14$) (5). Proportions of $CD56^+CD3^-$ NK cells and $CD56^+CD3^+$ NKT cells among the lymphocytes extracted from the liver perfusates (NK cells, 46.4% ± 4.2%; NKT cells, 17.2% ± 2.3%; $n = 14$) were significantly ($P < 0.05$) higher than those among the lymphocytes derived from the peripheral blood of the same donors (NK cells, 21.9% ± 3.7%; NKT cells, 3.8% ± 0.9%; $n = 14$). Extensive preclinical studies have shown that liver allograft–derived resident NK cells mediate remarkably higher cytotoxic activity against HCC cells than do peripheral blood NK cells (5). On this basis, we undertook a clinical trial of adjuvant immunotherapy with IL-2/OKT3–treated liver lymphocytes for preventing the recurrence of HCC after LT in 14 recipients with HCC (Figure 1 and Tables 1 and 2). The therapy involved administering a single intravenous injection of IL-2/OKT3–treated liver lymphocytes to recipients 3 days after LT ($2–5 \times 10^8$ cells injected per subject). In order to prevent graft-versus-host disease (GVHD), i.e., to inactivate $CD3^+$ alloreactive T cells, we added an anti-CD3 mAb, OKT3, to the culture medium a day before the inoculation. During the follow-up period (mean, 23.4 months; range, 10.7–32.9 months), neither any remarkable adverse effects nor rejection episodes occurred. All 14 subjects who received the immunotherapy were alive without recurrence of HCC after LT (including 5 patients with HCC exceeding the Milan criteria; ref. 17). At our institute, the survival rate and recurrence rate of historical control patients with HCC exceeding the Milan criteria were 78% (30 of 37) and 10.8% (4 of 37), respectively. The lymphocytes in the peripheral blood of LT recipients who received immunotherapy in the early postoperative period showed significantly enhanced cytotoxicity against an HCC cell line (HepG2) as compared with those in the peripheral blood of LT recipients who did not receive the therapy in the same period (Figure 2A). Although the gross proportions of NK/NKT cells in the peripheral blood of patients treated with immunotherapy did not differ from those in the peripheral blood of untreated patients, the proportions of $TRAIL^+$ NK cells significantly increased after immunotherapy in the peripheral blood of the former patients. This increase in the $TRAIL^+$ NK cells in the peripheral blood lymphocytes was not observed in untreated patients (Figure 2B). Furthermore, there was a significant correlation between the frequency of $TRAIL^+$ NK cells in the peripheral blood lymphocytes and the NK cytolytic activity of the peripheral blood lymphocytes at 7 days after LT (Spearman rank-order correlation coefficient = 0.54, $P = 0.01$; Figure 2C), indicating the anti-HCC effect of adoptively injected $TRAIL^+$ NK cells. It would be pertinent to conduct additional clinical trials of this immunotherapy for preventing HCC recurrence after LT.

Anti-HCV activity after adoptive immunotherapy. Of the 14 LT recipients who received the immunotherapy, 7 had chronic HCV infection. During the period of this trial, 5 other HCV-infected LT recipients who did not agree to receive immunotherapy served as controls; the background of the controls, including HCV genotype, age, and immunosuppressive therapy, was similar to that of the immunotherapy recipients (Table 3). It has been reported

Table 1
Recipient and tumor characteristics

Patient no.	Age (yr)	Sex	MELD	Hepatitis virus infection	HLA A	HLA B	HLA C	Milan criteria	AFP (ng/ml)	PIVKA-II (AU/ml)	Tumor no.	Maximum tumor size (mm)	Path. vascular invasion	Path. stage	Postop. months	Outcome
1	67	M	19	B	24,-	13,40	03,-	OUT	–	2,584	5	35	–	III	32.9	Alive
2	53	M	16	B	2603,3303	4002,4403	0304,1403	IN	25.3	43	4	11	–	II	31.0	Alive
3	54	M	7	B	0206,3101	3501,5101	0303,1402	OUT	5.7	213	11	26	–	III	29.4	Alive
4	64	F	16	C	2601,2603	3501,4801	0303,-	IN	5.9	142	–	–	–	–	28.5	Alive
5	59	F	14	B	0206,2601	4002,5502	0102,0304	OUT	<5	65	1	13	b1	II	27.8	Alive
6	47	F	8	C	2402,2601	3501,5201	0303,1202	IN	18	46	3	12	–	II	26.2	Alive
7	57	M	29	B	2402,3101	5101,5201	1202,1402	IN	40.3	514	1	25	–	II	25.4	Alive
8	65	F	18	C	1101,2402	5401,5901	0102,-	IN	–	–	3	6	–	II	24.4	Alive
9	60	F	8	–	1101,3001	1302,4006	0602,0801	OUT	32.8	3,026	2	40	vv1	IVA	22.7	Alive
10	56	M	8	C	2402,3303	5201,5801	0302,1202	OUT	–	304	11	22	–	III	19.1	Alive
11	56	M	9	C	0207,-	4601,-	0102,-	IN	47	20	3	25	–	III	17.5	Alive
12	58	M	22	C	1101,3101	1501,3501	0102,0415	IN	–	62	1	17	–	I	16.5	Alive
13	59	M	6	C	1101,2402	1507,1501	0303,0401	IN	202.9	19	3	16	–	II	15.8	Alive
14	51	M	16	B	1101,2601	4002,5401	0102,0304	IN	–	29	–	–	–	–	10.7	Alive

The Milan criteria specifies that liver cancer patients with a single tumor of 5 or fewer centimeters in diameter or 3 or fewer tumors, each no more than 3 cm in diameter, and with no macrovascular invasion, can expect an excellent outcome after LT, with only a 10% risk of cancer recurrence (31). AFP, alpha fetoprotein; F, female; M, male; MELD, model for end-stage liver disease; PIVKA-II, protein induced by vitamin K absence; Path., pathological; Postop., postoperative.

that HCV RNA concentrations sharply decrease a day after LT and increase rapidly thereafter (3). In some of the patients, who did not receive the immunotherapy, HCV RNA titers remained lower than that of the pretransplant titer 1 week after LT, suggesting the individual variation of increasing tempo. However, in almost all patients, HCV RNA titers exceeded the pretransplantation levels by 2 weeks after LT. Notably, HCV infection disappeared in 2 LT recipients after the immunotherapy, but this was not observed in the case of any HCV-infected LT recipients who did not receive the therapy. In one of these patients (who had the lowest HCV RNA levels before LT), HCV RNA has not been detected to date (20 months after LT), even with a qualitative assay. In the other patient, HCV RNA became detectable at 2 months after LT. On the other hand, the 2 patients with the highest HCV viral loads did not respond at all to the immunotherapy. Thus, the effects of immunotherapy were dependent on the HCV virus load before LT, probably because of the proportion of effectors and targets. All patients with HCV viremia are currently being treated with pegylated IFN-α2b and ribavirin. Nevertheless, during the first month after LT, the HCV RNA titers in the sera of LT recipients who received the immunotherapy were statistically lower than those in the sera of LT recipients who did not receive the therapy ($P < 0.05$) (Figure 3). Among the LT recipients who received the immunotherapy, at 2 weeks after LT, HCV RNA remained undetectable in 4 patients (responders), whereas it was detectable in the other 3 patients (nonresponders). The serum ALT levels did not differ between the responders and nonresponders (Supplemental Figure 1; supplemental material available online with this article; doi:10.1172/JCI38374DS1), suggesting that the immunotherapy did not inhibit HCV RNA by injuring HCV-infected hepatocytes.

In vitro evidence to prove the anti-HCV activity of IL-2/OKT3–treated liver lymphocytes by using HCV replicon–containing hepatic cells. The liver allograft-derived lymphocytes were cultured in complete medium with and without IL-2 for 3 days. This was followed by adding OKT3 to the culture medium 1 day before coculturing the lymphocytes with HCV replicon-containing hepatic cells in a transwell system, at an indicated time. While the freshly isolated liver allograft-derived lymphocytes inhibited HCV replication in the HCV replicon-containing hepatic cells to some extent, the cultivation of these lymphocytes with IL-2/OKT3 markedly promoted anti-HCV activity. Absence of exposure to either IL-2 or OKT3 resulted in reduced anti-HCV activity of the lymphocytes (OKT3 had a more profound influence than IL-2) (Figure 4A). When the lymphocytes were treated with IL-2 alone, the $CD56^+$ fraction, including NK and NKT cells, that had been isolated by magnetic cell sorting inhibited HCV replication more strongly than the $CD56^-$ fraction; further, the $CD3^-CD56^+$ NK cell and $CD3^+CD56^+$ NKT cell subfractions showed equivalent anti-HCV activity (Figure 4, B and C). On the other hand, when the lymphocytes were treated with both IL-2 and OKT3, the $CD56^+$ and $CD56^-$ fractions showed similar levels of anti-HCV activity (Figure 4B). After the treatment with IL-2 and OKT3, IFN-γ was the predominant cytokine in the culture supernatant of the lymphocytes (Figure 5A), and intracellular IFN-γ expression was induced in the $CD3^-CD56^+$ NK, $CD3^+CD56^+$ NKT, and $CD3^+CD56^-$ T cells (Figure 5B). There was no difference between the proportions of $TRAIL^+$ and $TRAIL^-$ $CD3^-CD56^+$ NK cells producing IFN-γ (Supplemental Figure 2). Adding mAb against IFN-γ to the coculture of lymphocytes with HCV replicon cells markedly weakened the anti-HCV effects. The incomplete restoration of the anti-HCV effect by anti–IFN-γ treat-

Table 2
Donor and graft characteristics

Donor no.	Donor age (yr)	Donor sex	HLA A	HLA B	HLA C	Relationship	Graft	Graft weight (g)	No. of cells administered ($\times 10^6$)
1	41	M	24,-	07,40	03,07	Offspring	Right	608	172
2	24	M	2402,2603	4002,2603	0304,5201	Offspring	Right	658	38
3	51	F	0201,2402	0702,3901	0702,-	Spouse	Right	670	129
4	34	M	2601,2603	4001,4801	0303,0401	Offspring	Left	414	143
5	31	M	0206,2402	4002,5401	0102,0304	Offspring	Posterior	702	135
6	53	F	2402,-	5201,5401	0102,1202	Sibling	Right	538	411
7	24	M	2601,3101	4006,5201	0801,1202	Offspring	Right	642	350
8	34	M	1101,-	4001,5401	0102,1502	Offspring	Right	846	229
9	37	M	0201,1101	1501,4006	0702,0801	Offspring	Left	402	811
10	28	M	1101,3303	5502,5801	0102,0302	Offspring	Right	686	517
11	28	M	0207,2402	4601,5201	0102,5201	Offspring	Right	558	414
12	27	M	0201,1101	1501,3501	0303,0415	Offspring	Right	628	509
13	54	F	1101,2402	1501,1507	0303,0401	Sibling	Right	650	460
14	21	F	2601,2603	1501,5401	0102,0303	Offspring	Right	436	382

ment suggests the possibility that other inflammatory cytokines may also be responsible for the anti-HCV effect, although we have not defined them at present (Figure 5C). Thus, the vigorous anti-HCV activity of IL-2/OKT3–treated liver lymphocytes was dependent, at least in part, on their IFN-γ–secreting activity.

IFN-γ–secreting activity in LT recipients after adoptive immunotherapy. At 14 days after LT, the number of IFN-γ–secreting cells in the peripheral blood of LT recipients who received adoptive immunotherapy was significantly higher than that in the peripheral blood of LT recipients who did not receive immunotherapy during the trial period (Figure 6). This result was consistent with the results of the in vitro studies showing the crucial role of IFN-γ produced in IL-2/OKT3–treated liver lymphocytes.

In vivo evidence to prove the anti-HCV activity of adoptive immunotherapy by using HCV-infected human hepatocyte–chimeric mice. HCV-infected mice have previously been developed by inoculating HCV-infected human serum into chimeric urokinase-type plasminogen activator-SCID (uPA-SCID) mice with engrafted human hepatocytes (18). This HCV-infected mouse model has been reported to be useful for evaluating anti-HCV drugs such as IFN-α and anti-NS3 protease (19). We also generated a human hepatocyte-chimeric mouse model, in which mouse hepatocytes were almost completely replaced by human hepatocytes (20). These mice consistently developed long-term HCV infections, showing high viral titers after inoculation with HCV genotype 1b-infected human serum (50 μl/mouse) (Supplemental Figure 3). Intraperitoneal injection of IL-2/OKT3–treated liver lymphocytes (20×10^6 cells/mouse), at 2 weeks after inoculation with the infected serum, consistently prevented the development of HCV infection in the human hepatocyte-chimeric mice (Figure 7A). Such anti-HCV effects were countered by anti-IFN-γ neutralizing antibodies in some chimeric mice, suggesting the potential role played by IFN-γ in the anti-HCV effects of the immunotherapy. The administration of recombinant human IFN-γ markedly and consistently prevented the development of HCV infection in the human hepatocyte–chimeric mice. Once the HCV RNA became undetectable in the sera of chimeric mice receiving either IL-2/OKT3–treated liver lymphocytes or recombinant IFN-γ, it could not be detected again. The constant levels of human serum albumin in the chimeric mice indicated that neither the immunotherapy nor recombinant IFN-γ administration had significant adverse effects on human hepatocytes in those mice (Figure 7B). Once HCV infection had developed in the human hepatocyte–chimeric mice, who showed high titers of HCV RNA in their sera (over 10^3 copies/ml) 4 weeks after the inoculation of HCV-infected serum, the preventive effects of the adoptive immunotherapy or recombinant IFN-γ on HCV infection were no longer observed (Figure 7C).

Table 3
Characteristics of HCV-infected LT recipients that received and did not receive immunotherapy

No.	Age	Sex	HCV genotype	MELD	Pre–HCV RNA (KIU/ml)	Postoperative months	Immunosuppressant
With immunotherapy							
4	64	F	1b	16	210	29	Basiliximab+FK506+MMF
6	47	F	1b	8	5,000	26	Basiliximab+CsA+MMF
8	65	F	1b	18	2,400	24	Basiliximab+CsA+MMF
10	56	M	1b	8	970	19	Basiliximab+FK506+MMF
11	56	M	1b	9	1,700	17	Basiliximab+FK506+MMF
12	58	M	1b	22	19	17	Basiliximab+FK506+MMF
13	59	M	1b	6	2,200	16	Basiliximab+FK506+MMF
Without immunotherapy							
A	51	M	1b	27	420	42	Basiliximab+FK506+MMF
B	44	M	1b	10	1,600	32	Basiliximab+FK506+MMF
C	54	M	1b	8	180	22	Basiliximab+CsA+MMF
D	56	M	2a	10	470	20	Basiliximab+FK506+MMF
E	57	M	1b	12	3,200	6	Basiliximab+FK506+MMF

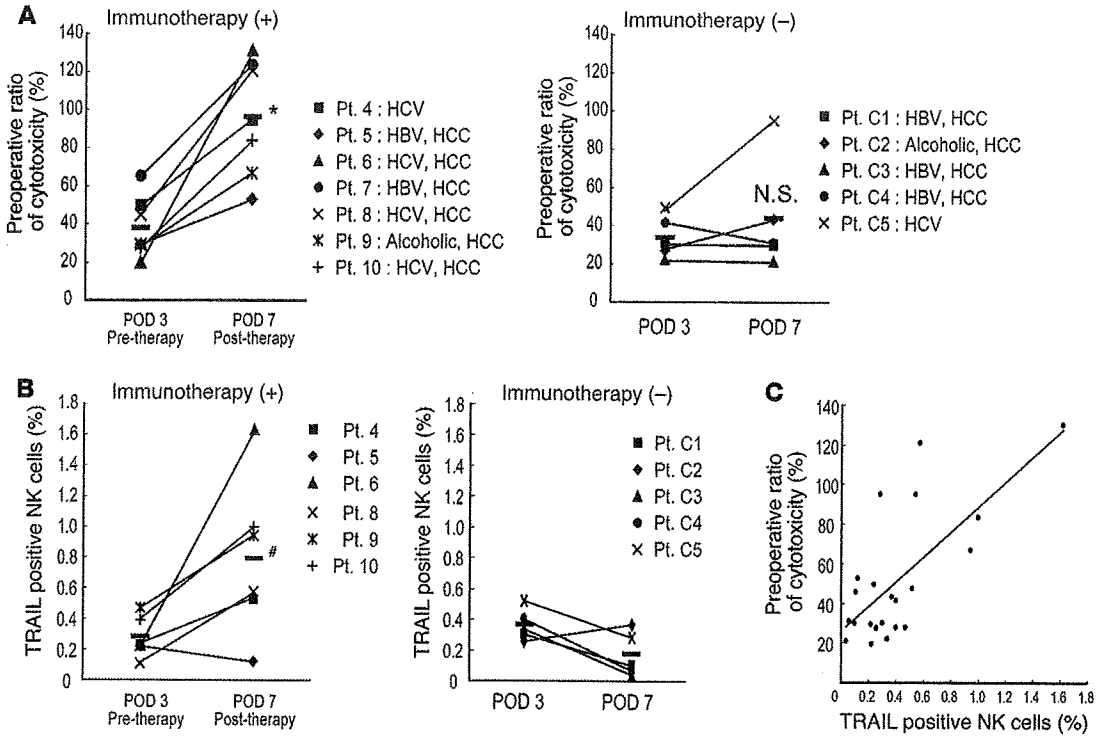

Figure 2

Adoptive immunotherapy with IL-2/OKT3–treated liver lymphocytes promoted the cytotoxic activity and TRAIL expression of NK cells in LT recipients. (**A**) The NK cytotoxic activities of the indicated effectors against their target cells were analyzed by the ^{51}Cr-release assay. The dot plot represents the NK cytotoxic activities of freshly isolated peripheral blood lymphocytes obtained from recipients who received immunotherapy (+) ($n = 7$) and did not receive immunotherapy (–) ($n = 5$) against HepG2 target cells (effector/target [E/T] ratio, 40:1) 3 and 7 days after LT. NK cytotoxic activities are represented as a proportion (percentage) of the preoperative cytotoxicity in each patient. Horizontal lines indicate the mean. Statistical analyses were performed using the 2-tailed, paired Student's *t* test. $^{*}P < 0.05$ for day 7 versus day 3. (**B**) The frequency of TRAIL^{+} NK cells increased remarkably in the peripheral blood of LT recipients who received the immunotherapy. Horizontal lines indicate the mean. Statistical analyses were performed using the Mann-Whitney *U* test. $^{\#}P = 0.013$ for immunotherapy group versus untreated group in postoperative day 7. (**C**) Correlation between TRAIL^{+} NK cell ratio and NK cytolytic activity after LT (Spearman rank-order correlation coefficient = 0.54, $P = 0.01$). Statistical analyses were performed using the Spearman rank-order correlation coefficient. The diagonal line indicates a linear regression line. Each dot indicates the cytotoxicity and TRAIL^{+} NK cell percentange of each patient. C1, control 1; POD, postoperative day; Pt., patient.

Discussion

The consequences of recurrent hepatitis C on the survival of graft and LT recipients can only be avoided by the development of safe and effective antiviral strategies that can not only prevent initial graft infection but also eradicate established hepatitis C recurrence (3, 4). With regard to initial graft infection, the circulating virions infect the liver graft immediately after LT. HCV RNA concentrations usually increase a few days after LT, reflecting active HCV replication in the liver graft. In general, in such an early phase of a viral infection, the first line of host defense may be effective in removing the virus; however, recent reports have indicated that HCV effectively escapes the innate immune system comprising NK and NKT cells, resulting in persistent infection (21, 22). It has been reported that cross-linking of CD81 on NK cells by the major envelope protein of HCV, HCV-E2, blocks NK cell activation, IFN-γ production, cytotoxic granule release, and proliferation (21). Engagement of CD81 on NK cells blocks tyrosine phosphorylation through a mechanism that is distinct from the negative signaling pathways associated with NK cell inhibitory receptors for major histocompatibility complex class I molecules (22). These facts prove that HCV-E2–mediated inhibition of NK cells is an efficient HCV evasion strategy, which involves targeting the early antiviral activities of NK cells and allowing the virus to establish itself as a chronic infection.

We have explored whether CD81 cross-linking–induced inhibitory effects occur even in IL-2–stimulated NK cells. CD81 cross-linking by a mAb specific for CD81 inhibited antitumor cytotoxicity and anti-HCV activity mediated by resting NK cells, but this manipulation did not alter both these activities of IL-2–stimulated NK cells (Supplemental Figure 4). This indicated that exposure to IL-2 before CD81 cross-linking abrogates subsequent inhibitory signals in the NK cells. This would be one mechanism whereby the adoptive immunotherapy with IL-2/OKT3–treated liver lymphocytes inhibited HCV replication at the early phase of infection after LT.

Although the role of NK cells in controlling HCV infection and replication has not been completely elucidated, a recent report has indicated that NK cells do not exert a direct cytolytic effect on the HCV replicon–containing hepatic cells but release IFN-γ, suppressing HCV RNA expression (11). The role of IFN-γ in the expression of NK cell–mediated anti-HCV activity has been proved by the observa-