

Fig. 1 IFN- $\alpha$  and IFN- $\lambda$ s inhibit HCV replicon in OR6 cells. Specific inhibition of the replication of a full-length HCV genotype 1b replicon by (a) IFN- $\alpha$  and (b) IFN- $\lambda$ 1, (c) IFN- $\lambda$ 2, (d) IFN- $\lambda$ 3 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.

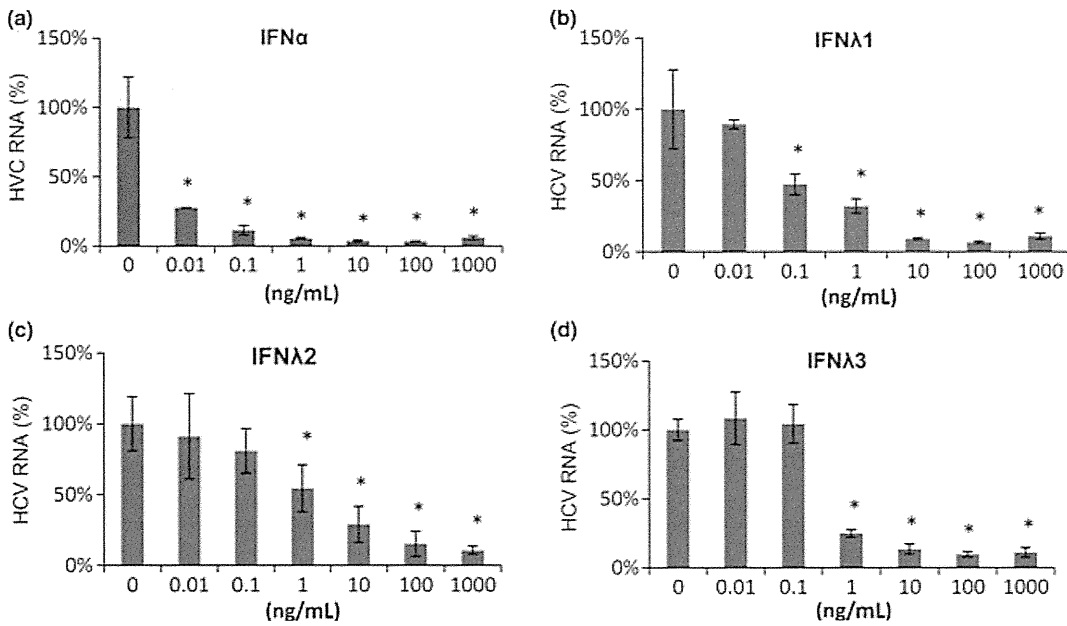
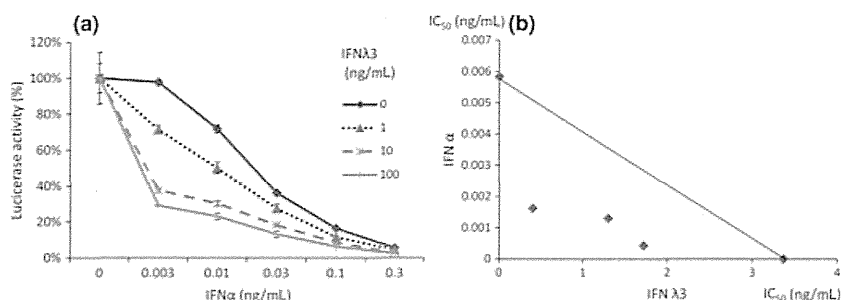
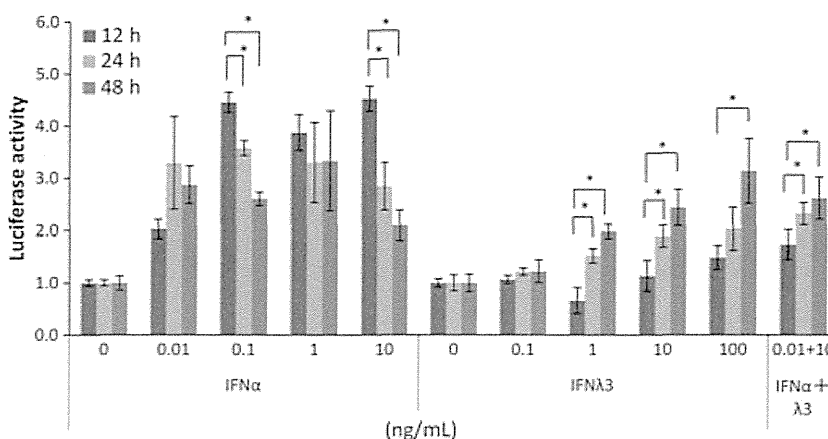


Fig. 2 IFN- $\alpha$  and IFN- $\lambda$ s inhibit HCV replicon in Huh7.5.1 cells. JFH1-infected Huh7.5.1 cells were incubated with various concentrations of (a) IFN- $\alpha$  and (b) IFN- $\lambda$ 1, (c) IFN- $\lambda$ 2, (d) IFN- $\lambda$ 3. After 48 h of treatment, total RNA was isolated and reverse 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- $\lambda$ 3 with IFN- $\alpha$  on hepatitis C virus replication. OR6/ORN/C-5B/KE cells were treated with combinations of IFN- $\lambda$ 3 with IFN- $\alpha$  at various concentrations. (a) The relative concentration-inhibition curves of IFN- $\alpha$  plotted for each fixed concentration of IFN- $\lambda$ 3 (0, 1, 10 and 100 ng/mL). (b) Classic isobologram for IC<sub>50</sub> of IFN- $\lambda$ 3 with IFN- $\alpha$  in combination.



**Fig. 4** IFN-stimulated response element (ISRE) promoter activity induced by IFN- $\alpha$ , IFN- $\lambda$ 3 or combination of IFN- $\alpha$  and IFN- $\lambda$ 3. OR6/ORN/C-5B/KE cells transfected with ISRE-firefly luciferase were cultured with various concentrations of IFN- $\alpha$  alone, IFN- $\lambda$ 3 alone or 0.01 ng/mL IFN- $\alpha$  plus 10 ng/mL IFN- $\lambda$ 3. 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- $\lambda$ 3-treated samples showed a tendency for the induction of a larger number of genes than samples treated with IFN- $\alpha$ . However, as shown in Table 1 listing the top 25 genes that were upregulated by both IFN- $\alpha$  and IFN- $\lambda$ 3 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- $\alpha$ and IFN- $\lambda$ 3*

By microarray analysis, ISGs were more rapidly induced after the addition of IFN- $\alpha$  vs IFN- $\lambda$ 3 (data not shown). To confirm the rapid induction of ISGs by IFN- $\alpha$ , 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- $\alpha$  peaked at 12 h and fell thereafter. In contrast, expression of IFN- $\lambda$ 3-induced genes peaked at 24 h

and lasted up to 48 h. Combination of IFN- $\alpha$  and IFN- $\lambda$ 3 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- $\lambda$  family members have distinctive time-dependent antiviral activities in an HCV replicon system and that IFN- $\lambda$ 3 and IFN- $\alpha$  have a synergistic effect in combination. Moreover, we attempted to identify the antiviral mechanism of IFN- $\lambda$ 3 by conducting a cDNA microarray analysis.

In previous studies, anti-HCV activity of IFN- $\lambda$ 1, IFN- $\lambda$ 2 and IFN- $\lambda$ 3 was reported in JFH-1 and OR6/C-5B systems [13]. Time-dependent anti-HCV activity has also been observed with IFN- $\lambda$ 1 [9]. In this study, we confirmed the previous results and added the further finding that time-dependent antiviral activity is not limited to IFN- $\lambda$ 1, but rather is common among all IFN- $\lambda$ s.

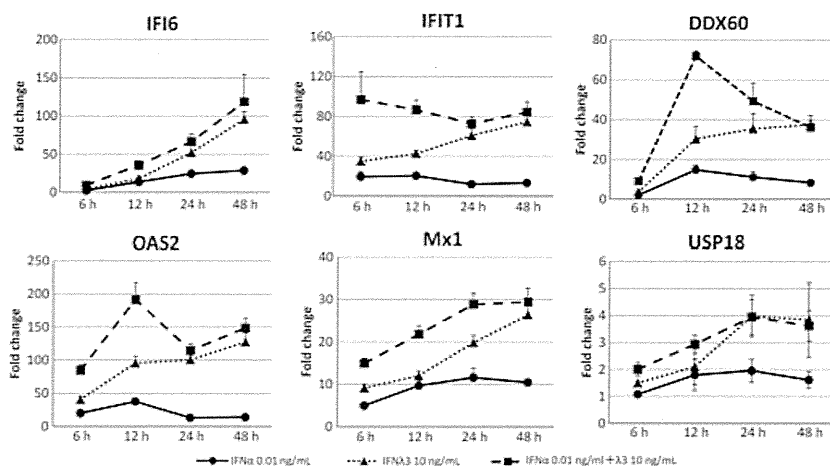
**Table 1** Top 25 genes that were upregulated by both IFN- $\alpha$  and IFN- $\lambda$ 3 at 12 h

Gene bank ID	Gene symbol	Gene description	IFN- $\alpha$ 0.01 ng/mL fold increase	IFN- $\lambda$ 3 10 ng/mL fold increase	IFN- $\alpha$ +IFN- $\lambda$ 3 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 <sup>l</sup> 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- $\lambda$ 3 and IFN- $\alpha$  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- $\lambda$ 1 and IFN- $\alpha$  [9, 10]. However, there have been no previous reports on the combined effects of IFN- $\lambda$ 3 and IFN- $\alpha$ . In this study, the focus was on IFN- $\lambda$ 3, because IFN- $\lambda$ 3 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- $\alpha$ . 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- $\lambda$  are similar to those induced by IFN- $\alpha$  [9, 14–16], there have been no previous reports on



**Fig. 5** Time course of ISG expression induced by 0.01 ng/mL IFN- $\alpha$ , 10 ng/mL IFN- $\lambda$ 3 or 0.01 ng/mL IFN- $\alpha$  plus 10 ng/mL IFN- $\lambda$ 3. 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- $\alpha$  alone, whereas *fine dashed lines* show 10 ng/mL IFN- $\lambda$ 3 alone, and *coarse dashed lines* show the combination of the 2 cytokines.

the genes induced by IFN- $\alpha$  and IFN- $\lambda$  in combination. In cDNA microarray analysis, as demonstrated in Table 1, the most strongly upregulated genes induced by IFN- $\alpha$ /IFN- $\lambda$ 3 alone or in combination were almost identical, and most of them were ISGs. As no genes showed upregulation specific to IFN- $\lambda$ 3, we speculate that IFN- $\alpha$  and IFN- $\lambda$ 3 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- $\alpha$  and IFN- $\lambda$ 3 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- $\lambda$ 3 and IFN- $\alpha$  did not synergistically enhance ISRE activity either.

Meanwhile, the peak time of the induction of ISG expression differs for IFN- $\alpha$  and IFN- $\lambda$ 1 [9, 17]; peak gene expression occurs earlier with IFN- $\alpha$  than with IFN- $\lambda$ 1. In our study, we confirmed that the peak induction of gene expression occurred later (24 h) and lasted longer (24–48 h) with IFN- $\lambda$ 3 than with IFN- $\alpha$  (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- $\alpha$  and IFN- $\lambda$ 3 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- $\alpha$  signalling while leaving IFN- $\lambda$  signalling unaffected [18, 19]. Actually, expression of USP18 is specifically upregulated with IFN- $\lambda$ 3 in this study as shown in Fig. 5. If the ISGs upregulated by IFN- $\alpha$  are downregulated by USP18, it is plausible that the expression of genes induced by IFN- $\alpha$  decreases early, while expression of genes induced by IFN- $\lambda$  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- $\lambda$ 1 (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- $\lambda$ 3 still needs to be investigated more thoroughly, if IFN- $\lambda$ 3 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- $\lambda$ 3 might improve IFN- $\alpha$ -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- $\lambda$ 3 (IL-

28B) protein used in the experiment was derived from cells with the rs8099917 TT genotype (data not shown). Therefore, the viral responses and/or cellular gene expression change in cells and/or proteins with different IL-28B genotypes *in vitro* should be determined in future studies.

In conclusion, we demonstrated that IFN- $\alpha$  and IFN- $\lambda$ 3 synergistically enhance anti-HCV activity *in vitro*. Although the ISGs upregulated by IFN- $\alpha$  and IFN- $\lambda$ 3 were similar, differences in time-dependent upregulation of these genes, especially prolonged ISGs expression by IFN- $\lambda$ 3, might contribute to their synergistic antiviral activity.

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#### CONFLICT OF INTEREST

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## SUPPORTING INFORMATION

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

**Figure S1:** IFN- $\alpha$  and IFN- $\lambda$ s inhibit HCV core protein secretion. JFH1-infected Huh7.5.1 cells were incubated with various concentrations of IFN- $\alpha$  and IFN- $\lambda$ 1, - $\lambda$ 2, - $\lambda$ 3. After 48 h of treatment, HCV core protein in the medium was measured. Symbols show the mean value of triplicate wells; error bars show the SD. \*:  $p < 0.05$  vs. control (IFN Ong/ml).

**Figure S2:** The dimethylthiazol carboxymethoxyphenyl sulfophenyl tetrazolium assay was performed after

OR6/ORN/C-5B/KE cells were cultured with various concentrations of (A) IFN- $\alpha$ , (B) IFN- $\lambda$ 1, (C) IFN- $\lambda$ 2, (D) IFN- $\lambda$ 3 and (E) combination of IFN- $\alpha$  and IFN- $\lambda$ 3 for 48 h. Symbols show the mean value of triplicate wells; error bars show the SD. \*:  $p < 0.05$  vs. control (IFN Ong/ml).

**Figure S3:** The dimethylthiazol carboxymethoxyphenyl sulfophenyl tetrazolium assay was performed after Huh7.5.1/JFH-1 cells were cultured with various concentrations of (A) IFN- $\alpha$ , (B) IFN- $\lambda$ 1, (C) IFN- $\lambda$ 2, (D)

IFN- $\lambda$ 3 and (E) combination of IFN- $\alpha$  and IFN- $\lambda$ 3 for 48 h. Symbols show the mean value of triplicate wells; error bars show the SD. \*:  $p < 0.05$  vs. control (IFN Ong/ml).

**Table S1:** Combination index after 48hr stimulation by CalucSyn.

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## Once-daily simeprevir in combination with pegylated-interferon and ribavirin: a new horizon in the era of direct-acting antiviral agent therapy for chronic hepatitis C

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Hepatitis C virus (HCV) is a leading cause of chronic hepatitis, liver cirrhosis, and hepatocellular carcinoma (HCC), and it is estimated that infected individuals total 185 million people worldwide. In Japan, around 2 million are infected with HCV, and more than 20 thousand die from HCV-induced HCC annually. Though viral eradication with antiviral therapies is the most important and effective choice for decreasing HCC-related deaths induced by HCV, complete viral eradication has been quite difficult till recently, especially in patients with genotype-1 HCV infection because of the low response rate to interferon (IFN)-based therapy [1, 2].

In this background, development of novel direct-acting antiviral agents (DAAs) specific for HCV was truly a revolutionary event. In 2011, two first-generation NS3 protease inhibitors (PIs), telaprevir and boceprevir, were firstly approved among all the DAAs for clinical use in USA and Europe for genotype-1 HCV in combination with pegylated-interferon and ribavirin (PR), while telaprevir was approved in Japan in the same 2011 period. As expected, a regimen including telaprevir in combination with pegylated-interferon and ribavirin dramatically improved the sustained viral response (SVR) rate to as high as 80 % in genotype-1 HCV infection. On the other hand, telaprevir has several undesirable problems. Among all, adverse events (AEs) of anemia and skin rash are serious problems of telaprevir, and Grade 3/4 skin disorders,

including Stevens–Johnson syndrome and drug rashes with eosinophilia and systemic symptoms, as well as Grade 3 anemia (<8.0 g/dL), might occur [3, 4]. Moreover, cumbersome frequent dosing three times a day (every 7–9 h) could induce poor medication adherence. Under the circumstances, it has been quite stressful for patients as well as clinicians to introduce and monitor this telaprevir-based regimen.

Simeprevir (SMV, TMC435) is classified as a second-generation PI with the macrocyclic structure having an advantage in the binding affinity and specificity for NS3 protease compared to the first-generation PI with the linear structure. Due to the difference in the structure, the drug-resistance profile is somewhat different from that of telaprevir. Though simeprevir shows cross-resistance with telaprevir at amino acid positions of 155 and 156, most of the resistant mutation occurs at the simeprevir-specific amino acid position of 168 [5]. Though simeprevir is effective in all viral genotypes (genotype 1–6), it has the strongest antiviral activity for genotype-1a and -1b HCV infection. In particular, low AE rate and its patient-friendly once-daily dosing are the important characters of simeprevir aside from its strong antiviral activity. In the international phase II trials of simeprevir in combination with PegIFN $\alpha$ -2a/RBV for treatment-naïve (PILLAR study) [6] and treatment-experienced patients (ASPIRE study) [7] for HCV genotype 1-infected patients, it was demonstrated that simeprevir was generally well tolerated and had a pharmacokinetic profile supporting once-a-day (QD) dosing resulting in high virologic response rates.

In this issue of the *Journal of Gastroenterology*, Hayashi et al. [8] reported the important results of the phase II Dose and duration Ranging study of Antiviral agent TMC435 in Genotype One HCV treatment-Naïve patients (DRAGON study; TMC435-C215) evaluating once-daily simeprevir

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with pegylated-interferon and ribavirin therapy for treatment-naïve, high viral-loaded hepatitis C genotype 1-infected patients in Japan. Due to the result of previous phase I study that simeprevir plasma concentration was higher in Japanese healthy volunteers compared with Caucasian volunteers, simeprevir doses of 50/100 mg QD were selected for this study, while simeprevir doses of 150 mg QD were selected in western countries [9]. Through investigating five treatment groups (SMV12/PR24 50 mg, SMV12/PR24 100 mg, SMV24/PR24 50 mg, SMV24/PR24 100 mg, and PR48), it was disclosed that simeprevir-combined groups all achieved high SVR rate (77–92 % compared to 46 % for PR). As to the AEs, simeprevir was well tolerated, and the incidence of anemia and skin rash were similar in their frequency and their grade between all the SMV groups and the PR group. Due to low AEs, therapy discontinuation rate and ribavirin dose reduction was also similar in the SMV groups and the PR group. While an AE of bilirubin elevation was specific to simeprevir, and it reached to grade 3 (2.6–5.0 mg/dL) to 4 (>5.0 mg/dL) in four patients (5 %) leading to the discontinuation of simeprevir in these individuals, the bilirubin level returned to baseline after the end of simeprevir in those patients. Since bilirubin elevation is considered to result from the blockade of bilirubin clearance-associated OATP1B1 and MRP transporters by simeprevir [10], it is considered that the bilirubin elevation by simeprevir does not reflect deterioration of liver function.

Following the results of this phase II DRAGON study, treatment dosage of simeprevir was determined as 100 mg QD in Japan, and successive phase III CONCERTO studies for simeprevir/pegylated-interferon/ribavirin therapy have been conducted (CONCERTO-1 for treatment-naïve, -2 for previous null responder, -3 for previous relapser, and -4 for naïve, null responder and relapser). After the completion of those CONCERTO studies with favorable outcomes for simeprevir-based regimens, once-daily simeprevir with pegylated-interferon and ribavirin therapy for high viral-loaded hepatitis C genotype 1-infected patients was just recently approved for clinical use in Japan.

Considering the history of HCV therapy, this new therapy of once-daily simeprevir with pegylated-interferon and ribavirin therapy is ideal in its high efficacy and low AEs. Of course, it is true that DAA combination therapies without IFN (IFN-free therapies) would appear in the near future, and that these IFN-free therapies are advantageous in that they are free from IFN-related AEs. However, in terms of DAA-resistant viral mutants, it is considered that

these mutant HCVs generally have low replication fitness, and are sensitive to IFN. Therefore, it is speculated that IFN-based DAA therapies compared to IFN-free DAA therapies are safer in preventing the development of multidrug resistant HCVs.

Taken together, the new regimen of once-daily simeprevir with pegylated-interferon and ribavirin therapy would surely be an important milestone in the therapy for high viral-loaded hepatitis C genotype-1 infected patients in the era of DAA therapy.

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1 **Hepatocellular carcinoma risk assessment using gadoxetic acid-enhanced**  
2 **hepatocyte phase magnetic resonance imaging**

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20 ***Short running title:*** HCC risk assessment using EOB-enhanced MRI

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## FOOTNOTES

### 5 **Competing interests**

6 All authors have no conflict of interest related to this manuscript.

7

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2 **List of Abbreviations**

3 HCC: Hepatocellular Carcinoma

4 MRI: Magnetic Resonance Imaging

5 US: Ultrasonography

6 CT: Computed Tomography

7 HBV: Hepatitis B Virus

8 HCV: Hepatitis C Virus

9 AASLD: American Association for the Study of Liver Diseases

10 T1WIs: T1-Weighted Images

11 T2WIs: T2-Weighted Images

12 ALT: Alanine Aminotransferase

13  $\gamma$ -GTP:  $\gamma$  - Glutamyl Transpeptidase

14 AFP: Alpha-fetoprotein

15 HR: Hazard Ratio

16 CI: Confidence Interval

17 DWIs: Diffusion-Weighted Images

## ABSTRACT

**Aim:** To investigate whether the patients with hypovascular liver nodules determined on the arterial phase and hypointensity on the hepatocyte phase gadoxetic acid-enhanced magnetic resonance imaging (hypovascular hypointense nodules) are at increased risk of hepatocarcinogenesis, we assessed subsequent typical hepatocellular carcinoma (HCC) development at any sites of the liver with and without such nodules.

**Methods:** One hundred and twenty-seven patients with chronic hepatitis B or C and without a history of HCC, including 68 with liver cirrhosis, were divided into those with (non-clean liver group, n = 18) and without (clean liver group, n =109) hypovascular hypointense nodules. All the patients were followed-up for 3 years, and HCC development rates and risk factors were analyzed with the Kaplan-Meier method and the Cox proportional hazard model, respectively.

**Results:** A total of 17 patients (10 in the non-clean liver group and 7 in the clean liver group) developed typical HCCs. Cumulative 3-year rates of HCC development were 55.5% in the non-clean liver group and 6.4% in the clean liver group ( $p < 0.001$ ), and those at the different sites from the initial nodules was also higher in the non-clean liver group (22.2%) than the clean liver group (6.4%) ( $p = 0.003$ ). Multivariate analysis identified older age ( $p = 0.024$ ), low platelet counts ( $p = 0.017$ ) and a non-clean liver ( $p < 0.001$ ) as independent risk factors for subsequent HCC development.

**Conclusions:** Patients with hypovascular hypointense liver nodules are at a higher risk for HCC development at any sites of the liver than those without such nodules.

## INTRODUCTION

Hepatocellular carcinoma (HCC) is one of the most common cancers worldwide and is a major cause of death in patients with chronic viral liver disease. Despite many advances in multidisciplinary treatment, complete curative treatment of early-stage HCC remains the only possible therapeutic choice for long-term survival. Therefore, surveillance programs for patients at a high-risk for HCC that include imaging-based evaluations are crucial for the detection and treatment of early-stage HCC.

The newly introduced magnetic resonance imaging (MRI) contrast agent, gadolinium ethoxybenzyl diethylenetriaminepentaacetic acid (gadoteric acid), has enabled concurrent assessment of tumor vascularity and unique hepatocyte-specific contrast (hepatocyte phase) (1-3). This has led to the frequent identification of hypovascular nodules determined on the arterial phase with hypointensity on the hepatocyte phase (hypovascular hypointense nodules) (4-8), while many of these nodules are difficult to be detected by ultrasonography (US) or computed tomography (CT). Recently, the natural history of hypovascular hypointense nodules themselves were reported in several studies (9-12), revealing the high risk of subsequent progress to typical HCCs from these nodules. However, it is not well known whether patients with such nodules has a higher risk of developing typical HCCs at any sites of the liver, including at the different sites from initial nodules, compared to those without such nodules.

If patients with these nodules may have a high risk of developing typical HCCs not only at the same sites but also at the different sites from initial nodules, significant proportion of these nodules are precancerous lesions or early-stage HCC as reported

1 (13-15), and more importantly, the liver with these nodules might reflect a higher  
2 potential for hepato-carcinogenesis or the presence of undetectable precursor lesions in  
3 other sites of the liver. Conversely, the absence of these nodules potentially identifies  
4 the patients at a low risk for subsequent typical HCC development at any sites. The  
5 purpose of this study was to assess the risk of subsequent typical HCC development at  
6 any sites of the liver with and without hypovascular hypointense nodules on gadoxetic  
7 acid-enhanced MRI.

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## METHODS

### *Ethical review*

3 The protocol of this retrospective study was approved by the ethics committee of  
4 Yamanashi University Hospital, which waived the requirement for written informed  
5 consent because the study was a retrospective data analysis, with appropriate  
6 consideration given to patient risk, privacy, welfare, and rights.  
7

8

### *Patients*

9 We recruited 559 consecutive outpatients with chronic hepatitis B virus (HBV) or  
10 hepatitis C virus (HCV) infection who underwent gadoxetic acid-enhanced MRI at  
11 Yamanashi University Hospital between January 2008 and December 2010. The  
12 exclusion criteria were as follows: 1) presence or history of typical HCC (n = 420),  
13 because intrahepatic metastasis does not always develop through the usual multistep  
14 hepatocarcinogenesis process, skipping the early pathological stage with  
15 hypovascularity to an advanced pathological stage even when the size is small (16, 17);  
16 2) Child-Pugh class C disease (n = 9), because the hepatocyte phase findings are not  
17 reliable in patients with this condition because of reduced gadoxetic acid uptake in the  
18 liver (18); and 3) patients who dropped out during the 3-year follow-up period (n = 3).  
19 After excluding 432 patients, 127 patients were included in this retrospective  
20 cohort study. They were divided into groups with hypovascular nodules determined on  
21 the arterial phase and hypointensity on the hepatocyte phase (non-clean liver group; n =  
22 18 patients) and without such nodules (clean liver group; n = 109 patients) as shown in  
23 Figure 1. In this study, we divided cases into two groups according to the presence or  
24

1 absence of these nodules at the baseline, even when such nodules were initially detected  
2 during the follow-up period; we assigned these patients to the clean liver group.

#### 3 4 *Follow-up and diagnosis of HCC*

5 All 127 patients were followed-up at the liver disease outpatient clinic of our  
6 institution with blood tests, including those for tumor markers, and diagnostic imaging  
7 modality (US, CT or MRI). The development of typical HCC that required treatment as  
8 proposed by the American Association for the Study of Liver Diseases (AASLD)  
9 guidelines (19) and that was diagnosed according to imaging criteria, showing arterial  
10 hypervascularity and venous phase washout, or based on histological examination of  
11 liver biopsies from hypovascular nodules that grew to >10 mm during follow-up.

12 Biopsies were obtained using a 21-gauge core needle. Two patients each had a liver  
13 nodule >10 mm in diameter on initial MRI (12mm and 13mm), was diagnosed on the  
14 basis of the biopsy as a dysplastic nodule.

15 The endpoint of this study was the development of typical HCC not only from the  
16 hypovascular hypointense nodules observed initially but also from other areas without  
17 these nodules (“*de novo* HCC”). Dynamic CT and/or MRI were also performed in cases  
18 with hepatic nodules detected by US, liver cirrhosis, a tendency of tumor marker  
19 elevation, and difficult evaluation of the liver parenchyma by US. All the 127 patients  
20 were followed-up for 3 years after the initial gadoxetic acid-enhanced MRI  
21 examination. When imaging modalities led to diagnosis of HCC, recognizing  
22 hypervascularization by more than one experienced radiologist and other imaging  
23 modalities was regarded as the time of diagnosis of HCC. When needle biopsy was  
24 performed to investigate nodules, the time of diagnosis of HCC was when the



1 pathologists and physicians examined pathological tissue and diagnosed as HCC.

2

### 3 ***MRI***

4 MRI was performed using a superconducting magnet that operated at 1.5 Tesla  
5 (Sigma EXCITE HD; GE Medical Systems, Milwaukee, WI) and an 8-channel  
6 phased-array coil. First, we obtained fast spoiled gradient-echo T1-weighted images  
7 (T1WIs) with dual echo acquisition and respiratory-triggered fat-saturated fast  
8 spin-echo T2-weighted images (T2WIs). Dynamic fat-suppressed gradient-echo T1WIs  
9 were obtained using a three-dimensional (3D) acquisition sequence before (precontrast)  
10 and 20-30 s, 60 s, 2 min, 5 min, 10 min, and 20 min after the administration of  
11 gadoxetic acid (Primovist; Bayer Schering Pharma, Berlin, Germany). This contrast  
12 agent (0.025 mmol/kg body weight) was administered intravenously as a bolus at a rate  
13 of 1 mL/s through an intravenous cubital line (20–22 gauge) that was flushed with 20  
14 mL saline from a power injector. The delay time for the arterial phase scan was adjusted  
15 according to a fluoroscopic triggering method (20). All images were acquired in the  
16 transverse plane. Sagittal plane T1WIs were also obtained during the hepatocyte phase  
17 at 20 min after the injection of the contrast agent.

18

### 19 ***Statistical analysis***

20 All continuous values are expressed as median (range). Fischer's exact probability  
21 test was used for comparisons between categorical variable and the non-parametric  
22 Mann-Whitney test was used to compare differences between continuous variables.  
23 Baseline clinical characteristics, including blood test results, were evaluated within 1  
24 month of the initial MRI. We investigated whether or not HCC development was

1 associated with age, gender, fibrosis, etiology (HBV or HCV), platelet count, serum  
2 alanine aminotransferase (ALT),  $\gamma$ -glutamyl transpeptidase ( $\gamma$ -GTP), alpha-fetoprotein  
3 (AFP), and the presence or absence of hypovascular hypointense nodules.

4 Cumulative HCC development was estimated according to the Kaplan-Meier  
5 method and differences in the curves were tested using the log-rank test. Risk factors for  
6 HCC development were determined according to the Cox proportional hazard model.  
7 Subgroup analyses with a Cox proportional hazard model were applied to estimation of  
8 the hazard ratio (HR) of the non-clean liver group versus clean liver group in the  
9 dichotomized subgroups. All statistical analyses were performed using JMP software,  
10 version 10 (SAS Institute Japan, Tokyo, Japan). A two-sided p value  $<0.05$  was  
11 considered statistically significant.

12

## RESULTS

### *Characteristics of the patients and nodules*

A total of 127 patients were enrolled, of whom 26 had chronic HBV infections and 101 had HCV infections, and 68 had virus-associated cirrhosis. No statistically significant differences in the initial clinical characteristics were found between the non-clean liver and clean liver groups (Table 1). Thirty five hypovascular hypointense nodules were found in 18 patients in the non-clean liver group (1–5 nodules per patient) at baseline (data not shown). Twenty-four of these 35 nodules were detectable only on the hepatocyte phase MRI and were undetectable by US, CT and non-hepatocyte phase MRI. None of the 35 nodules showed high intensity on T2WIs. The median nodule diameter was 8 mm (range: 4–13 mm, 33 nodules with 10mm or less, 2 nodules with 12 mm and 13 mm).

### *HCC incidence according to initial MRI findings*

HCC was diagnosed in 17 patients, 10 in the non-clean liver group and 7 in the clean liver group; 14 of these patients had HCV infection. Thirteen patients were diagnosed according to the AASLD imaging criteria (19). Four patients were diagnosed pathologically by liver biopsies that were performed, based on enlargement of the nodules of >10 mm in diameter during the observation period.

The cumulative 1-, 2-, and 3-year HCC incidence rates were 1.5%, 10.2%, and 13.4%. As determined by the Kaplan-Meier method, these rates were 11.1% (95% confidence interval [CI], 0.0-25.6%), 38.8% (95% CI, 16.3-61.4%), and 55.5% (95% CI, 32.6-78.5%) in the non-clean liver group and 0.0% (95% CI, 0.0-2.3%), 5.5% (95%

1 CI, 0.0-9.8%), and 6.4% (95% CI, 1.8-11.0%) in the clean liver group; the former group  
2 showed significantly higher rates of development of typical HCC than the latter (p  
3 <0.001) as shown in Figure 2. The median imaging intervals were 3 months (3-6  
4 months) in the non-clean liver group and 4 months (2-12 months) in the clean liver  
5 group. The imaging interval of the non-clean liver group was shorter than clean liver  
6 group (3 vs. 4 months: p = 0.015). The median intervals between the initial MRI and  
7 HCC diagnosis was 16 months (9-32 months) in the non-clean liver group and 21  
8 months (16-35 months) in the clean liver group.

9 In 11 of 17 patients with HCC development, HCCs developed at sites in which no  
10 nodules had been seen on the initial gadoxetic acid-enhanced MRI, *i.e.* "de novo HCC".

11 These HCCs were found 4 in 18 patients in the non-clean liver group (3-year HCC  
12 incidence rates: 22.2%, 95% CI, 4.3-51.0%) and 7 in 109 patients in the clean liver  
13 group (3-year HCC incidence rates: 6.4%, 95% CI, 1.8-11.0%). The incidence rates of  
14 "de novo HCC" was significantly higher in the non-clean liver group than the clean liver  
15 group (p = 0.003, Figure 3). In the remaining 6 patients, HCCs developed at the same  
16 site of the initial nodules exclusively in 18 patients of a non-clean liver group by  
17 definition, and those HCCs arose among the nodules  $\geq 8$  mm in the initial MRI study.

### 18 19 ***Risk factors for HCC development***

20 Univariate analyses showed that the significant risk factors for HCC development  
21 included older age (p = 0.039), cirrhosis (p = 0.009), a low platelet count (p = 0.003), a  
22 high AFP concentration (p = 0.006), and a non-clean liver (p < 0.001). Multivariate  
23 analysis with these variables revealed that older age (HR: 1.08; 95% CI, 1.01–1.16: p =  
24 0.024), a low platelet count (HR 1.17; 95% CI, 1.03–1.35: p = 0.017), and a non-clean