Table 4 Most common adverse events

n (%)	PEG IFN-α-2a† + ME3738 50 mg/day (*n* = 46)	PEG IFN-α-2a† + ME3738 200 mg/day (*n* = 45)	PEG IFN-α-2a† + ME3738 800 mg/day (*n* = 44)	Total (*n* = 135)
Eye disorders				
Retinopathy	14 (30.4%)	15 (33.3%)	13 (29.5%)	42 (31.1%)
Gastrointestinal disorders				
Diarrhea	19 (41.3%)	14 (31.1%)	9 (20.5%)	42 (31.1%)
General disorders and administration site conditions				
Malaise	21 (45.7%)	18 (40.0%)	18 (40.9%)	57 (42.2%)
Fever	27 (58.7%)	22 (48.9%)	31 (70.5%)	80 (59.3%)
Infections and infestations				
Nasopharyngitis	16 (34.8%)	15 (33.3%)	12 (27.3%)	43 (31.9%)
Metabolism and nutrition disorders				
Decreased appetite	8 (17.4%)	8 (17.8%)	13 (29.5%)	29 (21.5%)
Musculoskeletal and connective tissue disorders				
Arthralgia	14 (30.4%)	15 (33.3%)	11 (25.0%)	40 (29.6%)
Nervous system disorders				
Headache	17 (37.0%)	15 (33.3%)	16 (36.4%)	48 (35.6%)
Skin and subcutaneous tissue disorders				
Alopecia	13 (28.3%)	14 (31.1%)	8 (18.2%)	35 (25.9%)
Pruritus	11 (23.9%)	15 (33.3%)	17 (38.6%)	43 (31.9%)
Investigations				
White blood cell count decreased	40 (87.0%)	40 (88.9%)	37 (84.1%)	117 (86.7%)
Red blood cell count decreased	20 (43.5%)	14 (31.1%)	21 (47.7%)	55 (40.7%)
Hemoglobin decreased	24 (52.2%)	15 (33.3%)	23 (52.3%)	62 (45.9%)
Hematocrit decreased	18 (39.1%)	17 (7.8%)	21 (47.7%)	56 (41.5%)
Platelet count decreased	35 (76.1%)	39 (86.7%)	36 (81.8%)	110 (81.5%)
Neutrophil count decreased	32 (69.6%)	37 (82.2%)	38 (86.4%)	107 (79.3%)
Aspartate aminotransferase increased	11 (23.9%)	11 (24.4%)	10 (22.7%)	32 (23.7%)
Blood triglycerides increased	11 (23.9%)	8 (17.8%)	8 (18.2%)	27 (20.0%)
Hyaluronic acid increased	23 (50.0%)	21 (46.7%)	19 (43.2%)	63 (46.7%)
Blood immunoglobulin G increased	10 (21.7%)	8 (17.8%)	9 (20.5%)	27 (20.0%)
Total	46 (100%)	45 (100%)	43 (97.7%)	134 (99.3%)

†Pegylated interferon-α-2a.

regular clinical practice, these two events have not been previously reported, and it was unclear whether these events were caused by ME3738 plus PEG IFN-α-2a combination therapy or by the primary disease itself. Furthermore, in subjects who developed these two events, no particular symptoms or findings were reported, suggesting that these two events may not be clinically problematic.

In a double-blind clinical study conducted in Japan comparing PEG IFN-α-2a plus RBV combination therapy and PEG IFN-α-2a plus placebo (48-week treatment) combination therapy, the reported incidence of decreased hemoglobin was 89.9% and 49.5%, respectively,[12] and the incidence of decreased hemoglobin noted in the present study was 45.9%. Considering the severity of decreased hemoglobin, the proportion of subjects in whom the hemoglobin level decreased to less than 10 g/dL and that resulted in dose reduction or withdrawal of RBV was 33.0% in the group receiving the PEG IFN-α-2a plus RBV combination and 4.0% in the group receiving the PEG IFN-α-2a plus placebo combination.[12] In the present study, the proportion of subjects in whom the hemoglobin level decreased to less than 10 g/dL during the study period was 19.3%.

In terms of the incidence of decreased hemoglobin, when patient background factors were compared

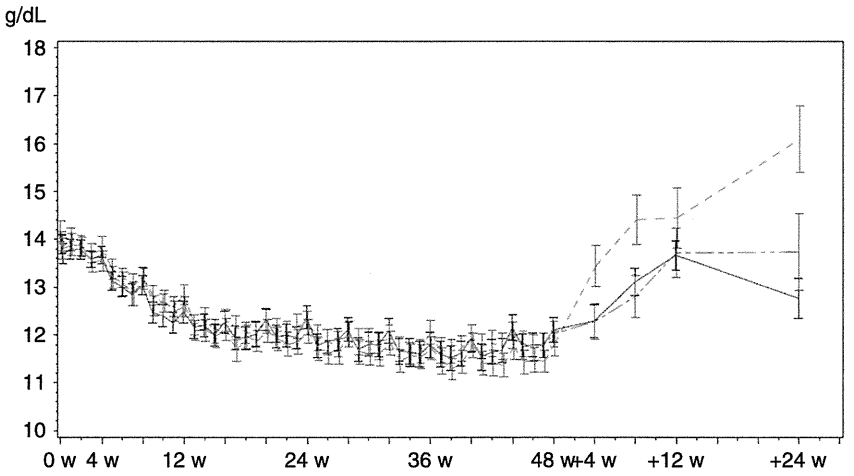

Figure 2 Time-course changes in hemoglobin levels. ----, ME3738 50 mg/day; ----, ME3738 200 mg/day; ——, ME3738 800 mg/day.

between the present study and the above double-blind study (the RBV co-administration study), the mean age was higher in the present study by approximately 5 years, and the male : female ratio was 4:6 in the present study, but 7:3 in the RBV co-administration study.[12] Furthermore, the mean baseline hemoglobin level was 14.0 g/dL in the present study, but 14.76 g/dL in the RBV co-administration study.[13] The incidence of decreased hemoglobin was lower in the present study than in the RBV co-administration study despite less favorable patient background factors in the present study.

As described, ME3738 was found to have a good safety profile and showed inflammatory suppression effects in the liver. In addition, Ogasawara *et al.* reported that ME3738 showed antiproliferative effects on liver cancer cells in an *in vitro* and *in vivo* liver tumor nude mouse model using hepatocellular carcinoma cell lines.[14] These findings suggest that long-term co-administration of ME3738 (which does not cause severe hemoglobin decrease) with PEG IFN is a therapeutic option anticipated to suppress inflammation in the liver, decrease the amount of HCV RNA, suppress proliferation of HCV, and suppress the onset of liver cancer in patients with chronic hepatitis C in whom the standard combination therapy with PEG IFN and RBV cannot be used because of a decrease in hemoglobin levels or because the patient is elderly.

ME3738 was concurrently used with PEG IFN-α-2a treatment; however, a clear additional effect on SVR was not confirmed in this trial.

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α-Fetoprotein Levels After Interferon Therapy and Risk of Hepatocarcinogenesis in Chronic Hepatitis C

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The effects of interferon (IFN) treatment and the post-IFN treatment α-fetoprotein (AFP) levels on risk of hepatocellular carcinoma (HCC) in patients with chronic hepatitis C (CHC) are unknown. To determine the relationship between AFP and alanine transaminase (ALT) levels and HCC risk, a cohort consisting of 1,818 patients histologically proven to have CHC treated with IFN were studied. Cumulative incidence and HCC risk were analyzed over a mean follow-up period of 6.1 years using the Kaplan-Meier method and Cox proportional hazard analysis. HCC developed in 179 study subjects. According to multivariate analysis, older age, male gender, advanced fibrosis, severe steatosis, lower serum albumin levels, nonsustained virological response (non-SVR), and higher post-IFN treatment ALT or AFP levels were identified as independent factors significantly associated with HCC development. Cutoff values for ALT and AFP for prediction of future HCC were determined as 40 IU/L and 6.0 ng/mL, respectively, and negative predictive values of these cutoffs were high at 0.960 in each value. The cumulative incidence of HCC was significantly lower in patients whose post-IFN treatment ALT and AFP levels were suppressed to less than the cutoff values even in non-SVR patients. This suppressive effect was also found in patients whose post-IFN treatment ALT and AFP levels were reduced to less than the cutoff values despite abnormal pretreatment levels. *Conclusion*: Post-IFN treatment ALT and AFP levels are significantly associated with hepatocarcinogenesis. Measurement of these values is useful for predicting future HCC risk after IFN treatment. Suppression of these values after IFN therapy reduces HCC risk even in patients without HCV eradication. (HEPATOLOGY 2013;58:1253-1262)

Hepatocellular carcinoma (HCC), one of the most frequent primary liver cancers,[1,2] is the third most common cause of cancer mortality worldwide.[3] Hepatitis C virus (HCV) infection is a common cause of chronic hepatitis, which progresses to HCC in many patients.[4] In the last two decades, interferon (IFN) therapy has been used to treat chronic hepatitis C (CHC) with the goal of altering the natural history of this disease. Although HCV eradication with IFN therapy for CHC has been shown to prevent HCC,[5-9] HCC sometimes develops even after achieving viral eradication.[5] Because the number of sustained virological responders (SVRs) is increasing along with recent advances in the development of effective anti-HCV therapy, it is very important to determine factors responsible for HCC

Abbreviations: AFP, α-fetoprotein; ALT, alanine aminotransferase; APRI, aspartate aminotransferase to platelet ratio index; CHC, chronic hepatitis C; CT computed tomography; γ-GTP, gamma-glutamyl transpeptidase; HCC, hepatocellular carcinoma; HCV, Hepatitis C virus; IFN, interferon; MRI, magnetic resonance imaging; PEG-, pegylated; RBV, ribavirin; ROC, receiver operator characteristic; SVR, sustained virological response.

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development among IFN-treated patients. However, this information is difficult to determine because of the paucity of large-scale, long-term cohort studies.

The 70-kDa glycoprotein α-fetoprotein (AFP), encoded by a gene located on chromosome 4, is the major serum protein during fetal life.[10] Shortly before birth, AFP is replaced by albumin as the major serum protein,[11,12] and thereafter, serum AFP levels remain extremely low throughout life (<10 ng/mL). Because serum AFP levels are frequently elevated in patients with HCC and germ-cell tumors, measurement of AFP is widely used as a serological marker for these tumors.[8,13] However, AFP levels are sometimes elevated in patients with chronic viral hepatitis and cirrhosis who do not have HCC.[3,19] While one possible explanation for this elevation is liver inflammation, in patients with CHC, the relationship between AFP and markers of liver inflammation such as alanine aminotransferase (ALT) is unclear. Moreover, although several reports suggest that pre-IFN treatment ALT and AFP levels in patients or those in patients who did not undergo subsequent treatment are associated with the development of HCC, it is unclear whether post-IFN treatment ALT and AFP levels are associated with hepatocarcinogenesis in patients with CHC. Hence, to clarify these associations we conducted a large-scale, long-term cohort study of patients with CHC to analyze the influence of ALT and AFP levels before and after IFN therapy on hepatocarcinogenesis in addition to other host and virological factors.

Patients and Methods

Patients. Patients chronically infected with HCV who had histologically proven chronic hepatitis or cirrhosis and had undergone IFN treatment between 1992 and 2010 were enrolled in the cohort. HCC was definitively ruled out by ultrasonography, dynamic computed tomography (CT), and/or magnetic resonance imaging (MRI) on enrollment. Patients were excluded if they had a history of HCC at the time of liver biopsy, autoimmune hepatitis, primary biliary cirrhosis, excessive alcohol consumption (≥50 g/day), hepatitis B surface antigen, or antihuman immunodeficiency virus antibody. Based on these criteria, a total of 2,689 patients were initially enrolled. Of these, 223 (8.3%) patients were excluded from the cohort because of loss to follow-up. In the remaining 2,466 patients, 133 and 515 patients were excluded from this analysis because of short follow-up and retreatment with IFN-based therapy during the follow-up period, respectively. Thus, the cohort comprising 1,818 patients was analyzed in the present study. Written informed consent was obtained from all patients and the Ethical Committee of Musashino Red Cross Hospital approved this study, which was conducted in accordance with the Declaration of Helsinki.

Histological Evaluation. To obtain liver specimens, laparoscopic or ultrasound-guided liver biopsies were performed with 13G or 15G needles, respectively. The median length of specimen was 18 mm (range, 11-41 mm), and the mean number of portal tracts was 17 (range, 9-35). The stage of fibrosis and the grade of inflammatory activity were scored by two pathologists according to the classification of Desmet et al.[24] The percentage of steatosis was quantified by determining the average proportion of hepatocytes affected.

IFN Therapy and Definitions of Response to IFN Therapy. All patients had chronic HCV infection at liver biopsy, which was confirmed by the presence of HCV-RNA in serum. All IFN therapies were initiated within 48 weeks after liver biopsy. Among the 1,818 patients, 535 received IFNα or IFNβ monotherapy for 24 weeks, 244 patients received IFNα ribavirin (RBV) combination therapy for 24 weeks, 299 patients received pegylated (PEG-) IFNα monotherapy for 48 weeks, and 760 patients received PEG-IFNα RBV combination therapy for 48-72 weeks.

Patients negative for serum HCV-RNA 24 weeks after IFN therapy completion were defined as SVRs. Patients who remained positive for HCV-RNA 24 weeks after therapy completion were defined as non-SVRs. HCV-RNA was determined by the qualitative Amplicor or TaqMan HCV assay (Roche Molecular Diagnostics, Tokyo, Japan).

Data Collection and Patient Follow-up. At enrollment, patient characteristics, biochemical,

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Additional Supporting Information may be found in the online version of this article.

Table 1. Characteristics of Patients Enrolled in the Present Study

Factors	Value
Patients, n	1818
Sex, n (%)	
Male	833 (45.8)
Female	985 (54.2)
Age (SD), year	57.1 (12.0)
BMI (SD), kg/m^2	23.1 (3.2)
Fibrosis stage, n (%)	
F1/2	1384 (76.1)
F3/4	434 (23.9)
Activity grade, n (%)	
A0/1	964 (53.0)
A2/3	854 (47.0)
%Severe steatosis (≥10%)	23.7
Albumin (SD), g/dL	4.0 (0.38)
ALT (SD), IU/L	78.3 (71.0)
γ-GTP (SD), IU/L	49.8 (50.6)
T. Bilirubin (SD), mg/dL	0.73 (0.34)
Fasting blood sugar (SD), mg/dL	113.4 (37.8)
LDL-Cholesterol (SD), mg/dL	101.6 (28.9)
T. Cholesterol (SD), mg/dL	176.2 (38.4)
AFP (SD), ng/mL	11.3 (28.3)
WBC counts (SD),/μL	4990 (1516)
Hb (SD), g/dL	14.0 (1.7)
Platelet counts (SD), x10^3/μL	164 (54)
HCV load (SD), KIU/mL	1097 (1263)
HCV genotype, n (%)*	
1a	11 (0.56)
1b	1183 (67.4)
2a	361 (20.6)
2b	180 (10.3)
Others	20 (1.1)
%Core 70 a.a. mutation†	34.2
%ISDR wild or 1 mutation‡	63.9
IFN regimen, n (%)	
IFN mono	758 (35.0)
IFN + RBV	275 (12.7)
PEG-IFN mono	307 (14.2)
PEG-IFN + RBV	758 (38.2)

Unless otherwise indicated, data are given as mean (SD).
*HCV genotype was determined in 1755 patients.
†HCV core mutation was determined in 409 patients with genotype 1b.
‡ISDR was determined in 1264 patients with genotype 1b.
Abbreviations: BMI, body mass index; ALT, alanine aminotransferase; γ-GTP, γ-glutamyl transpeptidase; LDL, low-density lipoprotein; AFP, α-fetoprotein; WBC, white blood cell; Hb, hemoglobin; HCV, hepatitis C virus; ISDR, interferon sensitivity determining region; IFN, interferon; RBV, ribavirin; PEG, pegylated.

hematological, virological, and histological data were collected. Age was determined at the time of primary liver biopsy. Patients were examined for HCC by abdominal ultrasonography, dynamic CT, and/or MRI every 3-6 months. Serum ALT and AFP levels were measured every 1-6 months. The surveillance protocols were in accordance with the standard of care in Japan. If HCC was suspected on the basis of the screening examination, additional procedures (e.g., dynamic CT, dynamic MRI, CT during hepatic arteriography, CT during arterial portography, contrast-enhanced ultrasonography, and tumor biopsy) were used to confirm the diagnosis. HCC diagnosis was confirmed by needle biopsy, histology of surgically resected specimens, or characteristic radiological findings. To evaluate the effects of changes in serum ALT and AFP levels during IFN therapy on hepatocarcinogenesis, the average integration values of ALT and AFP in each patient were calculated before and after IFN therapy. Data obtained more than 1 year prior to HCC development were used to exclude AFP elevation caused by HCC itself.

Follow-up was between the date of primary liver biopsy and HCC development or the last medical attendance until June 2011. The mean follow-up period was 6.1 years (range, 1.0-20.8 years).

Statistical Analyses. Categorical data were compared by the chi-square test or Fisher's exact test. Distributions of continuous variables were analyzed with Student t test for two groups. All tests of significance were two-tailed and $P < 0.05$ was considered statistically significant. The cumulative incidence curve was determined by the Kaplan-Meier method, and differences among groups were assessed using the log-rank test. Factors associated with HCC risk were determined by the Cox proportional hazard model. As covariates in the multivariate stepwise Cox model, age, sex, stage of liver fibrosis, grade of histological activity, presence of hepatic steatosis, serum albumin levels, γ-glutamyl transpeptidase (γ-GTP) level, fasting blood sugar levels, platelet counts, pre-IFN ALT levels, pre-IFN AFP levels, post-IFN ALT levels, post-IFN AFP levels, and virological response were included. HCC development was the dependent variable. Time zero was defined as the time of primary liver biopsy. The proportional assumption was supported by log[-log(survival)] versus log(time) plots that showed parallel lines. Statistical analyses were performed using the Statistical Package for the Social Sciences software v. 18.0 (SPSS, Chicago, IL).

Results

Patient Characteristics and Factors Associated With Risk of HCC. Table 1 shows patient characteristics at the time of enrollment. During follow-up, HCC developed in 179 patients. The cumulative incidence of HCC for 5 and 10 years was 6.5% and 15.0%, respectively. The final virological response to IFN therapy was determined in all patients. The overall rate of SVRs was 50.2% (913/1818). The cumulative incidence in SVRs was 2.3% and 5.5%, respectively, which was significantly lower than that in non-SVRs (6.9% and 21.9%, respectively; log-rank test, $P < 0.0001$).

Univariate analysis demonstrated factors that increase the risk for HCC development (Table 2). According to

multivariate stepwise Cox analysis, older age, male gender, advanced fibrosis, severe steatosis, lower serum albumin levels, non-SVR, and higher post-IFN treatment ALT and AFP levels, but not pre-IFN treatment ALT and AFP levels, were identified as independent factors that were significantly associated with HCC development (Table 2).

Association of Post-IFN Treatment ALT and AFP Levels With HCC Development in SVRs and Non-SVRs. Because our multivariate analysis identified post-IFN treatment ALT and AFP levels as independent factors associated with HCC risk, we determined the cutoff values of these factors for predicting the development of HCC by receiver operator characteristics (ROC) analysis. The area under the ROC curve for post-IFN treatment ALT and AFP levels were higher than that for pre-IFN treatment ALT and AFP levels, suggesting that quantification of post-IFN treatment ALT and AFP levels rather than pre-IFN treatment levels of these values is useful for predicting HCC (Fig. 1A). From this ROC analysis, ALT <40 IU/L and AFP <6.0 ng/mL were identified as cutoff values. Negative predictive values were extremely high at 0.960 in each value, suggesting patients with ALT and/or AFP levels below these cutoff values are at a lower risk for HCC.

As shown in Fig. 1B, the hazard ratio determined by Cox proportional hazard analysis after adjustment for age, sex, stage of liver fibrosis, degree of liver steatosis, serum albumin levels, and virological response to therapy demonstrated that the hazard ratio for HCC was dependent on post-IFN treatment ALT and AFP levels. These hazard ratios increased predominantly when post-IFN treatment ALT and AFP levels were more than the cutoff values.

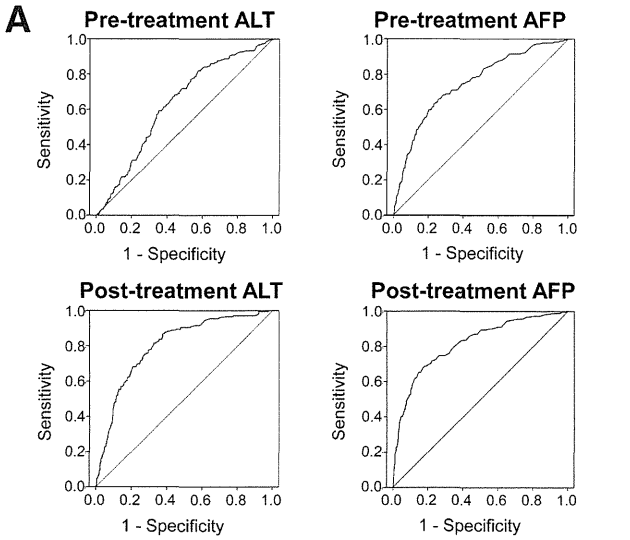
As shown in Fig. 2, the cumulative incidence of HCC was closely related to post-IFN treatment ALT and AST levels and was significantly lower in patients whose post-IFN treatment ALT and AFP levels was suppressed to <40 IU/L and 6.0 ng/mL, respectively. This suppressive effect was also notable in non-SVRs (Fig. 2C,D). Moreover, the cumulative incidence of HCC was significantly higher even in SVRs whose post-IFN treatment ALT and AFP levels were not <40 IU/L and 10 ng/mL, respectively (Fig. 2E,F).

Changes in ALT and AFP Levels With IFN Therapy and HCC Development. In the entire cohort, the mean ALT and AFP levels significantly decreased after IFN therapy (ALT = 78.4 to 36.6 IU/L, 95% confidence interval [CI] = 38.6-45.0, $P < 0.0001$; AFP = 11.3 to 6.9 ng/mL, 95% CI = 3.25-5.69, $P < 0.0001$; paired Student t test), and this significant decrease was found not only in SVRs, but also non-SVRs (Fig. 3A). Because post-IFN treatment ALT and AFP levels rather than pre-IFN treatment levels were

Table 2. Factors Associated With Hepatocellular Carcinoma

Risk Factor	Hazard Ratio (95% CI)	*P* Value
Univariate analysis		
Age (by every 10 year)	1.82 (1.52-2.20)	<0.0001
Sex		
Female	1	
Male	1.61 (1.20-2.17)	<0.0001
Fibrosis stage		
F1/F2	1	
F3/F4	4.90 (3.64-6.61)	<0.0001
Activity grade		
A0/A1	1	
A2/A3	3.38 (2.41-4.74)	<0.0001
Degree of steatosis		
<10%	1	
≥10%	3.84 (2.62-5.63)	<0.0001
Albumin (by every 1 g/dL)	0.18 (0.22-0.25)	<0.0001
Pre-ALT (by every 40 IU/L)	1.04 (0.96-1.08)	0.525
Post-ALT (by every 40 IU/L)	1.68 (1.55-1.81)	<0.0001
γ-GTP (by every 40 IU/L)	1.17 (1.08-1.27)	<0.0001
Fasting blood sugar (by every 100 mg/dL)	1.82 (1.35-2.45)	<0.0001
Pre-AFP (by every 10 ng/mL)	1.07 (1.05-1.09)	<0.0001
Post-AFP (by every 10 ng/mL)	1.08 (1.06-1.12)	<0.0001
Platelet counts (by every $10^4/\mu L$)	0.88 (0.85-0.90)	<0.0001
Genotype		
Non-1	1	
1	2.27 (1.51-3.45)	<0.0001
Core 70 mutation		
Wild	1	
Mutant	2.79 (1.19-6.53)	0.018
ISDR		
More than 1 mutation	1	
Wild or 1 mutation	1.27 (0.87-1.85)	0.216
Virological response		
SVR	1	
Non-SVR	3.66 (2.51-5.35)	<0.0001
Multivariate analysis		
Age (by every 10 year)	2.18 (1.71-2.81)	<0.0001
Sex		
Female	1	
Male	2.66 (1.86-3.80)	<0.0001
Fibrosis stage		
F1/F2	1	
F3/F4	2.27 (1.58-3.27)	<0.0001
Degree of steatosis		
<10%	1	
≥10%	2.29 (1.49-3.50)	<0.0001
Albumin (by every 1 g/dL)	0.35 (0.23-0.55)	<0.0001
Post-ALT (by every 40 IU/L)	1.81 (1.55-2.12)	<0.0001
Post-AFP (by every 10 ng/mL)	1.06 (1.02-1.10)	0.007
Virological response		
SVR	1	
Non-SVR	1.58 (1.01-2.48)	0.044

Hazard ratios for development of hepatocellular carcinoma were calculated by the Cox proportional hazards analysis. ALT, alanine aminotransferase; γ-GTP, gamma-glutamyl transpeptidase; AFP, alpha-fetoprotein; ISDR, interferon sensitivity determining region; SVR, sustained virological responder. As covariates in the multivariate stepwise Cox model, age, sex, stage of liver fibrosis, grade of histological activity, presence of hepatic steatosis, serum albumin levels, γ-GTP level, fasting blood sugar levels, platelet counts, pre-IFN ALT levels, pre-IFN AFP levels, post-IFN ALT levels, post-IFN AFP levels, and virological response were included.



Variables	AUC	95% CI	Cut-off	Sensitivity	Specificity	NPV	PPV
Pre ALT (IU/L)	0.634	0.595–0.673	73	0.592	0.649	0.935	0.154
Post ALT (IU/L)	0.803	0.770–0.835	40	0.754	0.728	0.960	0.233
Pre AFP (ng/mL)	0.748	0.709–0.786	7.3	0.682	0.716	0.954	0.208
Post AFP (ng/mL)	0.816	0.781–0.851	6.0	0.704	0.783	0.960	0.262

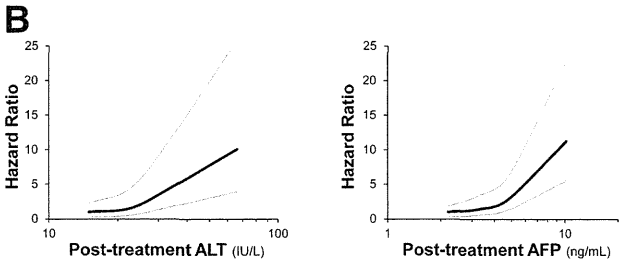


Fig. 1. Predictive values for ALT and AFP, and hazard ratios (HRs) according to post-IFN treatment ALT and AFP levels. (A) ROC curve for prediction of HCC. Area under the ROC curve, 95% CI, cutoff value, sensitivity, specificity, negative predictive value (NPV), and positive predictive value (PPV) are shown in the bottom of the figure. (B) Spline curves of HR (solid line) and 95% CI (dotted line) for HCC development according to post-IFN treatment ALT and AFP levels. Curves were fitted using polynomial regression.

significantly associated with the development of HCC in non-SVRs, we determined the effects of changes in ALT and AFP levels by IFN therapy on hepatocarcinogenesis. Even in non-SVRs with equal or higher pre-IFN treatment ALT or AFP levels than the cutoff values, the cumulative incidence of HCC was significantly suppressed in patients whose post-IFN treatment ALT or AFP level was reduced to less than the cutoff values (Fig. 3B). In contrast, persistence of post-IFN treatment ALT or AFP levels to more than the cutoff values after IFN therapy was associated with a significantly higher incidence of HCC (Fig. 3B).

Relation Between AFP and ALT or Histological Findings. Univariate analysis using logistic regression determined factors that were associated with post-IFN treatment ALT or AFP levels (Supporting Table). Although many clinical factors were associated with post-IFN ALT and/or AFP levels, post-IFN ALT and AFP levels were not correlated with each other ($r^2 = 0.050$). Therefore, the cumulative incidence of HCC was significantly higher in patients with higher post-IFN treatment AFP levels, even when patients were stratified by post-IFN treatment ALT levels (Fig. 4A,B).

As shown in Fig. 4C-F, the cumulative incidence of HCC development was significantly lower in patients whose post-IFN treatment AFP level was <6.0 ng/mL in all subgroups stratified by stage of fibrosis and grade of activity. Therefore, reduction in post-IFN treatment AFP levels reduces HCC risk even in patients with advanced fibrosis. Although pre-IFN treatment AFP levels correlated with the advance of histological fibrosis and grade of activity, such correlations became less significant with post-IFN treatment AFP levels (data not shown).

Platelet Counts and Aspartate Aminotransferase-to-Platelet Ratio Index (APRI) in Patients Without Advanced Fibrosis. Because a substantial amount of HCC cases developed in the patients without histologically advanced fibrosis (Fig. 4C), we characterized these individuals using platelet counts and APRI,[25] which are the readily available surrogate markers for liver fibrosis. We first determined the cutoff values of platelet counts and APRI for predicting HCC development by ROC analyses. Accordingly, platelet counts $<150 \times 10^3/\mu L$ and APRI >0.96 were identified as cutoff values, and the areas under the ROC curve for platelet counts and APRI were 0.715 (95% CI: 0.675-0.755) and 0.740 (95% CI: 0.701-0.779), respectively (Supporting Figure). Even in individuals without advanced fibrosis (F1 and F2 patients), the proportion of patients with platelet counts $<150 \times 10^3/\mu L$ or APRI >0.96 was significantly higher in patients with HCC than in those without HCC (platelet counts, 53.0% [35/66] versus 31.3% [387/1238], $P = 0.0002$; APRI, 53.0% [35/66] versus 26.4% [325/1229], $P < 0.0001$). Moreover, the cumulative incidence of HCC development was significantly higher in patients with platelet counts $<150 \times 10^3/\mu L$ or APRI >0.96 in the subgroups without advanced fibrosis (Supporting Figure). Therefore, patients with low platelet counts or high APRI still have a substantial risk for HCC development even though they were diagnosed with mild fibrosis by liver biopsy.

Hepatic Steatosis and Post-IFN ALT and AFP Levels in SVRs. To characterize SVRs without ALT and AFP normalization after IFN therapy, we evaluated the percentage of severe hepatic steatosis in these patients. Accordingly, the percentages of severe hepatic steatosis were significantly higher in SVRs without ALT and AFP normalization than in those with normal

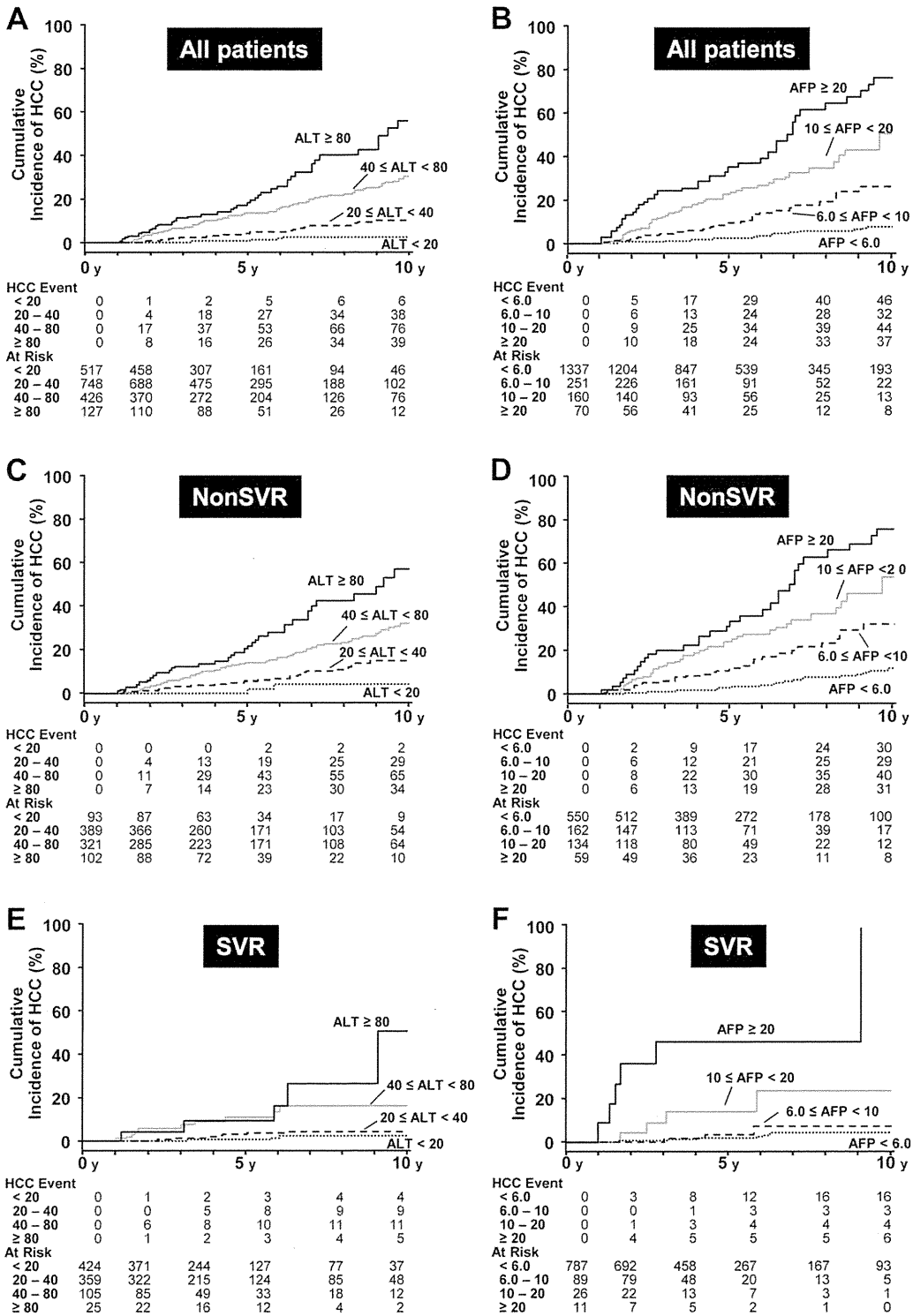
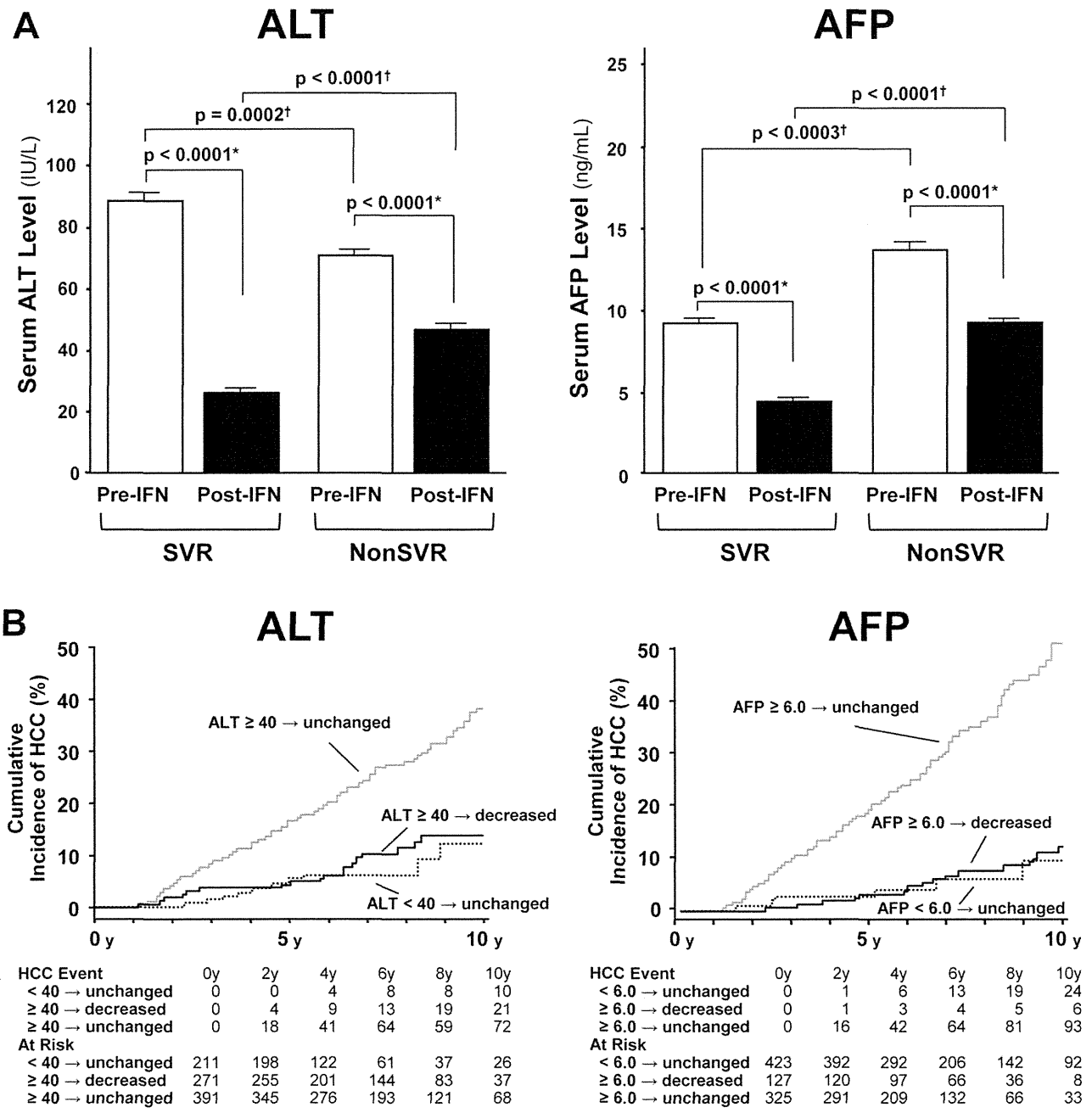


Fig. 2. Cumulative incidence of HCC according to post-IFN treatment ALT and AFP levels. (A) Entire cohort stratified by post-IFN treatment ALT levels (log-rank test: $P < 0.0001$). (B) Entire cohort stratified by post-IFN treatment AFP levels (log-rank test: $P < 0.0001$). (C) Non-SVRs stratified by post-IFN treatment ALT levels (log-rank test: $P < 0.0001$). (D) Non-SVRs stratified by post-IFN treatment AFP levels (log-rank test: $P < 0.0001$). (E) SVRs stratified by post-IFN treatment ALT levels (log-rank test: $P < 0.0001$). (F) SVRs stratified by post-IFN treatment AFP levels (log-rank test: $P < 0.0001$). The number of HCC events and patients at risk at each timepoint are shown below the graphs.

ALT and AFP (ALT, 37.9% [36/95] versus 13.8% [77/557], $P < 0.0001$; AFP, 31.6% [31/98] versus 14.8% [82/554], $P < 0.0001$). Therefore, it is likely that presence of hepatic steatosis is associated with ALT and/or AFP elevation, and it is one of the risks for HCC development even after achieving SVR.



HCC Event	0y	2y	4y	6y	8y	10y
< 40 → unchanged	0	0	4	8	8	10
≥ 40 → decreased	0	4	9	13	19	21
≥ 40 → unchanged	0	18	41	64	59	72
At Risk						
< 40 → unchanged	211	198	122	61	37	26
≥ 40 → decreased	271	255	201	144	83	37
≥ 40 → unchanged	391	345	276	193	121	68

HCC Event	0y	2y	4y	6y	8y	10y
< 6.0 → unchanged	0	1	6	13	19	24
≥ 6.0 → decreased	0	1	3	4	5	6
≥ 6.0 → unchanged	0	16	42	64	81	93
At Risk						
< 6.0 → unchanged	423	392	292	206	142	92
≥ 6.0 → decreased	127	120	97	66	36	8
≥ 6.0 → unchanged	325	291	209	132	66	33

Fig. 3. Changes in pre- and post-IFN treatment ALT and AFP levels, and their effects on HCC development. (A) Mean serum pre- (open columns) and post-IFN treatment (solid columns) ALT and AFP levels in SVRs and non-SVRs. Error bars indicate the standard error. *Paired Student *t* test. †Unpaired Student *t* test. (B) Cumulative incidence of HCC stratified by changes in pre- and post-IFN treatment ALT and AFP levels (log-rank test: $P < 0.0001$). ALT <40 → unchanged, patients with ALT <40 IU/L before IFN therapy unchanged after IFN therapy; ALT ≥40 → decreased, patients with ALT ≥40 IU/L before IFN therapy decreased to ALT <40 IU/L after IFN therapy; ALT ≥40 → unchanged, patients with ALT ≥40 IU/L before IFN therapy unchanged at ALT not <40 IU/L after IFN therapy. AFP <6.0 → unchanged, patients with AFP <6.0 ng/mL before IFN therapy unchanged at AFP <6.0 ng/mL after IFN therapy; AFP ≥6.0 → decreased, patients with AFP ≥6.0 ng/mL before IFN therapy decreased to AFP <6.0 ng/mL after IFN therapy; AFP ≥6.0 → unchanged, patients with AFP ≥6.0 ng/mL before IFN therapy unchanged at AFP ≥6.0 ng/mL after IFN therapy.

Discussion

This large-scale, long-term cohort study establishes important findings, which demonstrate a strict association between hepatocarcinogenesis and post-IFN treatment ALT and AFP levels in patients with CHC. This association was notable in both SVR and non-SVR subgroups, and suppression of these values by IFN therapy reduced the hepatocarcinogenesis risk despite failure of HCV eradication. These data, which

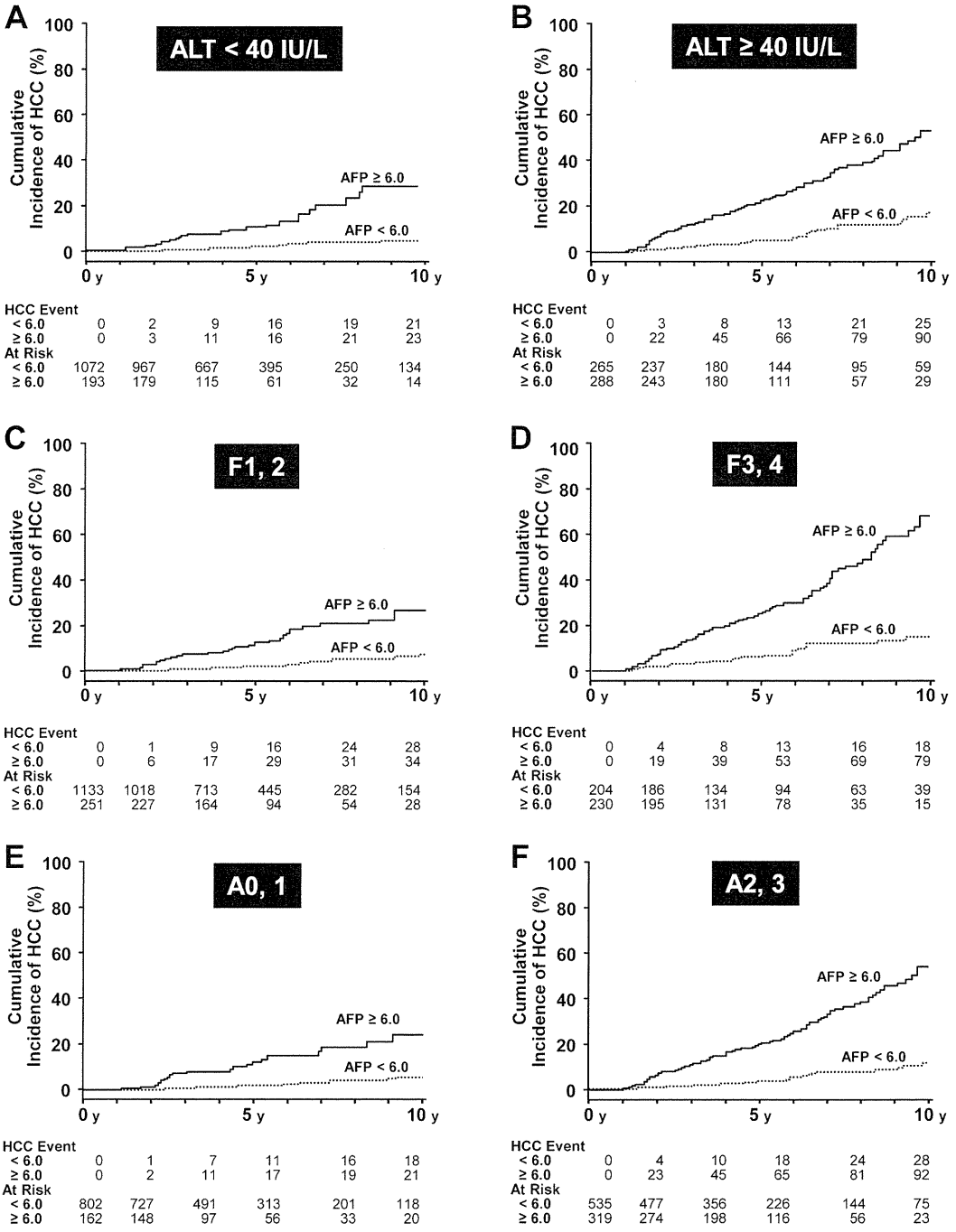


Fig. 4. Relationship between AFP and ALT or histological findings. (A) The cumulative incidence of HCC stratified by post-IFN treatment AFP levels in subgroups according to the post-IFN treatment ALT (log-rank test: $P < 0.0001$ in both subgroups). (B) Cumulative incidence of HCC stratified by post-IFN treatment AFP levels in subgroups according to the histological stage of fibrosis (log-rank test: $P < 0.0001$ in both subgroups). (C) Cumulative incidence of HCC stratified by post-IFN treatment levels of AFP in subgroups according to the histological grade of activity (log-rank test: $P < 0.0001$ in both subgroups).

demonstrate the efficacy of IFN against HCC development associated with suppression of AFP, have clinically important implications for physicians.

Although there have been reports on the association between baseline pretreatment AFP levels and HCC risk,[26-35] little is known regarding the effects of IFN therapy on change in post-IFN treatment AFP and its relation to HCC risk.[36] Although a previous report demonstrated that a decrease in AFP levels in patients receiving IFN therapy reduced the incidence of HCC,[37] this study was performed in a small number of patients (n = 382), and cutoff values, relation to ALT, or histological findings were not determined. Our study, performed in a large well-characterized

cohort, had a greater advantage in that it allowed determination of cutoff values for post-IFN treatment ALT and AFP levels useful for predicting HCC development. Although a higher cutoff value of 20 ng/mL was used to determine the incidence of HCC in the previous study,[36] we propose a lower value for negatively predicting HCC. From our results, those with AFP levels ≥6.0 ng/mL have a substantial HCC risk, even if it is <20 ng/mL. Therefore, post-IFN treatment AFP levels should be <6.0 ng/mL to suppress HCC risk in patients with CHC.

It should be noted that AFP produced by HCC itself was carefully excluded in our study. Serum AFP elevation is frequently observed in patients with advanced CHC in the absence of HCC.[19-23] Although the precise mechanisms accounting for this observation are unknown, Hu et al.[38] found a correlation between AFP and measures of liver disease activity, suggesting that AFP production is enhanced in the presence of necroinflammatory injury of the liver. However, in our study post-IFN treatment ALT and AFP levels were not correlated, and the cumulative incidence of HCC was significantly higher in patients with higher post-IFN treatment AFP levels, even when patients were stratified by post-IFN treatment ALT levels. Moreover, multivariate analysis confirmed that AFP and ALT are independently associated with HCC risk. Therefore, observed elevation in AFP levels in patients with subsequent HCC development is not necessarily caused by necroinflammation of the liver. Alternatively, increased AFP levels have been reported during liver regeneration following hepatic resection and during recovery from massive hepatic necrosis,[39-41] suggesting that elevated AFP levels are a surrogate for proliferative activity of liver cells, which may cause hepatocarcinogenesis in patients with CHC.

Other possible reasons accounting for HCC risk related to AFP are the close association between AFP levels and the stage of liver fibrosis, which is consistent with a previous report.[35] However, we further clarified the fact that correlation between post-IFN treatment AFP levels and liver fibrosis was less notable in patients without subsequent development of HCC (data not shown). Cumulative incidence of HCC was significantly higher in patients with higher post-IFN treatment AFP levels at each stage when patients were stratified by the histological stage of fibrosis (Fig. 4). Therefore, post-IFN treatment AFP is not just a surrogate marker for liver fibrosis, and elevation of post-IFN treatment AFP as a potential risk for hepatocarcinogenesis is not only the result of advanced liver fibrosis. Conversely, suppression of post-IFN treatment AFP levels may reduce HCC risk even in patients with advanced fibrosis.

This study has a few limitations, the first being the heterogeneity of our cohort, which included various treatment regimens with different treatment responses. However, we obtained similar results in a more uniform subgroup of HCV genotype 1b patients treated with PEG-IFNα/RBV (data not shown). The second limitation is the ethnic homogeneity of the Japanese population. Because the baseline incidence of HCC development differs among population groups, longer-term longitudinal studies in larger cohorts with various population subgroups are required to verify the generality of our results.

With the development of potent direct-acting antiviral agents combinations, IFN-free therapy is likely to be approved in the near future. This raises the question of whether posttreatment ALT and/or AFP levels will remain a significant predictor of HCC risk. Moreover, it is uncertain whether the suppressive effect of viral eradication by IFN-free regimens on hepatocarcinogenesis will be identical to that obtained by IFN-based regimens. Therefore, it is extremely interesting to prove these issues in future studies.

In conclusion, post-IFN treatment ALT and AFP levels are strictly associated with hepatocarcinogenesis risk in patients with CHC. Measurement of these values is useful for predicting future HCC risk in IFN-treated patients. Suppression of these values after IFN therapy reduces HCC risk even in patients without HCV eradication, while SVRs with increased ALT and/or AFP levels are at risk for HCC development. The present results have potentially important clinical implications for physicians and may influence their decisions regarding treatment strategy and HCC surveillance for individual patients.

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IL-28B (IFN-λ3) and IFN-α synergistically inhibit HCV replication

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SUMMARY. Genetic variation in the IL-28B (interleukin-28B; interferon lambda 3) region has been associated with sustained virological response (SVR) rates in patients with chronic hepatitis C treated with peginterferon-α and ribavirin. However, the mechanisms by which polymorphisms in the IL-28B gene region affect host antiviral responses are not well understood. Using the HCV 1b and 2a replicon system, we compared the effects of IFN-λs and IFN-α on HCV RNA replication. The anti-HCV effect of IFN-λ3 and IFN-α in combination was also assessed. Changes in gene expression induced by IFN-λ3 and IFN-α were compared using cDNA microarray analysis. IFN-λs at concentrations of 1 ng/mL or more exhibited concentration- and time-dependent HCV inhibition. In combination, IFN-λ3 and IFN-α had a synergistic anti-HCV effect; however, no synergistic enhancement was observed for interferon-stimulated response element (ISRE) activity or upregulation of interferon-stimulated genes (ISGs). With respect to the time course of ISG upregulation, the peak of IFN-λ3-induced gene expression occurred later and lasted longer than that induced by IFN-α. In addition, although the genes upregulated by IFN-α and IFN-λ3 were similar to microarray analysis, interferon-stimulated gene expression appeared early and was prolonged by combined administration of these two IFNs. In conclusion, IFN-α and IFN-λ3 in combination showed synergistic anti-HCV activity *in vitro*. Differences in time-dependent upregulation of these genes might contribute to the synergistic antiviral activity.

Keywords: HCV, IFN-λ, IL-28B, ISG, synergistic inhibition, microarray.

INTRODUCTION

In 2009, reports from three genome-wide association studies revealed that several single-nucleotide polymorphisms (SNPs) (rs12979860, rs12980275 and rs8099917) around the IL-28B (interleukin-28B; interferon lambda 3) gene are strongly associated with sustained viral response (SVR) to PEG-IFN and RBV treatment for chronic hepatitis C [1–3]. Specifically, patients with the TG or GG genotype at rs8099917 infected with genotype 1b are more resistant to PEG-IFN and RBV treatment than patients with the TT genotype. IL-28B haplotypes were also reported to be strongly associated with spontaneous HCV clearance [1, 4, 5].

IL-28B is a member of the type III IFN family [6], consisting of IFN-λ1 (IL-29), IFN-λ2 (IL-28A) and IFN-λ3 (IL-28B). IFN-λs bind to their cognate receptor, composed of IL28R1 and IL10R2, and then activate the receptor-associated Janus-activated kinases (Jak) 1 and tyrosine kinase (Tyk) 2, leading to the activation of downstream signal transducer and activator of transcription (STAT) proteins, STAT1 and STAT2. Similar to type I IFN signalling, the Jak-STAT signalling pathway activates the IFN-stimulated response element (ISRE) within the promoter region of interferon-stimulated genes (ISGs) [7].

Concerning the functional role of IL-28B in HCV infection, two of *in vivo* studies assessed the correlation of IL-28A/B mRNA levels in whole blood and peripheral blood mononuclear cells (PBMC) with IL-28B haplotypes at position rs8099917. IL-28A mRNA and IL-28B mRNA levels in subjects with the TT genotype were higher than in subjects with other genotypes (TG or GG), suggesting an association between higher amounts of endogenous IFN-λs and HCV clearance [2, 3]. On the other hand, subjects

Abbreviations: DMEM, Dulbecco's modified Eagle's medium; FBS, foetal bovine serum; ISG, interferon-stimulated genes; MTS, dimethylthiazol carboxymethoxyphenyl sulphophenyl tetrazolium; PBMC, peripheral blood mononuclear cells; SNP, single-nucleotide polymorphisms; STAT, signal transducer and activator of transcription; SVR, sustained viral response.

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with the TT genotype at SNP rs8099917 were reported to have lower expression levels of ISGs in the liver during the pretreatment period as compared with subjects with the TG or GG genotypes [8]. Several *in vitro* studies support a direct role of IFN-λs in the control of HCV replication through the innate immune pathway. In a cell culture system, Marcello *et al.* [9] showed that IFN-λ1 inhibited HCV replication with similar kinetics to that of IFN-α, although IFN-λ1 induced stronger upregulation of ISGs and this effect lasted longer. Moreover, combinations of IFN-λ1 and IFN-α had a greater inhibitory effect on HCV replication compared with the individual agents [10].

As suggested by the studies performed to date, a change in IFN-λ3 expression might be a key mechanism by which IL-28B SNPs determine the response to PEG-IFN and RBV. Considering that IFN-λ1 plays a direct role in the control of HCV replication and that IFN-λ1 enhances the antiviral activity of IFN-α, it seems reasonable to speculate that IFN-λ3 plays a similar antiviral role. Therefore, in this study, we investigated the direct antiviral role of IFN-λ3 alone and in combination with IFN-α using an HCV replicon system. In addition, we used microarray analysis to investigate the influence of IFN-λ3, alone or in combination with IFN-α, on the regulation of ISG-mediated antiviral pathways.

MATERIALS AND METHODS

Cell culture and HCV replicon

The human hepatoma cell lines OR6 and Huh7.5.1 were maintained in Dulbecco's modified Eagle's medium (DMEM; Sigma, St. Louis, MO, USA) supplemented with 10% foetal bovine serum (FBS) at 37°C in 5% CO_2. JFH-1-infected Huh7.5.1 cells were grown in DMEM supplemented with 10% FBS. The OR6 cell line, harbouring full-length genotype 1b HCV RNA and co-expressing *Renilla* luciferase (ORN/C-5B/KE) [11], was established in the presence of 500 μg/mL G418 (Promega, Madison, WI, USA).

Reagents

IL-28A (IFN-λ2), IL-28B (IFN-λ3) and IL-29 (IFN-λ1) were obtained from R&D Systems (Minneapolis, MN, USA). IL-28A and IL-29 are recombinant proteins generated from an NSO-derived murine myeloma cell line, and IL-28B is a recombinant protein generated from the CHO cell line. Interferon alpha-2b (INTRON®A 300 IU) was obtained from Schering-Plough Corporation (Kenilworth, NJ, USA).

Reporter plasmids and luciferase assay

HCV replication in OR6 replicon cells was determined by monitoring *Renilla* luciferase activity (Promega). To monitor IFN signalling directed by the interferon-stimulated response element (ISRE), the plasmids pISRE-luc expressing firefly luciferase were cotransfected using FuGENE®6 Transfection Reagent (Roche, Indianapolis, IN, USA) following the manufacturer's protocol. Luciferase activity was quantified using the dual-luciferase assay system (Promega) and a GloMax 96 Microplate Luminometer (Promega). Assays were performed in triplicate, and the results were expressed as mean ± SD percentage of the control values.

Quantification of HCV core protein and RNA

We quantified HCV core protein in culture supernatant using Lumipulse Ortho HCV Ag (Ortho Clinical Diagnostics, Tokyo, Japan) as specified by the manufacturer. The principle of the measurement method is based on the chemiluminescent enzyme immunoassay (CLEIA) [12].

Real-time reverse transcription polymerase chain reaction (RT-PCR)

Intracellular genomic JFH-1 HCV RNA as well as cellular mRNA of IFI-6, IFIT1 (ISG56), DDX60, OAS2, Mx1 and USP18 was quantified by TaqMan RT-PCR. The cells were lysed and subjected to reverse transcription without purification of RNA using a Cells-to-Ct kit (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's protocol. Quantitative PCR was performed in triplicate using a 7500 Real-Time PCR System (Applied Biosystems) and TaqMan Gene Expression Assays (Applied Biosystems) according to the manufacturer's instructions. The sequences of the sense and antisense primers and the TaqMan probe for 5′UTR region of HCV were 5′-TGCGG AACCGGTGAGTACA-3′, 5′-CTTAAGGTTTAGGATTCGTGCT CAT-3′ and 5′-(FAM)CACCCTATCAGGCAGTACCACAAGG CC(TAMRA)-3′, respectively. TaqMan probes for IFI-6, IFIT1 (ISG56), DDX60, OAS2, Mx1 and USP18 were purchased from Applied Biosystems. Primers for 18s rRNA (Applied Biosystems) were used as internal control.

Microarray analysis

OR6 replicon cells were harvested by centrifugation after exposure to 0.01 ng/mL IFN-α, 10 ng/mL IFN-λ3 or a combination of both for 6, 12, 24 and 48 h. Total RNA was isolated from cells using the RNeasy Mini Kit (Qiagen, Valencia, CA, USA). On-column DNase digestion was performed using the RNase-Free DNase Set (Qiagen). Quality control of extracted RNA was performed with the 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA).

The RNA was then amplified and labelled using the Ambion® WT Expression Kit and GeneChip® WT Terminal Labelling and Control Kit (Affymetrix, Santa Clara, CA, USA). cDNA was synthesized, labelled and hybridized to the GeneChip® array according to the manufacturer's protocol, starting with 200-ng total RNA. The GeneChips were finally washed

and stained using the GeneChip® Fluidics Station 450 (Affymetrix) and then scanned with the GeneChip® Scanner 3000 7G (Affymetrix).

Affymetrix CEL files were imported into GeneSpring GX v.11.5 (Agilent Technologies, Santa Clara, CA, USA) analysis software. Data were normalized using robust multichip average analysis (RMA).

Dimethylthiazol carboxymethoxyphenyl sulphophenyl tetrazolium (MTS) assays

To evaluate the cell viability, dimethylthiazol carboxymethoxyphenyl sulphophenyl tetrazolium (MTS) assays were performed using a CellTiter 96 AQueous One Solution Cell Proliferation Assay kit (Promega) according to the manufacturer's instructions.

Statistical analyses

Statistical analyses were performed using an unpaired, two-tailed Student's *t*-test. *P* values of < 0.05 were considered to be statistically significant.

RESULTS

IFN-λ1, IFN-λ2 and IFN-λ3 demonstrate antiviral activity against HCV

To determine the antiviral effect of IL-29 (IFN-λ1), IL-28A (IFN-λ2) and IL-28B (IFN-λ3) against HCV, OR6/ORN/C-5B/KE cells were seeded in 96-well plates for 24 h and then treated with IFN-λ1, IFN-λ2, IFN-λ3 or IFN-α at various concentrations for another 24, 48 and 72 h. In this system, the *Renilla* luciferase activity reflects the amount of HCV RNA synthesized. As shown in Fig. 1, at concentrations of 1 ng/mL or more, all IFN-λs led to a concentration- and time-dependent decrease in luciferase activity of the OR6/C-5B replicon. IFN-λ3 at 10 ng/mL inhibited HCV replication (32% reduction, $P < 0.05$) to a similar extent as 0.01 ng/mL IFN-α (49% reduction, $P < 0.05$) by 48 h.

We also assessed the effects of IFN-λ1, IFN-λ2 and IFN-λ3 on Huh7.5.1/JFH-1 cells. JFH-1 cells were seeded in 96-well plates for 24 h and then treated with IFN-λ1, IFN-λ2, IFN-λ3 or IFN-α at various doses for another 48 h. To determine their antiviral effect, HCV core protein in the medium and intracellular HCV RNA were measured by CLEIA and quantitative real-time RT-PCR, respectively. HCV RNA quantitative PCR assays were multiplexed for 18s ribosomal RNA to control for the amount of input RNA. As shown in Fig. 2, all IFN-λs inhibited HCV replication in JFH-1 cells in a concentration-dependent manner. Similarly, all of the IFN-λs caused suppression of HCV core protein secretion into the cell culture medium (Figure S1).

In C-5B system, there was no evident cytotoxicity below 100 ng/mL in any interferons except for IFN-λ1 (Figure S2). On the other hand, cytotoxicity was observed in lesser concentrations by those IFNs in JFH-1 system. However, as demonstrated in Fig. 2 and Figure S3, antiviral effect exceeded the cytotoxicity in the JFH-1 system.

Synergistic inhibition of HCV replication by IFN-λ3 and IFN-α in combination

We examined whether the combination of IFN-λ3 and IFN-α induces greater antiviral activity as compared with the individual cytokines alone. OR6/ORN/C-5B/KE cells were treated with the combinations of IFN-λ3 and IFN-α at various concentrations for 48 h. As shown in Fig. 3a, the relative concentration–inhibition curves of IFN-α were plotted for each fixed concentration of IFN-λ3, and the curves shifted to the left with increasing concentrations of IFN-λ3. The results indicate a synergistic effect of IFN-λ3 and IFN-α against HCV replication. We confirmed the synergistic effect of IFN-λ3 and IFN-α by isobologram (Fig. 3b). The inhibitory effects of the combination were quantified according to the method of Chou *et al.* using the CalcuSyn software program (Biosoft, Cambridge, UK). At the ED_{50} of each drug, the combination index was 0.40-0.61, indicating significant synergism. We also assessed the effect of the combination on Huh7.5/JFH-1 cells by HCV RNA quantitative PCR assays and HCV core protein secretion. At the ED_{50} of each drug, the combination index was 0.55 and 0.48, respectively (Table S1). The cytotoxicity was not observed at the range of concentration tested (Fig. S2E, S3E).

IFN-λ3 induces ISRE promoter activity

We used the ISRE luciferase reporter assay to assess activity downstream of the JAK-STAT signalling pathway. The ISRE-firefly luciferase plasmid was transfected into OR6/ORN/C-5B/KE cells for 24 h, and these cells were cultured with various concentrations of IFN-λ3 and IFN-α for another 12, 24 or 48 h. Firefly and *Renilla* luciferase activity was then measured.

IFN-λ3 induced ISRE luciferase activity in a time-dependent manner; activity was elevated threefold after treatment with 100 ng/mL IFN-λ3 for 48 h (Fig. 4). In contrast, IFN-α induced ISRE luciferase more rapidly, producing maximal activation of the response to IFN-α at 12 h. The combination of IFN-λ3 and IFN-α induced ISRE luciferase activity similarly to IFN-λ3 alone.

IFN-α and IFN-λ3 induce expression of similar genes in HCV 1b replicon cells

OR6/ORN/C-5B/KE cells were stimulated for 6, 12, 24 and 48 h with 0.01 ng/mL IFN-α, 10 ng/mL IFN-λ3 or a combination of both, while controls were left unstimulated for the same time interval. Induction of gene expression by IFNs was analysed in microarray experiments.

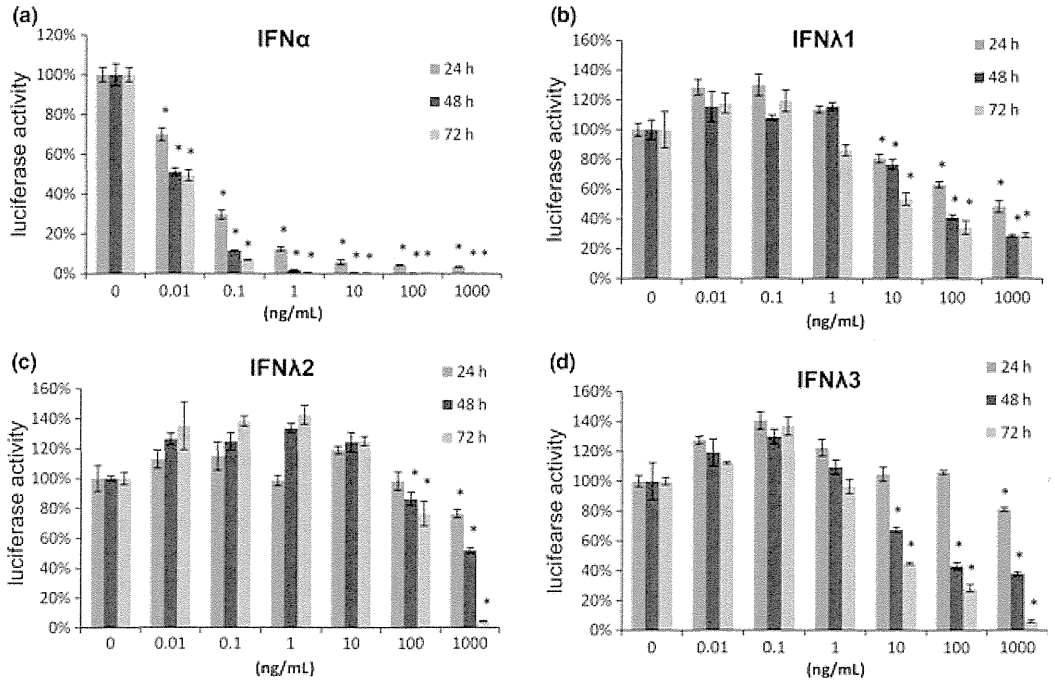

Fig. 1 IFN-α and IFN-λs inhibit HCV replicon in OR6 cells. Specific inhibition of the replication of a full-length HCV genotype 1b replicon by (a) IFN-α and (b) IFN-λ1, (c) IFN-λ2, (d) IFN-λ3 were quantified on the basis of luciferase activity. Symbols show the mean value of triplicate wells; error bars show the SD. *: $P < 0.05$ *vs* control (IFN 0 ng/mL) of each time point.

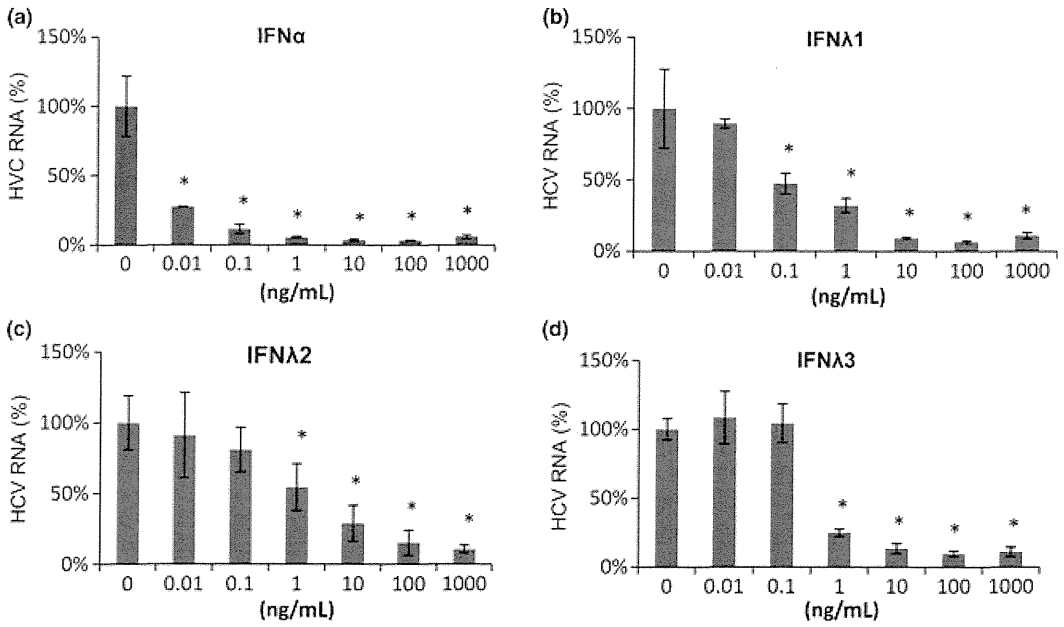

Fig. 2 IFN-α and IFN-λs inhibit HCV replicon in Huh7.5.1 cells. JFH1-infected Huh7.5.1 cells were incubated with various concentrations of (a) IFN-α and (b) IFN-λ1, (c) IFN-λ2, (d) IFN-λ3. After 48 h of treatment, total RNA was isolated and reverse transcribed, after which quantitative PCR was performed. Symbols show the mean value of triplicate wells; error bars show the SD. *: $P < 0.05$ *vs* control (IFN 0 ng/mL).

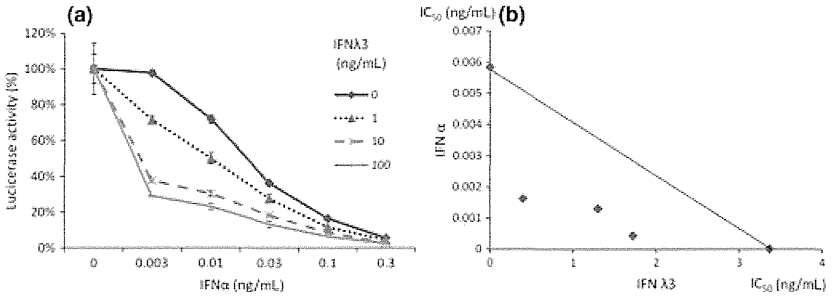

Fig. 3 Synergistic inhibitory effect of IFN-λ3 with IFN-α on hepatitis C virus replication. OR6/ORN/C-5B/KE cells were treated with combinations of IFN-λ3 with IFN-α at various concentrations. (a) The relative concentration–inhibition curves of IFN-α plotted for each fixed concentration of IFN-λ3 (0, 1, 10 and 100 ng/mL). (b) Classic isobologram for IC_{50} of IFN-λ3 with IFN-α in combination.

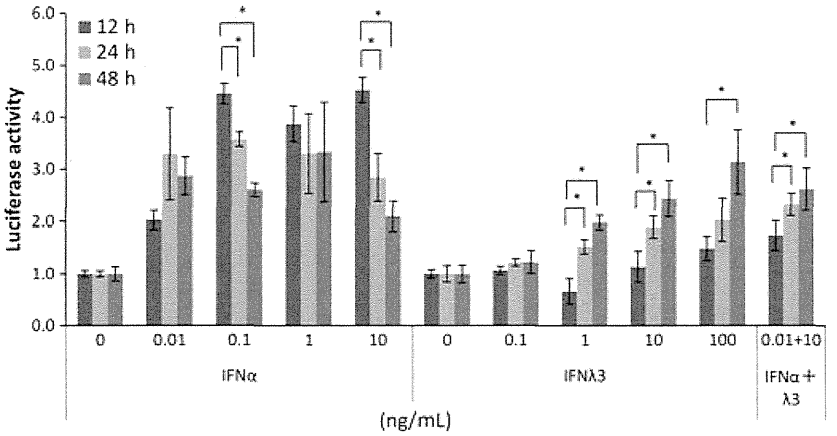

Fig. 4 IFN-stimulated response element (ISRE) promoter activity induced by IFN-α, IFN-λ3 or combination of IFN-α and IFN-λ3. OR6/ORN/C-5B/KE cells transfected with ISRE-firefly luciferase were cultured with various concentrations of IFN-α alone, IFN-λ3 alone or 0.01 ng/mL IFN-α plus 10 ng/mL IFN-λ3. ISRE-firefly luciferase activity at 24 h after transfection. Symbols show the mean value of triplicate wells; error bars show the SD. *: $P < 0.05$.

At all time points, the IFN-λ3-treated samples showed a tendency for the induction of a larger number of genes than samples treated with IFN-α. However, as shown in Table 1 listing the top 25 genes that were upregulated by both IFN-α and IFN-λ3 at 12 h, most of the upregulated genes are previously identified ISGs and the genes with high ranks were similar irrespective of the type of IFN or time point.

The time course of ISGs regulation differs between IFN-α and IFN-λ3

By microarray analysis, ISGs were more rapidly induced after the addition of IFN-α *vs* IFN-λ3 (data not shown). To confirm the rapid induction of ISGs by IFN-α, six ISGs, that is, IFI-6, IFIT1 (ISG56), DDX60, OAS2, Mx1 and USP18, were quantified for time-dependent expressional change by real-time RT-PCR. Expression of most of the genes upregulated by IFN-α peaked at 12 h and fell thereafter. In contrast, expression of IFN-λ3-induced genes peaked at 24 h and lasted up to 48 h. Combination of IFN-α and IFN-λ3 induced ISG with peak effects occurring at 12–24 h and lasting up to 48 h (Fig. 5).

DISCUSSION

In this study, we demonstrated that IFN-λ family members have distinctive time-dependent antiviral activities in an HCV replicon system and that IFN-λ3 and IFN-α have a synergistic effect in combination. Moreover, we attempted to identify the antiviral mechanism of IFN-λ3 by conducting a cDNA microarray analysis.

In previous studies, anti-HCV activity of IFN-λ1, IFN-λ2 and IFN-λ3 was reported in JFH-1 and OR6/C-5B systems [13]. Time-dependent anti-HCV activity has also been observed with IFN-λ1 [9]. In this study, we confirmed the previous results and added the further finding that time-dependent antiviral activity is not limited to IFN-λ1, but rather is common among all IFN-λs.

Table 1 Top 25 genes that were upregulated by both IFN-α and IFN-λ3 at 12 h

Gene bank ID	Gene symbol	Gene description	IFN-α 0.01 ng/mL fold increase	IFN-λ3 10 ng/mL fold increase	IFN-α+IFN-λ3 fold increase
BC007091	IFIT1	Interferon-induced protein with tetratricopeptide repeats 1	4.01	4.49	4.87
BC049215	OAS2	2′-5′-oligoadenylate synthetase 2, 69/71kDa	3.06	3.88	4.48
M33882	MX1	Myxovirus (influenza virus) resistance 1	3.24	3.29	3.69
AF095844	IFIH1	Interferon induced with helicase C domain 1	2.73	3.02	3.54
BC038115	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	2.70	2.92	3.51
BC011601	IFI6	Interferon, alpha-inducible protein 6	3.07	3.24	3.42
BC042047	HERC6	Hect domain and RLD 6	2.56	2.75	3.34
AF442151	RSAD2	Radical S-adenosyl methionine domain containing 2	1.32	2.59	3.28
U34605	IFIT5	Interferon-induced protein with tetratricopeptide repeats 5	2.47	2.91	3.25
AY730627	OAS1	2′,5′-oligoadenylate synthetase 1, 40/46kDa	2.32	2.57	3.05
AB006746	PLSCR1	Phospholipid scramblase 1	2.37	2.51	3.03
AF307338	PARP9	Poly (ADP-ribose) polymerase family, member 9	2.39	2.46	2.94
M87503	IRF9	Interferon regulatory factor 9	2.61	2.59	2.85
AK297137	IFIT3	Interferon-induced protein with tetratricopeptide repeats 3	1.90	2.36	2.79
AK290655	EIF2AK2	Eukaryotic translation initiation factor 2-alpha kinase 2	2.47	2.45	2.77
BX648758	PARP14	Poly (ADP-ribose) polymerase family, member 14	2.07	2.25	2.66
BC132786	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.83	2.17	2.59
AF445355	SAMD9	Sterile alpha motif domain containing 9	2.07	2.08	2.56
	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	1.63	1.92	2.39
BC014896	USP18| USP41	Ubiquitin-specific peptidase 18/ubiquitin-specific peptidase 41	1.52	1.78	2.11
AB044545	OAS3	2′-5′-oligoadenylate synthetase 3, 100kDa	1.44	1.57	2.10
BC010954	CXCL10	Chemokine (C-X-C motif) ligand 10	0.76	1.66	1.99
BC014896	USP18	Ubiquitin-specific peptidase 18	1.33	1.55	1.99
AL832618	IFI44L	Interferon-induced protein 44-like	0.58	1.31	1.95

We also assessed whether IFN-λ3 and IFN-α in combination could produce additive or synergistic effects on antiviral activity. In previous studies, additive antiviral activity against HCV was reported with the combination of IFN-λ1 and IFN-α [9, 10]. However, there have been no previous reports on the combined effects of IFN-λ3 and IFN-α. In this study, the focus was on IFN-λ3, because IFN-λ3 is suspected to be the key molecule, mediating the effect of SNPs in the IL-28B gene region on the anti-HCV response to IFN-α. As shown in Fig. 3 and Table S1, synergistic induction of anti-HCV activity occurred in both the OR6/C-5B and Huh7.5/JFH-1 HCV replicon systems. Synergy was demonstrated by the combination index values (Table S1).

Although it has been reported that the upregulated genes induced by IFN-λ are similar to those induced by IFN-α [9, 14–16], there have been no previous reports on

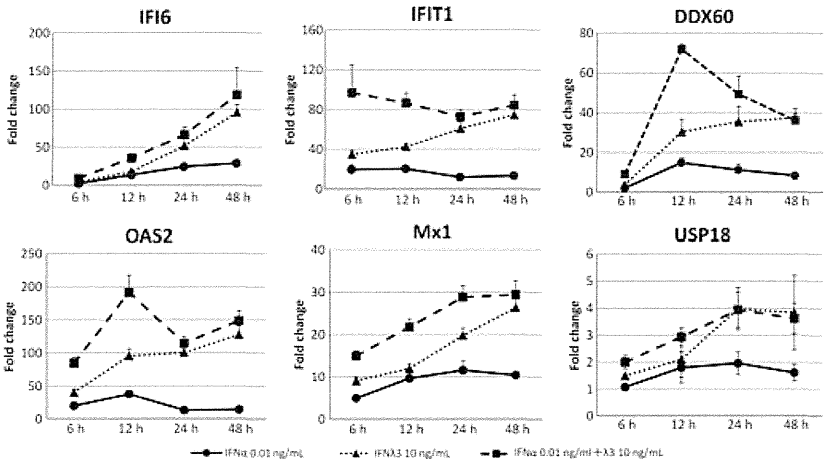

Fig. 5 Time course of ISG expression induced by 0.01 ng/mL IFN-α, 10 ng/mL IFN-λ3 or 0.01 ng/mL IFN-α plus 10 ng/mL IFN-λ3. Expression of the ISGs – IFI-6, IFIT1 (ISG56), DDX60, OAS2, Mx1 and USP18 – in OR6/ORN/C-5B/KE cells treated 6, 12, 24 and 48 h were determined by qRT-PCR. Results are presented as the relative fold induction. Symbols show the mean value of triplicate wells; error bars show the SD. *Solid lines* represent 0.01 ng/mL IFN-α alone, whereas *fine dashed lines* show 10 ng/mL IFN-λ3 alone, and *coarse dashed lines* show the combination of the 2 cytokines.

the genes induced by IFN-α and IFN-λ in combination. In cDNA microarray analysis, as demonstrated in Table 1, the most strongly upregulated genes induced by IFN-α/IFN-λ3 alone or in combination were almost identical, and most of them were ISGs. As no genes showed upregulation specific to IFN-λ3, we speculate that IFN-α and IFN-λ3 share a similar antiviral intracellular mechanism at the molecular level.

Unexpectedly in microarray analyses, synergistic upregulation of ISGs was not observed. In the same manner, TaqMan real-time RT-PCR analysis showed that the combination of IFN-α and IFN-λ3 did not upregulate ISGs synergistically (Fig. 5). In addition to cDNA microarray analysis, ISRE reporter assays were performed to determine the activation of components of the JAK-STAT pathway common to both type I and III IFNs. As shown in Fig. 4, each IFN upregulated ISRE activity, and the combination of IFN-λ3 and IFN-α did not synergistically enhance ISRE activity either.

Meanwhile, the peak time of the induction of ISG expression differs for IFN-α and IFN-λ1 [9, 17]; peak gene expression occurs earlier with IFN-α than with IFN-λ1. In our study, we confirmed that the peak induction of gene expression occurred later (24 h) and lasted longer (24–48 h) with IFN-λ3 than with IFN-α (12 h). Importantly, gene expression appeared early (12 h) and was prolonged (48 h) by the combination of both IFNs. Similarly to the peak time difference between IFN-α and IFN-λ3 seem for ISG expression, a time-dependent increase in ISRE activation was observed with the combination of both IFNs. While the precise mechanism remains to be clarified, differential regulation of the time-dependent induction of ISG gene expression could be one of the mechanisms underlying the synergistic antiviral effect. One of the molecules contributing to time-dependent ISG upregulation is the ISG known as ubiquitin-specific peptidase 18 (USP18), which has been reported to bind to IFNAR2 and inhibit the interaction of Jak1 with its receptor, thereby preventing IFN-α signalling while leaving IFN-λ signalling unaffected [18, 19]. Actually, expression of USP18 is specifically upregulated with IFN-λ3 in this study as shown in Fig. 5. If the ISGs upregulated by IFN-α are downregulated by USP18, it is plausible that the expression of genes induced by IFN-α decreases early, while expression of genes induced by IFN-λ lasts longer.

A number of clinical studies have confirmed that SNPs around the IL-28B gene are associated with the response to PEG-IFN and RBV therapy, and as previously indicated, various investigations have been performed to clarify the underlying mechanism. Specifically, increased IL-28B mRNA expression in PBMC [2, 3], high serum concentrations of IFN-λ1 (IL-29) [20], low expression of ISGs in the liver prior to IFN treatment [8, 21] and high upregulation of ISG expression by IFN treatment [8, 22] were found in subjects with IL-28B SNP genotypes associated with SVR (rs12979860 CC and rs8099917 TT). Although the functional role of IFN-λ3 still needs to be investigated more thoroughly, if IFN-λ3 expression change is the essential difference in determining the clinical treatment response to PEG-IFN and RBV therapy and if its expression is decreased in patients with the specific IL-28B genotype, which is associated with non-SVR, it is possible that exogenous administration of IFN-λ3 might improve IFN-α-induced viral clearance and that such treatment would be beneficial for patients with the IFN-resistant IL-28B genotype.

In present study, the OR6-cultured cells harboured the rs8099917 TT genotype, and recombinant IFN-λ3 (IL-