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# G-to-A Hypermethylation in Hepatitis B Virus (HBV) and Clinical Course of Patients with Chronic HBV Infection

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**Background.** The apolipoprotein B messenger RNA editing enzyme, catalytic polypeptide-like family of cytidine deaminases induce G-to-A hypermethylation in hepatitis B virus (HBV) genomes and play a role in innate antiviral immunity. The clinical relevance of this protein family is unknown.

**Methods.** We analyzed 33 instances in which 17 patients with chronic HBV infection experienced >2 increases of >100 IU/L in alanine aminotransferase (ALT) level; we used a quantitative differential DNA denaturation polymerase chain reaction assay to quantify the hypermutated HBV genomes observed during 21 of these 33 increases in ALT level.

**Results.** Of the 9 increases in ALT level that involved a >5-fold increase (relative to basal levels) in the number of hypermutated genomes observed, 8 were associated with a >2-log reduction in plasma HBV DNA level. In contrast, a corresponding decrease in plasma HBV DNA level was observed for only 1 of the 12 increases in ALT level that did not involve an increase in the number of hypermutated genomes ( $P < .001$ ). Hepatitis B e antigen clearance was often observed in patients who experienced an increase in the number of hypermutated genomes. Interferon treatment induced hypermethylation in HBV genomes in an animal model. However, there was no apparent increase in the number of hypermutated genomes among the majority of patients who received interferon therapy, probably because the number of hypermutated genomes had already increased prior to the initiation of therapy.

**Conclusion.** Our results suggest that a marked increase in the number of hypermutated genomes represents a strong immunological host response against the virus and is predictive of hepatitis B e antigen clearance and plasma HBV DNA level reduction.

Despite the availability of safe and effective vaccines for >2 decades, hepatitis B virus (HBV) infection is still a global health problem. Worldwide, >2 billion people are infected with HBV, and chronic HBV infection affects ~400 million people [1, 2]. It is estimated that

>500,000 people die annually because of cirrhosis and/or hepatocellular carcinoma due to HBV infection [3].

Recent reports have shown that cellular cytosine deaminase (apolipoprotein B messenger RNA [mRNA] editing enzyme, catalytic polypeptide-like 3G [APOBEC3G]), packaged in human immunodeficiency virus type 1 (HIV-1), induces G-to-A hypermethylation to a nascent reverse transcript of HIV-1 and reduces the infectivity of HIV, thus contributing in part to innate antiviral activity [4–8]. HIV-1 overcomes this innate defense barrier in T cells with HIV virion infectivity factor, a protein that specifically targets APOBEC3G to proteasomal degradation [9–12]. HIV-1 can infect resting CD4 T cells in lymphoid tissues but not those circulating in peripheral blood [13–16]. Resting CD4 T cells in peripheral blood are protected from HIV infection through the action of the deaminase-active

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**Table 1. Clinical profiles of 17 patients with chronic hepatitis B virus (HBV) infection who experienced >2 increases of >100 IU/L in alanine aminotransferase (ALT) level.**

Patient	Sex	Age, years	ALT level, IU/L		Plasma HBV DNA level, log copies/mL	HBV serum marker status <sup>a</sup>		HBV subtype	Histologic result <sup>b</sup>	Receipt of IFN treatment
			Minimum	Maximum		HBeAg	HBeAb			
1	M	50	26	2000	8.1	+	-	C	F2, A2	Yes
2	M	31	22	230	8.2	+	-	C	F3, A2	Yes
3	F	23	14	313	8.7	+	-	C	F2, A2	Yes
4	M	22	16	846	6.9	+	-	C	F2, A1	Yes
5	F	42	10	100	7.8	+	-	C	L	No
6	F	33	21	748	8.8	+	-	C	F2, A3	Yes
7	M	23	22	339	8.4	+	-	C	L	Yes
8	F	54	22	108	6.7	-	+	C	F2, A2	No
9	M	44	17	512	9.5	+	-	C	F2, A3	No
10	M	27	39	115	8.8	+	-	C	F1, A1	Yes
11	M	36	16	452	3.8	+	-	C	F4, A3	Yes
12	M	20	21	1295	7.2	+	-	C	F2, A2	No
13	M	36	24	481	5.7	-	+	C	F2, A2	Yes
14	M	22	20	696	5.9	+	-	C	F1, A1	Yes
15	F	24	14	1544	7.7	+	-	C	F2, A2	Yes
16	M	35	10	1618	4.7	+	-	C	F2, A1	Yes
17	M	30	21	1655	6.7	+	-	C	L	Yes

**NOTE.** HBeAg, HBV e antigen; HBeAb, antibody against HBV e antigen; IFN, interferon; L, liver cirrhosis.

<sup>a</sup> Before increase in ALT level.

<sup>b</sup> Histologic evaluation of chronic hepatitis by use of the scoring system of Desmet et al. [29].

APOBEC3G [17]. Recent reports have shown that interferon (IFN)- $\alpha$  is a potent inducer of APOBEC3G [18–21]. It has also been reported that some of the HIV restriction exerted by APOBEC3G may be independent of its cytidine deaminase activity [17, 22–24].

We and others have reported the presence of small numbers of hypermutated genomes in serum samples obtained from HBV-infected patients [25–27]. Studies using HepG2 cell lines and primary human hepatocytes showed that such hypermutation is induced by the cytidine deaminase activity of the APOBEC family of proteins [27]. In our previous study, IFN induced little hypermutation in the HBV genome [27]. However, after extensive investigation supported by development of a quantitative analysis of hypermutation, we showed that both IFN- $\alpha$  and IFN- $\gamma$  actually increase transcription of APOBEC3G mRNA in HepG2 cell lines and induce an increase in the number of hypermutated genomes [28]. We also showed that APOBEC3G induces hypermutation in HBV and reduces HBV replication levels in the absence of the deaminase activity. Thus, APOBEC3G has dual antiviral actions against HBV and is thought to be part of the host defense mechanisms, as has been shown for HIV infection. Although it is assumed that APOBEC3G is important in the host anti-HBV defense system, little is known about the clinical importance of this enzyme, because there are no methods available for the precise quantification of small amounts of hypermutated genomes.

Using a method that can measure small amounts of hypermutated genomes (differential DNA denaturation polymerase chain reaction [3D-PCR] combined with TaqMan PCR [28]), we analyzed fluctuations in the number of hypermutated genomes observed in patients with chronic HBV infection who experienced increased alanine aminotransferase (ALT) levels. The study group included patients who received IFN treatment and patients who did not.

## METHODS

**Patients.** From 2002 through 2006 at Hiroshima University Hospital (Hiroshima, Japan), there were 17 consecutive patients with chronic hepatitis B who experienced >2 increases of >100 IU/L in ALT level and for whom stored serum samples were available. These 17 patients were enrolled in this study, among whom 33 such increases in ALT level were observed. Thirteen of 17 patients received IFN treatment, usually during an increase in ALT level. The clinical profiles of these 17 patients are shown in table 1. Written informed consent was obtained from all patients, and the study was approved by the Hiroshima University Ethics Committee.

**HBV markers.** Hepatitis B e antigen and antibody against e antigen were quantified by use of enzyme immunoassay kits (Abbott Diagnostics). HBV DNA was measured by use of real-time PCR performed with the 7300 Real-Time PCR System (Applied Biosystems), in accordance with the manufacturer's instructions. The primers used for amplification were 5'-TT-

TGGGCATGGACATTGAC-3' (nt 1893–1912; nucleotide numbers are those of HBV subtype C as reported by Norder et al. [30]) and 5'-GGTGAACAATGTTCCGGAGAC-3' (nt 2029–2049). For real-time PCR, we used 25  $\mu$ L of SYBR Green PCR Master Mix (Applied Biosystems) with 1  $\mu$ L of the DNA solution and 200 nmol/L of each primer. The amplification conditions were as follows: 2 min at 50°C, 10 min at 95°C, followed by 40 cycles of amplification (denaturation at 95°C for 15 s and annealing and extension at 60°C for 1 min). The lower detection limit of this assay was 10<sup>3</sup> copies/mL.

**Extraction of HBV DNA and quantitative analysis of hypermutated genomes.** HBV DNA was extracted from 100- $\mu$ L serum samples by use of the SMITEST DNA Extraction Kit (Genome Science Laboratories) and dissolved in 20  $\mu$ L of water. Hypermutated genomes were quantified by use of TaqMan 3D-PCR performed with the 7300 Real-Time PCR System (Applied Biosystems); we used a procedure described elsewhere [28], with slight modifications. In brief, the HBV DNA fragments were amplified by use of 3D-PCR in which the denaturation temperature was set lower than usual so that only G-to-A hypermutated genomes would be amplified. The amplification conditions were as follows: activation at 95°C for 10 min; followed by initial denaturation at 89°C for 20 min, to allow nonhypermutated genomes reanneal; and 45 cycles of amplification (denaturation at 89°C for 20 s, annealing at 50°C for 30 s, and extension at 62°C for 90 s). TaqMan PCR was performed using the following primers: 5'-ACTTCAACCCCAACAMRRATCA-3' (nt 2978–2999) and 5'-AGAGYTTGKTGGAATGTKGTGGA-3' (nt 24–1), where M is A or C, R is G or A, Y is T or C, and K is G or T. The probe was a 6-carboxyfluorescein (FAM)-labeled MGB probe, 5'-(FAM)-TTAGAGGTGGAGAGATGG-(MGB)-3' (nt 3184–3167). The detection limit of hypermutated genomes was 10<sup>2</sup> copies/mL, and nonhypermutated genomes were not amplified by 3D-PCR [28]. The reproducibility of the assay was quite high (as indicated by the small standard deviation relative to the results of the quantitative PCR control reaction), as reported in our previous study [28].

**Cell culture and transfection.** HepG2 cell lines were grown in Dulbecco's modified Eagle medium supplemented with 10% (vol/vol) fetal calf serum at 37°C in 5% CO<sub>2</sub>. Cells were seeded to semiconfluence in 6-well tissue culture plates and transfected with the plasmid pTRE-HB-wt, which contained 1.4-genome length wild-type HBV genomes [31], by calcium phosphate precipitation. Seventy-two hours after transfection, the supernatant was collected for HBV DNA quantification by real-time PCR and for quantitative analysis of G-to-A hypermutated genomes [28]. The remaining supernatant was stored at –80°C for infection experiments using human hepatocyte–chimeric mice.

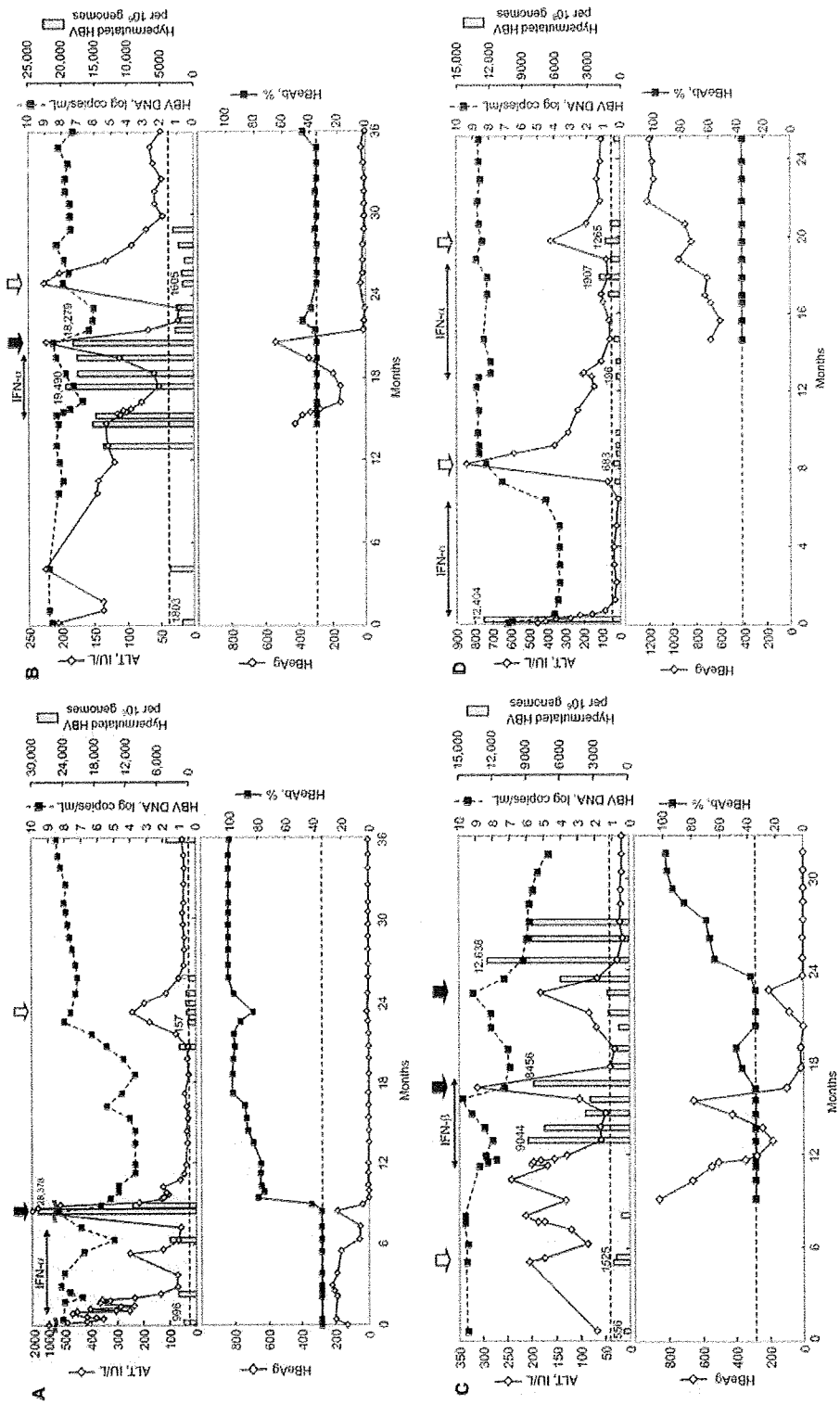
**Quantitative analysis of G-to-A hypermutated genomes with human hepatocyte–chimeric mice.** A human hepatocyte–chimeric mouse model was developed, as described previously [32], and used in infection and IFN-treatment experiments.

The human hepatocytes progressively repopulated the murine host liver and were susceptible to HBV produced in cultured cell lines [31]. All animal protocols were in accordance with the guidelines of the local animal experimentation committee. The experimental protocol was approved by the Ethics Review Committee for Animal Experimentation of the Graduate School of Biomedical Sciences, Hiroshima University. Hepatocyte–chimeric mice were inoculated with 500  $\mu$ L of the supernatant produced by transiently transfected cell lines. After confirmation of high-level HBV viremia, the mice were treated with 7000 IU/g/day of IFN- $\alpha$ , injected intramuscularly, for 14 days (the IFN- $\alpha$  was a gift from Hayashibara Biochemical Labs in Okayama, Japan). Human serum albumin in mouse serum was measured with the Human Albumin ELISA Quantitation Kit (Bethyl Laboratories), used in accordance with the manufacturer's instructions.

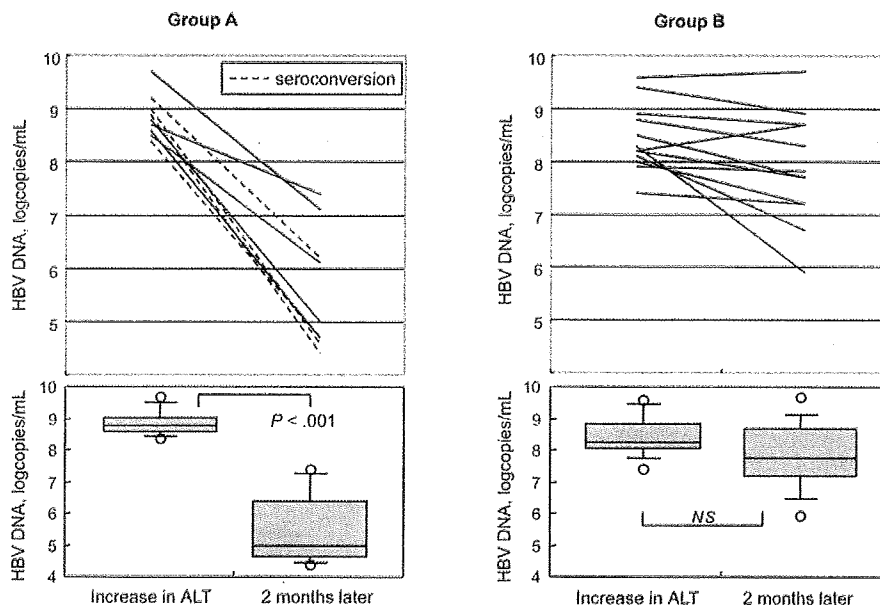
**Statistical analysis.** Differences between clinical groups with respect to HBV DNA and e antigen levels were examined for statistical significance, using the Mann-Whitney *U* test. A *P* value <.05 was considered to indicate a statistically significant difference. All statistical analyses were performed with StatView (version 5.0; SAS Institute).

## RESULTS

**Clinical course of disease in patients with increased ALT levels and fluctuations in the number of hypermutated genomes.** Figure 1A–1D shows clinical courses for 4 representative patients (patients 1–4 in Table 1) with chronic HBV infection who experienced increases in ALT level. We observed marked decreases in HBV DNA level in association with marked increases in hypermutated genomes (figure 1A–1C, black arrows). In contrast, there was no apparent reduction in HBV level in the absence of an increase in hypermutated genomes (1A–1D, white arrows). We also analyzed the effect of IFN therapy on the number of hypermutated genomes. In some patients, we observed an increase in the number of hypermutated genomes during IFN therapy (figure 1B and 1C) as well as a marked increase in the number of hypermutated genomes and a reduction of the virus accompanied by an increase in ALT level just after cessation of IFN therapy (1A–1C, black arrows). However, in some patients, such as patient 1 (figure 1A), we observed no apparent increase in the number of hypermutated genomes in response to IFN therapy. However, the number of hypermutated genomes observed in samples from this patient obtained just before the initiation of IFN therapy (996/10<sup>6</sup> genomes) was already higher than the baseline level (157/10<sup>6</sup> genomes). Samples from patient 4 (figure 1D) showed an increase in the number of hypermutated genomes during IFN therapy (1907/10<sup>6</sup> genomes), though this is less than the increase observed during natural exacerbation (12,404/10<sup>6</sup> genomes). In fact, there was no significant difference between IFN-treated patients and untreated patients with respect to the number of hypermutated genomes observed (data not shown). These results suggest that the host's antiviral immunity level was higher at baseline than it was after



**Figure 1.** Clinical courses for 4 patients (A–D) with chronic hepatitis B virus (HBV) infection who experienced exacerbation of infection. *Black arrows*, exacerbation associated with an increase in the number of hypermutated genomes (>5 times basal levels); *white arrows*, exacerbation not associated with an increase in the number of hypermutated genomes; *horizontal dotted lines*, upper normal limit of alanine aminotransferase (ALT) (40 IU/mL; A–D) and the detection limit for antibody against e antigen (HBeAb) (35%; lower panel, A–D). HBeAb, antibody against HBV e antigen; HBeAg, HBV e antigen; IFN, interferon.



**Figure 2.** Relationship between increase in the number of hypermutated genomes and plasma levels of hepatitis B virus (HBV) DNA in 17 patients with chronic HBV infection who experienced  $>2$  increases of  $>100$  IU/L in alanine aminotransferase (ALT) level. Patients' exacerbations were divided into 2 groups, A and B, according to the extent of increase in the number of hypermutated genomes, relative to the basal number (group A included 9 exacerbations that involved a  $>5$ -fold increase in the number of hypermutated genomes; group B included 12 exacerbations that involved a  $\leq 5$ -fold increase in the number of hypermutated genomes). *Upper panel* for groups A and B, individual HBV DNA levels at the time the ALT level increased and 2 months later; in the upper panel for group A, *dashed lines* indicate 4 exacerbations associated with seroconversion to positivity for antibody against e antigen. *Lower panel* for groups A and B, box-and-whisker plots for HBV DNA levels at same 2 time points. In the plots, the lines in the boxes indicate median values; the upper and lower lines of the boxes indicate the 25th and 75th percentiles, respectively; and the upper and lower whiskers represent the 90th and 10th percentiles, respectively.

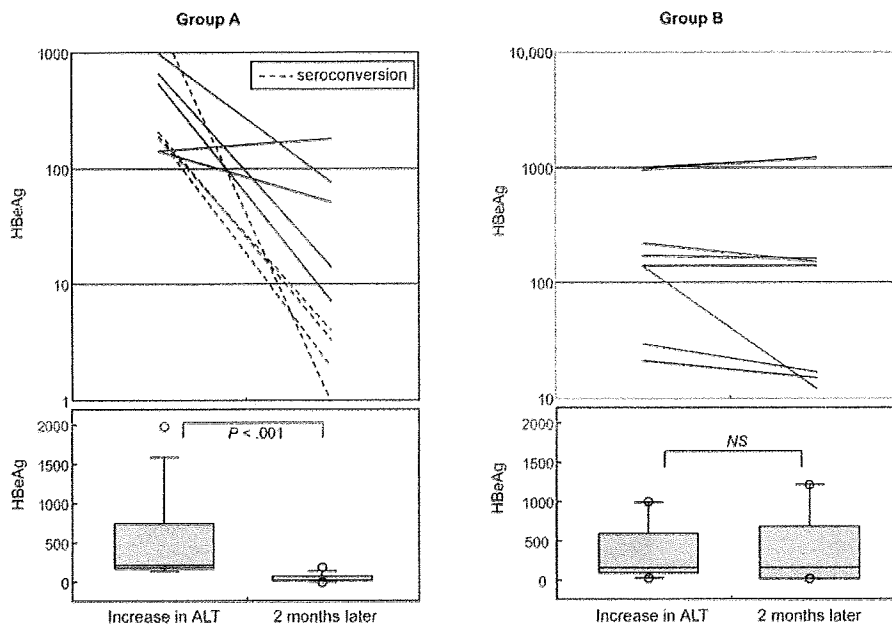
IFN or that the feedback system for IFN signaling was already active before initiation of therapy.

We also compared the degree of reduction in the plasma HBV DNA level for exacerbations (i.e., increases in ALT level) associated with a marked increase in the number of hypermutated genomes (i.e., those in which the peak number was  $>5$  times the number observed prior to exacerbation) and for exacerbations not associated with such an increase. As shown in figure 2, 8 of 9 exacerbations that were coupled with a marked increase in the number of hypermutated genomes (group A) were associated with a  $>2$ -log reduction in the HBV DNA level. In contrast, only 1 of the 12 exacerbations not associated with a marked increase in the number of hypermutated genomes (group B) was associated with a  $>2$ -log reduction in plasma HBV DNA level. The median serum HBV DNA level decreased from 8.8 to 5.0 log copies/mL among the patients in group A ( $P < .001$ ) but did not decrease for patients in group B (figure 2).

In addition, we compared the reduction in e antigen level for these 2 groups. Levels were reduced in both groups, but the median reduction was more prominent for patients in group A than for those in group B (figure 3). All 4 exacerbations coupled with e antigen seroconversion (from positive to negative) were associated with marked increase in hypermutated genomes (figure 3).

**Effect of IFN treatment on the rate of HBV hypermutation in chimeric mice.** Next, we examined the effect of IFN treatment on G-to-A hypermutation in HBV genomes in human hepatocyte-chimeric mice. Two mice were intravenously injected with supernatant produced by HepG2 cells transiently transfected with a plasmid containing 1.4-genome length wild-type HBV genomes. Ten weeks later, after confirmation of high-level HBV viremia, the mice were treated with 7000 IU/g/day of IFN- $\alpha$ , injected intramuscularly, for 14 days. We observed an  $\sim 1.5$ -log reduction in plasma HBV DNA level accompanied by an increase in the number of hypermutated genomes in both mice (figure 4A). In a mouse inoculated with HBV but treated with phosphate-buffered saline, no increase of hypermutated genomes was observed (figure 4B). We also observed a 36-fold increase in the level of APOBEC3G mRNA, as determined by human oligonucleotide microarray (data not shown).

**Infectivity of hypermutated genomes.** To study the biological significance of hypermutated genomes, culture supernatant from HepG2 cells transfected with both HBV and APOBEC3G (5  $\mu$ g each) was injected into a chimeric mouse. As shown in figure 5, the culture supernatant contained a large number of hypermutated genomes. In contrast, we could not detect hypermutated genomes in the chimeric mouse inoculated with this



**Figure 3.** Relationship between increase in the number of hypermutated genomes and hepatitis B virus (HBV) e antigen (HBeAg) levels in 15 HBeAg-positive patients with chronic HBV infection who experienced  $>2$  increases of  $>100$  IU/L in alanine aminotransferase (ALT) level. Patients' exacerbations were divided into 2 groups, A and B, according to the extent of increase in the number of hypermutated genomes, relative to the basal number (group A included 9 exacerbations that involved a  $>5$ -fold increase in the number of hypermutated genomes; group B included 8 exacerbations that involved a  $\leq 5$ -fold increase in the number of hypermutated genomes). *Upper panel* for groups A and B, individual e antigen levels at the time the ALT level increased and 2 months later; in the upper panel for group A, *dashed lines* indicate 4 exacerbations associated with seroconversion to positivity for antibody against e antigen. *Lower panel* for groups A and B, box-and-whisker plots for e antigen levels at these same 2 time points. In the plots, the lines in the boxes indicate median values; the upper and lower lines of the boxes indicate the 25th and 75th percentiles, respectively; and the upper and lower whiskers represent the 90th and 10th percentiles, respectively.

supernatant (figure 5A and 5B). These results suggest that the infectivity (or replication ability) of HBV with hypermutated genomes is very poor. It is possible that the inoculum contained less abundantly mutated genomes. To test this, we cloned and sequenced 72 clones of 217-bp DNA fragments amplified at a denaturation temperature of 95°C. Of 72 clones obtained from the inoculum, we found 1 clone with 8 G-to-A substitutions, 1 clone with 5 substitutions, 2 clones with 3 substitutions, and 1 clone with 1 substitution (figure 5C). In contrast, 1 of the 72 clones obtained from the mouse serum had 1 G-to-A substitution. If G-to-A substitutions were excluded, the only other nucleotide substitution observed in the 144 clones sequenced was a single C-to-T substitution.

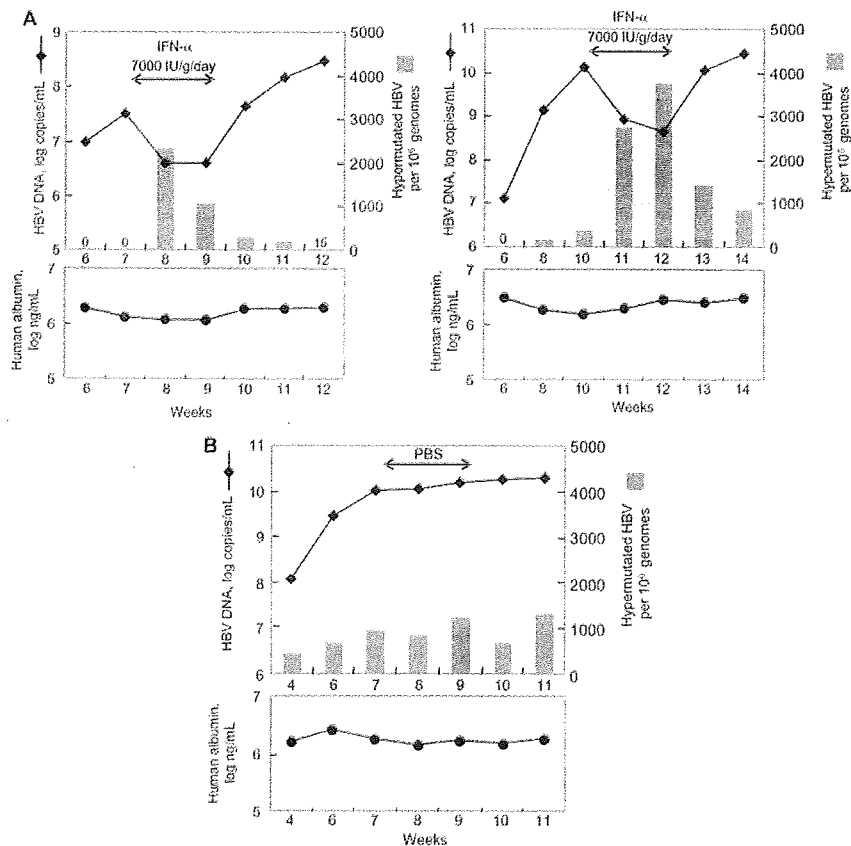
## DISCUSSION

In a previous study, we found that the majority of serum samples obtained from HBV-infected patients contained a small number of hypermutated genomes [27]. Recently, we developed a method (TaqMan 3D-PCR) to measure small numbers of hypermutated genomes [28]. Using this method, we reported dual antiviral effects for APOBEC3G, namely induction of hypermutation and reduction of viral replication. We also reported that

IFN increased the transcription of APOBEC3G and enhanced the effect of the protein in vitro [28]. Other investigators also showed that IFN enhances the action of APOBEC proteins against HIV [18–21]. It is thus assumed that the antiviral effect of APOBEC proteins should be enhanced by IFN and other cytokines in vivo.

In the present study, we showed that an increase in ALT level accompanied by an increase in the number of hypermutated genomes was associated with reduction in the plasma HBV DNA level. In contrast, no decrease in HBV DNA level was observed if the increase in ALT level occurred in the absence of an increase in the number of hypermutated genomes. It is difficult to know which of the dual antiviral effects of APOBEC3G (or other APOBEC proteins) reduced the viral level. It is also impossible to estimate the importance of APOBEC proteins in this reduction. However, it is clear that the increase in the number of hypermutated genomes of HBV correlates with activation of the host antiviral defense against HBV.

We also demonstrated that exacerbations of HBV infection associated with a marked increase in the number of hypermutated genomes were associated not only with a decrease in the plasma HBV DNA level but also with clearance of e antigen.



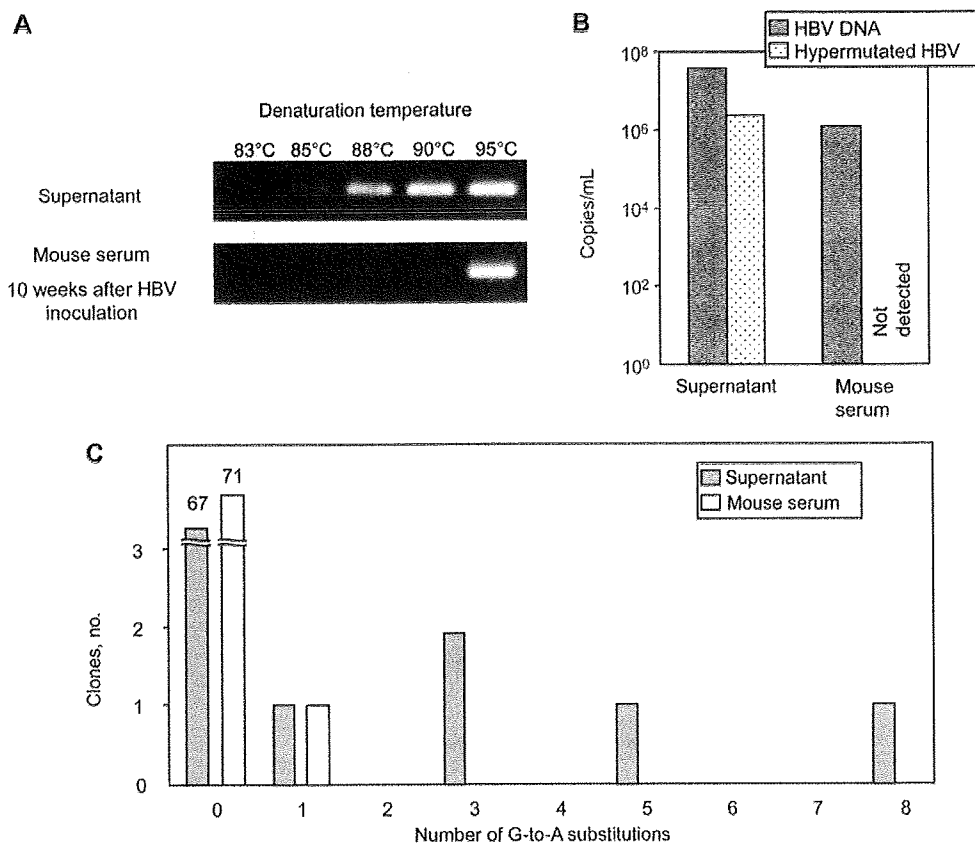
**Figure 4.** Effect of interferon (IFN)- $\alpha$  therapy on hepatitis B virus (HBV) hypermutation in HBV-infected, human hepatocyte–chimeric mice. Two chimeric mice (A) were inoculated with recombinant wild-type HBV produced by transfected HepG2 cells; 10 weeks later, after confirmation of high-level HBV viremia, they were treated with IFN- $\alpha$  at 7000 IU/g/day for 14 days, by intramuscular injection. Upper panels in both parts of A, serum HBV DNA levels and the number of hypermutated genomes; lower panels in both parts of A, human serum albumin concentrations. Note that the albumin levels are stable during IFN- $\alpha$  therapy. A control mouse (B) was inoculated with recombinant wild-type HBV produced by transfected HepG2 cells and treated with phosphate-buffered saline (PBS). Upper and lower panels of B show the same information as in A.

Furthermore, all exacerbations followed by seroconversion to positivity for antibody against e antigen were associated with a marked increase in the number of hypermutated genomes. Clearance of e antigen often results from a G-to-A nucleotide substitution at the first position of a 5'-GGGG stretch in the pre-core coding sequence (the G1896A mutation). Because this substitution (changing TGGGG to TAGGG) is in agreement with the dinucleotide pattern preferentially edited by APOBEC3G, one might assume that G-to-A substitution in this region could be caused by this enzyme and is related to the clearance of e antigen. However, we observed that hypermutation was induced in only some genomes, whereas the majority of genomes were unaffected. Thus, it seems unlikely that APOBEC proteins play a role in seroconversion to positivity for antibody against e antigen, although it is still possible that the 5'-GGGG stretch in the precore region is the preferred editing site for the enzyme. Importantly, such substitution of the 5'-GGGG stretch should result in the occurrence of multiple stop codons (TAG, TGA, and TAA) in HBV genomes, as we observed and reported in our

previous study [28], which makes the replication of mutated genomes impossible.

In the present study, we did not observe any increase in the number of hypermutated genomes during IFN therapy in some patients. This finding is discrepant from the results of previous in vitro experiments that showed increased numbers of hypermutated genomes after the application of IFN [28]. Interestingly, our experimental results also showed the induction of APOBEC3G gene expression, an increase in the number of hypermutated genomes, and a reduction of plasma HBV DNA level in 2 human hepatocyte–chimeric mice treated with IFN (figure 4). What is the reason for the lack of increase in hypermutation in some IFN-treated patients? We usually administer IFN to patients who have high ALT levels. The patients in this study had abnormal ALT levels prior to treatment with IFN—that is, their livers were inflamed, and the levels of many cytokines produced by the immune cells in the liver were already high. We presume that the effect of these elevated cytokine levels masked the effect of the IFN we administered. It could also be argued that the effect





**Figure 5.** Results for a human hepatocyte–chimeric mouse inoculated with hepatitis B virus (HBV) produced by HepG2 cells transfected with an equal amount (5  $\mu$ g each) of HBV and apolipoprotein B messenger RNA editing enzyme, catalytic polypeptide–like 3G plasmids. The inoculum contained ~6.25% hypermutated genomes. A serum sample was obtained 10 weeks after the inoculation. *A*, HBV DNA was amplified by polymerase chain reaction (PCR) that used different denaturation temperatures and run on 2% agarose gel. *B*, Quantitative measurement of HBV DNA and hypermutated DNA in the inoculum and mouse serum. *C*, Number of G-to-A substitutions found in each of 72 clones obtained from products of PCR of culture supernatant or mouse serum.

observed in mice represents the absence of the immune response in mice, whereas the lack of a clear response to IFN in the study patients was the result of the complex immune response in human beings. Alternatively, the concentrations of IFN in treated patients might be lower than those used for the cell culture or the chimeric mice. Although we did not perform this analysis in the present study, it would be interesting to determine the expression levels of APOBEC proteins and IFN-stimulated genes in the liver of IFN-treated patients.

The present study showed that the number of hypermutated genomes increased during some increases in ALT level, probably as a result of IFN-activated APOBEC proteins and other cytokines in patients with chronic hepatitis B. However, the number of hypermutated genomes was very small, only 28,378 in 10<sup>6</sup> HBV genomes at most (figure 1A). Because it was possible that the less abundantly hypermutated genomes were not detected (i.e., that genomes with only 1 or 2 G-to-A substitutions were not amplified by 3D-PCR), cloning and sequencing were performed to detect such genomes. However, the number of ge-

nomes containing G-to-A substitutions was still low (5 [6.9%] of 72 clones), even in the culture medium of HepG2 cells cotransfected with APOBEC3G and HBV (figure 5C). This means that the number of genomes with only a small number of G-to-A substitution was not high, suggesting that only selected DNA molecules were heavily mutated while the remaining DNA was not. Does this mean that the effect of APOBEC proteins in antiviral defense is trivial in patients with chronic HBV infection? It is a possible that the heavily deaminated genomes are an easy target for uracil DNA glycosylase. Although the dual antiviral effects of APOBEC proteins are currently known to reduce the amount of HBV, the importance and magnitude of APOBEC proteins with respect to in vivo virus reduction should be investigated further.

Treatment of patients with chronic HBV infection has improved with the advent of new nucleoside and nucleotide analogues. However, reactivation of HBV and flare-ups of hepatitis are often seen in patients who stop such therapy. Furthermore, hepatitis B surface antigen clearance is rare in patients treated

with these antiviral drugs. On the other hand, most patients with chronic HBV infection achieve sufficient viral suppression and disease quiescence through immunological suppression of the virus. As we showed in this study, the immunological suppression of HBV is much stronger than that achieved with IFN therapy, but it is often transient. It is thus necessary to clarify the mechanism of transient immune response and to develop treatment that produces persistent suppression of HBV. Quantitative measurement of hypermutated genomes should be useful in monitoring the immune response in this context.

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## Deletion of angiotensin II type I receptor reduces hepatic steatosis<sup>☆</sup>

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**Background/Aims:** A distinct subgroup of angiotensin II type 1 receptor (AT1R) blockers (ARBs) have been reported to suppress the development of hepatic steatosis. These effects were generally explained by selective peroxisome proliferator-activated receptor (PPAR)  $\gamma$  modulating properties of ARBs, independent of their AT1R blocking actions. Here, we provide genetic evidence of the direct role for AT1R in hepatic steatosis.

**Methods:** The effect of AT1R deletion on steatohepatitis was investigated in *AT1a*<sup>-/-</sup> mice. Furthermore, the influence of AT1R inhibition by telmisartan as well as gene silencing of AT1R by siRNA was assessed in an *in vitro* experiment using HepG2 cells.

**Results:** Compared to wild-type (WT), *AT1a*<sup>-/-</sup> mice fed methionine–choline deficient (MCD) diet resulted in negligible lipid accumulation in the liver with marked induction of PPAR $\alpha$  mRNA. *In vitro* experiments also demonstrated reduced cellular lipid accumulation by telmisartan and AT1R knockdown following exposure of long chain fatty acids. This is presumably explained by the observation that the expression of PPAR $\alpha$  and its target genes were significantly up-regulated in specific siRNA treated HepG2 cells.

**Conclusions:** Our data indicate, in addition to pharmacological effect of ARBs on PPAR $\gamma$  activation, a key biological role for AT1R in the regulation of hepatic lipid metabolism.

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**Keywords:** Lipid metabolism; Renin-angiotensin system; Non-alcoholic fatty liver disease; Non-alcoholic steatohepatitis; Peroxisome proliferator-activated receptor  $\alpha$

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**Abbreviations:** AT1R, angiotensin II type 1 receptor; ARB, angiotensin II type 1 receptor blocker; PPAR, peroxisome proliferator-activated receptor; Ang, angiotensin; WT, wild-type; MCD, methionine–choline deficient; TBARS, thiobarbituric acid-reactive substances; TG, triglyceride; NAFLD, nonalcoholic fatty liver disease; NASH, nonalcoholic steatohepatitis; HSC, hepatic stellate cell; siRNA, small interfering RNA; DMSO, dimethyl sulfoxide; FFA, free fatty acid; PBS, phosphate buffered saline; AST, aspartate aminotransferase; ALT, alanine aminotransferase; ApoB, apolipoprotein B; ACSL, acyl-CoA synthetase; VLDL, very low density lipoprotein.

### 1. Introduction

Non-alcoholic fatty liver disease (NAFLD) encompasses a wide spectrum of liver pathology – from simple steatosis alone, through necroinflammatory disorder referred to as non-alcoholic steatohepatitis (NASH), to cirrhosis and liver cancer. Because of the high prevalence and the potential mortality, NAFLD/NASH has emerged as a serious public concern and therefore therapeutic strategies need to be established. Recent animal studies and clinical trials have demonstrated several pharmacological treatments as potential therapeutic targets, which include insulin sensitizers (e.g., thiazolidinediones, metformin), lipid lowering agents (e.g., statins, fibrates), antioxidants, angiotensin (Ang) II type I receptor (AT1R) blockers (ARBs), etc. [1–7]. Among

these therapeutic options, ARBs are initially expected to suppress the development of hepatic fibrosis in NASH. Hepatic stellate cell (HSC), which is a major fibrogenic cell type in the liver and also contributes to hepatic inflammation through induction of cytokines, expresses AT1R, and blockade of Ang II signaling markedly attenuates hepatic inflammation and fibrosis in experimental models of chronic liver fibrosis [8,9]. A clinical report has also demonstrated that losartan, an ARB, improved hepatic necroinflammation and fibrosis in NASH patients [10].

In addition to anti-fibrotic/inflammatory effect, emerging data have suggested that ARBs improve glucose and lipid metabolism. In a large clinical trial, losartan substantially lowered the risk for type 2 diabetes compared with other antihypertensive therapies [11]. An animal study using obese Zucker rats has also demonstrated that high dose of irbesartan improved insulin sensitivity [12]. More recently, it has been shown that telmisartan, unlike other ARBs improved the development of hepatic steatosis in animal models [7,13,14]. These metabolic effects of ARBs might be explained in part by the *in vitro* study, in which a distinct subtype of ARBs induced transcriptional activities of peroxisome proliferator-activated receptor (PPAR)  $\gamma$ , independent of their AT1R blocking actions [15,16]. However, it is noteworthy that PPAR $\gamma$ -activating potency by ARBs appears rather modest as determined by transcription reporter assays, with median effective concentration (EC<sub>50</sub>) of telmisartan, the most potent PPAR $\gamma$  activator among ARBs, 5.02  $\mu\text{mol/L}$  compared to 0.2  $\mu\text{mol/L}$  of pioglitazone, a full agonist of PPAR $\gamma$  [15,16]. Interestingly, treatment with olmesartan, which has no impact on PPAR $\gamma$  activation, has been proved to attenuate the development of hepatic steatosis, suggesting the possibility that the blockade of AT1R itself might contribute to hepatic lipid homeostasis [17]. To further investigate the direct role for AT1R in hepatic steatosis, we applied two different approaches: (1) animal model of steatohepatitis using mice lacking AT1aR (*AT1a*<sup>-/-</sup>), which is the only Ang II receptor subtype expressed in rodent liver, and (2) *in vitro* cellular steatosis model in which gene silencing by RNA interference targeting AT1R was performed [18]. Our data demonstrated reduced lipid accumulation in the absence of AT1R with significant induction of PPAR $\alpha$ . Apart from PPAR $\gamma$  modulating action of ARBs, these data support the potential efficacy of AT1R blockade in the treatment of NAFLD/NASH.

## 2. Materials and methods

### 2.1. Animal

*AT1a*<sup>-/-</sup> mice were provided by Mitsubishi Tanabe Pharma (Osaka, Japan) and C57BL/6 mice were obtained from Charles River Laboratories (Yokohama, Japan) [19]. Both strains of the mice have

the same genetic background. The mice were housed in a standard 12 h light/dark cycle facility, and fed either standard chow diet or methionine–choline deficient (MCD) diet (Oriental Yeast Co., Tokyo, Japan) for 8 weeks with free access to drinking water. Male mice at 6–8 weeks of age were used in this study, and all animal procedures were performed according to the guidelines of Institute of Laboratory Animal Science, Hiroshima University.

### 2.2. Histological examination

Liver samples were fixed in 4% formaldehyde solution, embedded in paraffin, and cut into 5  $\mu\text{m}$ -thick sections. Staining for hematoxylin and eosin (H-E) or Azan-Mallory was carried out with standard techniques.

### 2.3. Analytical techniques

Serum triglyceride (TG) concentration was determined enzymatically using a Triglyceride E-test (Wako Chemicals, Osaka, Japan). To quantify hepatic TG content, hepatic lipid was extracted as previously described by Bligh and Dyer and subjected to the same procedure as serum assay followed by the standardization of protein concentrations [20]. Hepatic thiobarbituric acid-reactive substances (TBARS) levels were quantified using an OXI-TEK TBARS Assay Kit (Zepromatrix Corporation, New York) with protein standardization. Serum TBARS levels were assayed using the same kit.  $\beta$ -Hydroxybutyrate was assayed using an assay kit (BioVision, Mountain View, CA). The activities of serum transaminases were determined enzymatically.

### 2.4. Cell culture and gene silencing by small interfering RNA (siRNA)

HepG2 cells (human hepatoma cell line) were cultured in Dulbecco's modified Eagle's medium supplemented with 10% (v/v) fetal bovine serum. For gene silencing, two different sequences of small interfering RNA (siRNA) targeting human AT1R were purchased from Sigma–Aldrich (siRNA ID: SASI\_Hs01\_00206672, SASI\_Hs02\_00206672). Cells were transfected using Lipofectamine RNAiMAX (Invitrogen) in 6-well plates containing  $2.5 \times 10^5$  cells in each well with 10 nM of siRNA duplex. siPerfect Negative Controls (Sigma–Aldrich) was utilized as a negative control siRNA. In the preliminary experiment, siRNA duplex of SASI\_Hs02\_00206672 effectively knocked down AT1R expression compared to SASI\_Hs01\_00206672, and this was used for the following experiments. After 24 and 48 h of transfection, cells were subjected to gene quantification by real-time PCR and *in vitro* steatosis experiment, respectively.

### 2.5. *In vitro* model of cellular steatosis

Palmitic acid (C16:0) and oleic acid (C18:1) (Sigma, St. Louis, MO) were dissolved in isopropanol to obtain 20 or 40 mM stock mixture solution (2:1 oleate: palmitate), and the concentration of vehicle was 1% in final incubations [21]. Telmisartan (provided by Boehringer Ingelheim, Germany) was resolved in dimethyl sulfoxide (DMSO) to obtain 10 mM stock solution. To investigate the effect of telmisartan on cellular steatosis, cells were exposed to 200 or 400  $\mu\text{M}$  of free fatty acids (FFAs) mixture with or without 2 h preincubation of 10  $\mu\text{M}$  telmisartan. To assess the influence of AT1R knockdown on cellular steatosis, cells were treated with FFAs after 48 h of siRNA transfection. Following 24 h of incubation with FFAs, cells were subjected to determination of cellular lipid content by Nile Red assay and  $\beta$ -hydroxybutyrate levels in the media.

### 2.6. Nile Red assay

The lipid content in cultured cells was quantified fluorometrically using Nile Red, a vital lipophilic dye as previously described [22].

Briefly, cell monolayers were washed twice with phosphate buffered saline (PBS) followed by fixation with 4% formaldehyde solution for 15 min, and washed with PBS twice again. Cells were stained for 30 min with Nile Red solution at a final concentration of 200 µg/ml in PBS. Monolayers were washed thereafter with PBS and measured fluorometrically (excitation; 488 nm. emission; 550 nm) [23].

### 2.7. Quantitative real-time PCR

Total RNA was isolated using RNeasy Mini Kit (Qiagen, Germany). cDNA was synthesized from 1 µg of total RNA with GeneAmp Gold RNA PCR Core Kit (Applied Biosystems, Foster City, CA). To quantify AT1R mRNA expression in human heart and kidney, PCR Ready First Strand cDNA (BioChain, Hayward, CA) was utilized. Specific primers except AT1R from PrimerBank, a public resource for PCR primers (<http://pga.mgh.harvard.edu/primerbank/>, ID: 14043066) were designed using Primer3 (<http://frodo.wi.mit.edu>) with nucleotide sequences from GenBank™ as listed in Table 1. Real-time PCR was carried out with Lightcycler 1.5 system using Lightcycler FastStart DNA Master plus SYBR Green I (Roche Applied Science). The relative expression levels were calculated with the formula  $2^{-\Delta C_t}$ , where  $\Delta C_t$  is the difference in threshold cycle ( $C_t$ ) values between target gene and ribosomal protein S18 as a control.

### 2.8. Western blot analysis for AT1R

Fifty microgram of protein prepared from HepG2 cells using RIPA buffer supplemented with protease inhibitors (Roche Diagnostics), as well as Total Protein-Human Adult Normal Tissues (Biochain, Hayward, CA) were fractionated by SDS-PAGE and subjected to Western blot analysis using rabbit polyclonal antibodies against human AT1R (N-10) (Santa Cruz Biotechnology, Santa Cruz, CA). The blots were visualized by enhanced chemiluminescence.

### 2.9. Statistical analysis

The data are expressed as the means ± SE. The statistical analysis was performed using Student's *t* test, and differences were considered statistically significant for a two-tailed  $p < 0.05$ .

## 3. Results

### 3.1. Mice lacking AT1R are resistant to steatohepatitis

MCD diet has been reported to cause steatohepatitis which represents most of histological features of human NASH [24,25]. As shown in Fig. 1A, histological analy-

sis of the livers demonstrated that MCD diet for 8 weeks resulted in apparent steatosis with inflammatory cell infiltration mainly in portal area in wild-type (WT) mice. However, in contrast to WT mice, *AT1a*<sup>-/-</sup> mice displayed no significant changes in the liver (Fig. 1A, right panel). Azan-Mallory staining of the liver from WT mice revealed mild pericellular fibrosis, which was absent in *AT1a*<sup>-/-</sup> mice (Fig. 1A, lower panels). In accordance with these histological observations, hepatic TG content increased by 3-fold in WT and remained no significant 1.5-fold increase in *AT1a*<sup>-/-</sup> mice following 8 weeks of MCD diet (Fig. 1B, left panel). Serum TG level following MCD diet was reduced in both genetic groups with more drastic change in WT mice (Fig. 1B, right panel). The substantial changes in hepatic TG content suggested the possibility that the expression of PPAR $\alpha$ , a central player in hepatic lipid metabolism, might be influenced by AT1aR expression. This was assessed by quantitative real-time PCR. While MCD diet did not affect hepatic PPAR $\alpha$  expression in both genetic strains, absence of AT1aR was associated with significant 3-fold increase in PPAR $\alpha$  mRNA in chow diet-fed mice (Fig. 1C). Since PPAR $\alpha$  mediates hepatic expression of genes regulating lipid oxidation, we next assessed serum level of  $\beta$ -hydroxybutyrate, an end product of hepatic fatty acid oxidation. Fig. 1D demonstrates 3-fold increase in serum  $\beta$ -hydroxybutyrate in *AT1a*<sup>-/-</sup> mice compared to WT mice following MCD diet. This might be a potential explanation for reduced hepatic lipid accumulation in *AT1a*<sup>-/-</sup> mice.

### 3.2. Lack of AT1R ameliorates liver injury

As shown in Fig. 2, there were no differences in aspartate aminotransferase (AST) and alanine aminotransferase (ALT) levels between WT and *AT1a*<sup>-/-</sup> mice when fed chow diet. MCD diet caused significant increase in AST and ALT levels in WT mice, whereas there was no significant increase of these liver enzymes in *AT1a*<sup>-/-</sup> mice.

**Table 1**  
Primer used for quantitative real-time PCR.

Gene	Forward	Reverse	GenBank Accession No.
mPPAR $\alpha$	tgcaactggacttgaacg	tgatgtcacagaacggcttc	BC016892
AT1	atccaagatgattgtccaaagc	gcccatagtgcgaagctagtaa	
PPAR $\alpha$	cagtggagcattgaacatcg	gttgtgtgacatcccagacag	NM_001001928
ApoB100	agccttgctgaagaaaacca	atgccctcttgatgttcag	M14162
ACSL1	ccagaaggccttcaagactg	gccttctctggcctgtcaac	NM_001995
RPS18	atagccttggccatcactgc	ggacctggctgtattttcca	NM_022551
PPAR $\gamma$	atacaagtggagcctgcatc	acccttgcatccttcacaag	NM_138711
PPAR $\beta$ ( $\delta$ )	ctatccgtttggcggatg	cgatgtcgtggatcacaaaag	NM_006238

mPPAR $\alpha$ , mouse peroxisome proliferator-activated receptor  $\alpha$ ; AT1, angiotensin II type I receptor; PPAR, human PPAR; ApoB100, apolipoprotein B-100; ACSL1, acyl-CoA synthetase long-chain family member 1; RPS18, ribosomal protein S18.

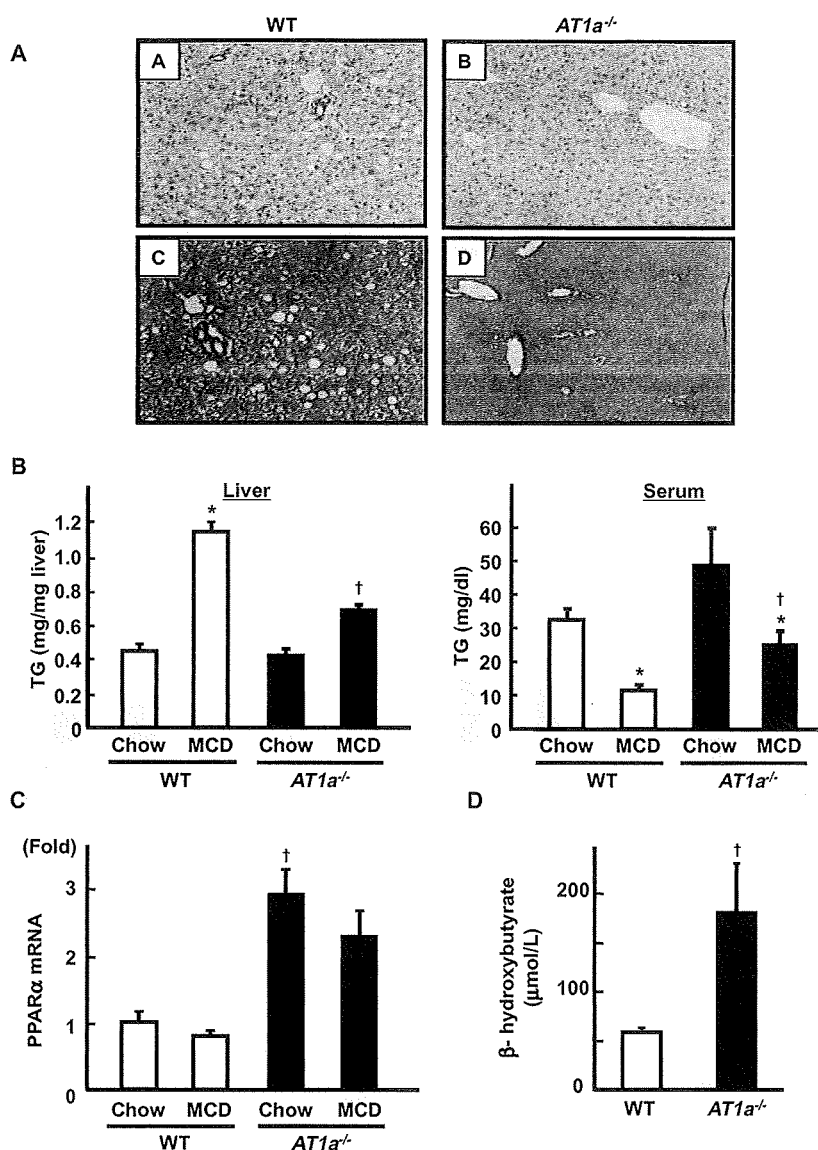


Fig. 1. The absence of AT1aR expression attenuates the development of MCD diet-induced hepatic steatosis in mice. (A) Liver sections from MCD diet-fed WT (A and C) and *AT1a*<sup>-/-</sup> mice (B and D) were processed for haematoxylin & eosin (HE) (upper panels) or Azan-Mallory staining (lower panels). Hepatic steatosis as well as fibrosis are evident only in WT mice (original magnification 100×). (B) TG concentrations in liver (left panel) and serum (right panel) obtained from WT (open bars) and *AT1a*<sup>-/-</sup> (closed bars) mice (*n* = 6/each group) were determined after feeding either normal chow or MCD diet. (C) Hepatic PPARα mRNA expression was quantified (*n* = 5/each group) by quantitative real-time PCR. (D) The serum level of β-hydroxybutyrate in WT (*n* = 5) and *AT1a*<sup>-/-</sup> (*n* = 6) mice fed MCD diet was determined. \**p* < 0.05, chow-fed vs. MCD diet-fed mice. †*p* < 0.05, WT vs. *AT1a*<sup>-/-</sup> mice. [This figure appears in colour on the web.]

### 3.3. Influence of AT1R expression on oxidative stress

Since lipid peroxidation product plays an important role as a “2nd hit” in the pathogenesis of NASH, we next examined serum and hepatic levels of TBARS [26]. Fig. 3 demonstrates marked increase in TBARS levels in serum and liver of WT mice following MCD diet. In contrast, *AT1a*<sup>-/-</sup> mice showed no significant changes in TBARS levels, which presumably reflected

the reduction of liver injury as demonstrated in AST and ALT levels.

### 3.4. Expression of AT1R in the liver and HepG2 cells

To further explore the protective effect of AT1R blockade in hepatic steatosis observed in animal model, we performed *in vitro* studies using HepG2 cells. We first ascertained AT1R expression in HepG2 cells comparing

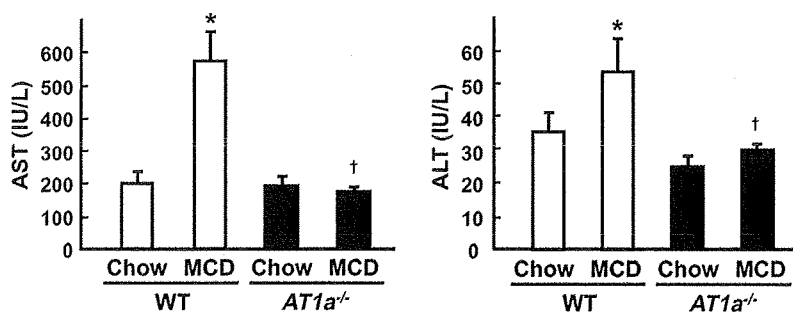


Fig. 2. Diminished hepatic injury following 8 weeks of MCD diet in the absence of AT1aR. AST and ALT levels were determined in WT (open bars) and *AT1a*<sup>-/-</sup> (closed bars) mice fed either normal chow or MCD diet for 8 weeks ( $n = 6$ /each group). \* $p < 0.05$ , chow-fed vs. MCD diet-fed mice. † $p < 0.05$ , WT vs. *AT1a*<sup>-/-</sup> mice.

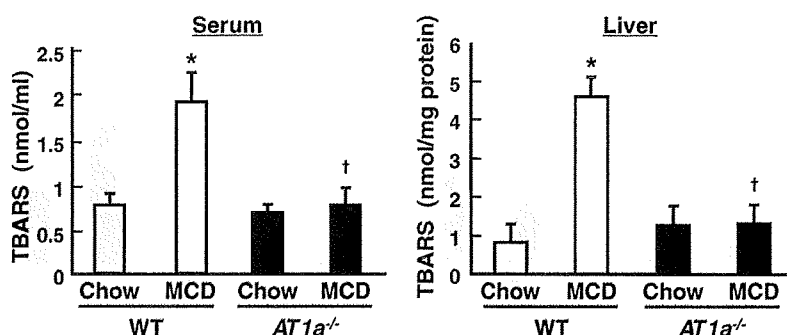


Fig. 3. Influence of AT1aR expression on TBARS levels in serum and liver. TBARS levels were assayed in serum (left panel) and liver (right panel) from WT (open bars) and *AT1a*<sup>-/-</sup> (closed bars) mice after feeding either normal chow or MCD diet ( $n = 6$ /each group). \* $p < 0.05$ , chow-fed vs. MCD diet-fed mice. † $p < 0.05$ , WT vs. *AT1a*<sup>-/-</sup> mice.

that of heart, kidney, and liver tissues, which are known to express functional AT1R. As displayed in Fig. 4, Western blot analysis revealed AT1R protein expression in HepG2 cells, supporting the previous *in vivo* binding assay of Ang II that detected a homogeneous signal pattern throughout the liver parenchyma [27]. Although the quantities of loaded protein were the same among samples, the band intensity in HepG2 appeared to be weaker compared to whole liver homogenate, which comprises non-parenchymal liver cells such as hepatic stellate cells and Kupffer cells. However, real-time PCR demon-

strated similar level of AT1R in HepG2 as compared to kidney (Fig. 4, right panel).

### 3.5. AT1R blockade reduces lipid accumulation in hepatocellular *in vitro* model

To examine whether AT1R expression in HepG2 was functional, we utilized *in vitro* model of steatosis in which HepG2 cells were treated with FFAs mixture with or without 10  $\mu$ M of telmisartan. As shown in Fig. 5A, Nile Red assay quantified 4- to 5-fold increase in cellular

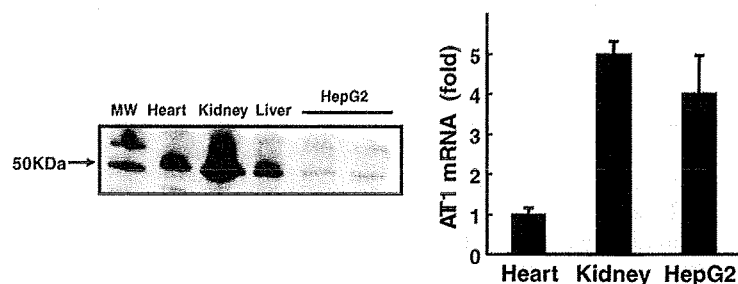


Fig. 4. Expressions of AT1R in the liver and HepG2 cells. Western blots of AT1R protein expression in homogenates from human liver and HepG2 cells by comparison with heart and kidney as positive tissues for AT1R expression (50 KDa) (left panel). Quantitative real-time PCR analysis for AT1R in HepG2 (right panel). Results represent from at least three independent experiments.

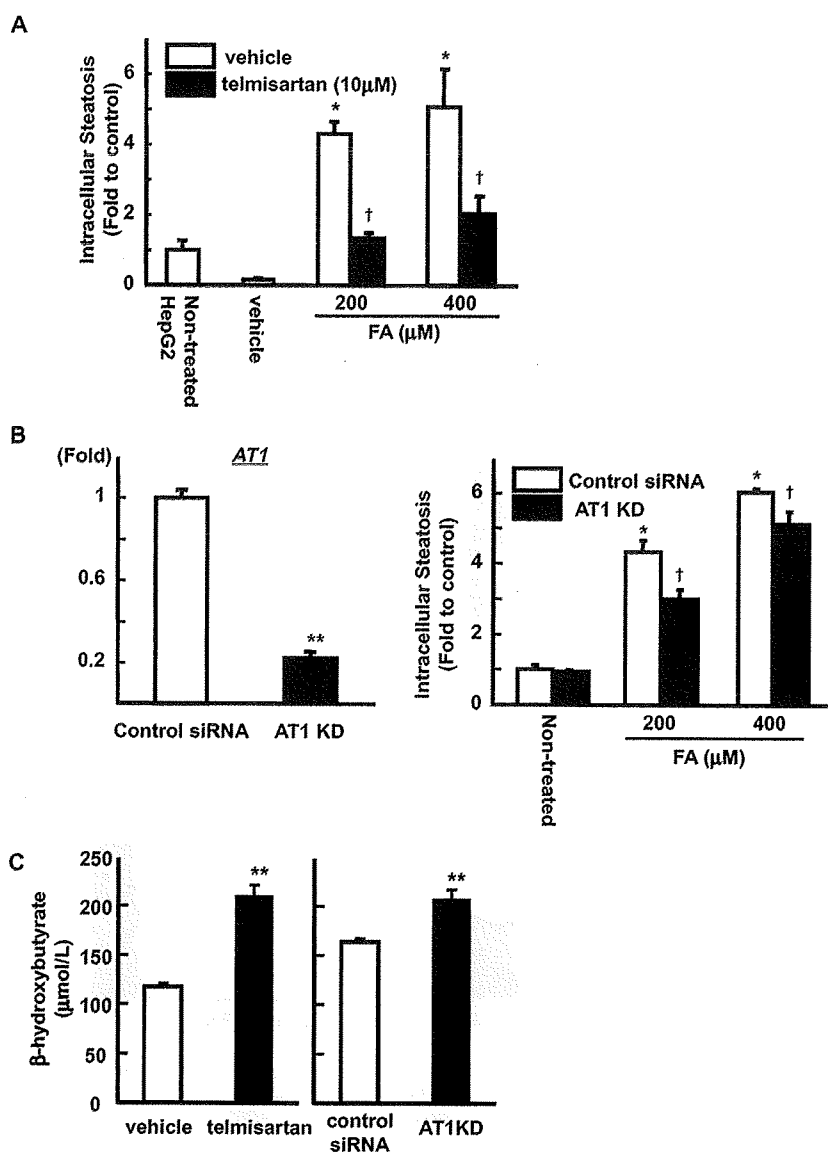


Fig. 5. AT1R blockade attenuates cellular steatosis following fatty acids overload. (A) Influence of telmisartan on intracellular steatosis induced by free fatty acids (FFAs) overload (2:1 oleate: palmitate) ( $n = 6$ /each group). (B) Effect of siRNA targeting AT1R on *AT1* mRNA expression (left panel) and influence of AT1 knockdown (KD) on cellular steatosis induced by FFAs overload (2:1 oleate: palmitate, right panel) ( $n = 6$ /each group). (C) Influence of AT1R blockade on  $\beta$ -hydroxybutyrate levels in media ( $n = 6$ /each group). \*\* $p < 0.005$ , vs. control siRNA. \* $p < 0.05$ , vs. non-treated groups. † $p < 0.05$ , AT1R blockade (either by telmisartan or AT1 knockdown) vs. control (either vehicle or control siRNA) HepG2.

lipid accumulation when cells were treated with FFAs for 24 h in the absence of telmisartan. These changes were markedly attenuated by the presence of telmisartan by 60–70%. To exclude the possibility that these anti-steatotic effects might be attributable to pharmacological property of telmisartan, we investigated the influence of AT1R knockdown using siRNA in the same experimental model. As shown in Fig. 5B, transfection of HepG2 cells with siRNA targeting AT1R successfully depleted its mRNA expression by 80% when compared

to control siRNA. This siRNA knockdown of AT1R resulted in significant 15–30% decrease in cellular lipid deposition following FFAs exposure (Fig. 5B, right panel). Compared to the treatment of telmisartan, the influence of AT1R knockdown appeared modest. This might be because siRNA suppression of AT1R was not sufficient to elicit complete inhibition of the AT1R signaling pathway. In connection with the observed ketogenesis in *AT1a*<sup>-/-</sup> mice, we examined  $\beta$ -hydroxybutyrate levels in the culture media. Under the condition



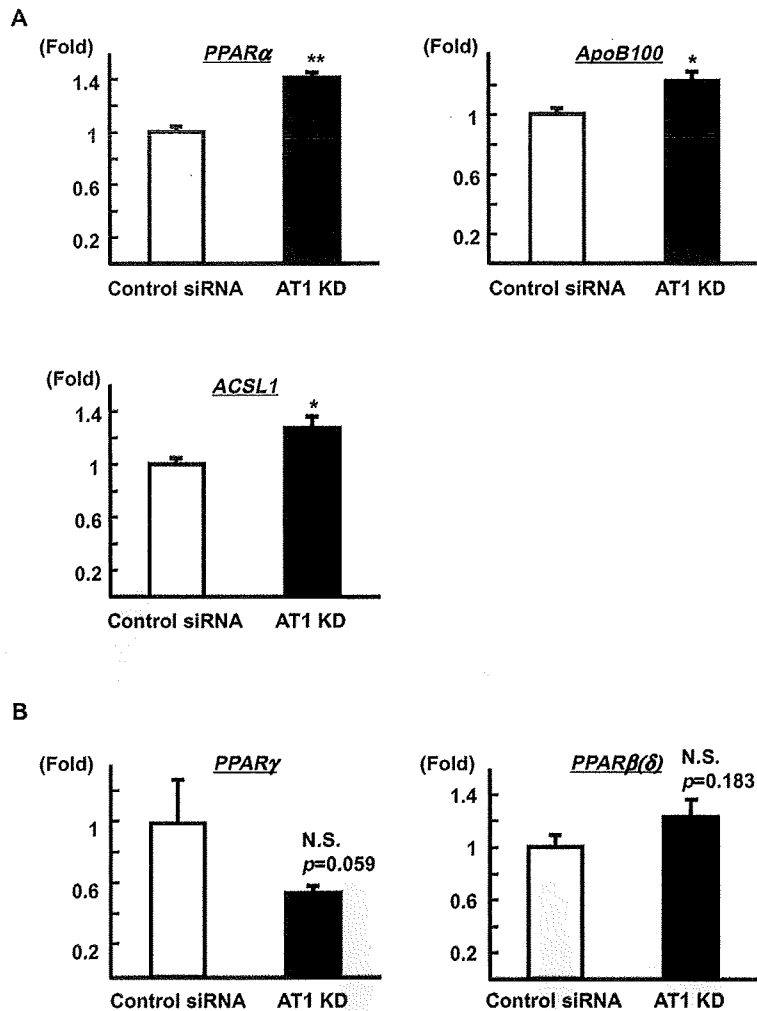


Fig. 6. Influence of AT1R knockdown on the expression of PPAR $\alpha$  target genes (A) and the other PPAR isoforms (B). Real-time PCR quantified the expression of genes regulated by PPAR $\alpha$  as well as of the other PPAR isoforms, PPAR $\gamma$  and PPAR $\beta(\delta)$  in HepG2 cells transfected with either siRNA targeting AT1R ( $n = 6$ ) or negative control siRNA ( $n = 6$ ). \* $p < 0.05$ , vs. control siRNA. \*\* $p < 0.005$ , vs. control siRNA. NS, not statistically significant.

of 200  $\mu$ M of FFAs overload, the treatment of telmisartan as well as AT1R knockdown significantly increased  $\beta$ -hydroxybutyrate levels (Fig. 5C).

### 3.6. AT1R knockdown induces PPAR $\alpha$ and its target genes

The observation that hepatic PPAR $\alpha$  expression was up-regulated in *AT1a*<sup>-/-</sup> mice suggests the possible link between AT1R signaling and PPAR $\alpha$  expression. In this setting, our working hypothesis was that AT1R down-regulation might in turn influence the hepatocellular expressions of PPAR $\alpha$  and its target genes. As shown in Fig. 6A, transient AT1R silencing by siRNA resulted in significant up-regulation of PPAR $\alpha$  by 41%. In addition, PPAR $\alpha$  target genes, acyl-CoA synthetase 1 (*ACSL1*) and apolipoprotein B (*ApoB*) 100 were also

induced by 27% and 21%, respectively. These data exclude the possibility that PPAR $\alpha$  up-regulation in *AT1a*<sup>-/-</sup> mice might be resulted from chronic adaptation to the absence of AT1R. To exclude the possible contribution of the other PPAR isoforms in hepatocellular steatosis, the expression of PPAR $\gamma$  and PPAR $\beta(\delta)$  were assessed by real-time PCR, which resulted in no significant changes following AT1R depletion (Fig. 6B).

## 4. Discussion

The present study indicates a major role for AT1R in hepatic steatosis by providing a precise genetic approach. Homozygous disruption of AT1R in mice resulted in marked reduction of hepatic lipid accumulation as determined morphologically and by hepatic TG

content. Recent studies have demonstrated that ARBs improve insulin resistance and hyperinsulinemia. Because the improvement of insulin resistance leads to reduction of FFAs flux to the liver together with increased uptake and storage of FFAs in adipose tissue, ARBs are expected to reduce hepatic steatosis. However, the effect of ARBs on hepatic steatosis is still controversial [7,14,17,28–30]. These conflicting findings might be explained by differences in selective PPAR $\gamma$  modulating properties of ARBs [15,16], or attributed to differences in the dose and length of ARBs supplementation as well as potential differences in the mechanisms of steatosis in the different experimental models. Our data reinforces the theory that blockade of AT1R, unrelated to pharmacological properties of ARBs, ameliorates the development of hepatic steatosis.

The pathophysiology of NASH remains poorly understood, but is often described as “two-hit process” consisting of hepatic TG accumulation (the 1st step) and development of oxidative stress and proinflammatory cytokines (the 2nd step), which leads to hepatocyte injury, inflammation, and fibrosis [26]. Previous reports have demonstrated that pharmacological blockade or gene deletion of renin-angiotensin system (RAS) significantly attenuates hepatic fibrosis in experimental animal models [31,32]. Moreover, Ang II, the effector peptide for AT1R, has been reported to stimulate an array of fibrogenic actions in activated HSCs through the mediation of reactive oxygen species [33]. More recent data has revealed that angiotensin converting enzyme (ACE) deficient (*ACE*<sup>-/-</sup>) mice which exhibit reduced levels of Ang II by 70% in plasma and by 85–97% in tissues [34] showed pronounced increase in hepatic gene expression related to lipolysis and fatty acid oxidation, suggesting close link between RAS and hepatic lipid metabolism [35]. Taken together with our finding of the anti-steatotic effect, the blockade of AT1R appears to contribute to wide range of steps and phases in the pathogenesis of NASH.

The up-regulation of PPAR $\alpha$  in the liver of *AT1a*<sup>-/-</sup> mice is intriguing because PPAR $\alpha$  plays a central role in hepatic lipid homeostasis. It is well known that many of the genes encoding enzymes involved in the mitochondrial and peroxisomal fatty acid  $\beta$ -oxidation pathways are regulated by PPAR $\alpha$ . To exclude the possibility that adaptation to persistent AT1R absence may induce PPAR $\alpha$  expression in mice, we performed *in vitro* siRNA experiments, which confirmed induction of PPAR $\alpha$  and its target genes by transient AT1R knockdown. In support of these observations, previous experiments have demonstrated telmisartan-mediated induction of PPAR $\alpha$  [36]. Whereas induction of PPAR $\alpha$  was observed in *AT1a*<sup>-/-</sup> mice, the present study lacks the direct evidence that suppressive effect of AT1R blockade on hepatic steatosis is mediated by PPAR $\alpha$ . In this connection, we examined  $\beta$ -hydroxybutyrate levels since it is

documented that PPAR $\alpha$  activation leads to stimulation of ketogenesis [37,38]. This yielded marked increase in serum  $\beta$ -hydroxybutyrate in *AT1a*<sup>-/-</sup> mice. In addition, our *in vitro* experiments demonstrated significant increase in  $\beta$ -hydroxybutyrate in the culture media in response to AT1R blockade. These findings support the detected changes in gene expressions of PPAR $\alpha$  and ACSL1 following AT1R deletion. Although it remains controversial whether the blockade of AT1R directly stimulates PPAR $\alpha$ , up-regulation of PPAR $\alpha$  likely increases the sensitivity to agonist and thus clinical usage of ARBs together with PPAR $\alpha$  ligand such as fibrates might have synergistic effects on hepatic lipid metabolism.

A potential limitation of the present study is the use of MCD dietary animal model. Although this model develops steatohepatitis morphologically similar to human NASH with an increase in oxidative stress and has been widely used for the study of NASH, absence of insulin resistance has been reported [24,25,39,40]. Since insulin resistance is considered to be pivotal in the development of NASH, this model might not entirely reflect the natural course and the etiological background of human NASH [41,42]. Some other potential dietary models include *ad libitum* feeding of the high fat diet, which develops obesity and insulin resistance but not noticeable steatohepatitis [43]. Additionally, intragastric overfeeding of high fat diet induces NASH pathology, but some of the biological changes observed in the liver did not mimic human NASH [44]. Altogether, the study of pathophysiological process of NASH is limited by the lack of suitable experimental animal models [45]. Interestingly, the effect of olmesartan has been investigated in a genetically diabetic rat fed MCD diet [30]. In contrast to our findings, olmesartan reduced hepatic steatosis only in diabetic but not in control rats. In the present study, MCD diet caused increase in hepatic TG content associated with decrease in serum TG level, suggesting that impaired TG secretion from liver might contribute to hepatic steatosis. These changes were blunted in the absence of AT1R, implying improvement of TG secretion in *AT1a*<sup>-/-</sup> mice. This might be in part explained by the observation of *in vitro* experiment that AT1 knockdown induced ApoB which is requisite for the formation of very low density lipoprotein (VLDL).

In the present study, human hepatoma cell line HepG2 instead of rodent primary hepatocytes was utilized for *in vitro* model of cellular steatosis. This was based on the previous report that human primary hepatocytes and HepG2 cells reached similar levels of intracellular lipid accumulation close to that determined in hepatocytes from human steatosis liver [23]. In addition, the observed up-regulation of hepatic PPAR $\alpha$  in *AT1a*<sup>-/-</sup> mice led to the speculation that PPAR $\alpha$  might play a role in the anti-steatotic effect of AT1 blockade.

Because hepatic expression of PPAR $\alpha$  and the sensitivity to it notably differ among species [46], human-derived cell line was applied.

In conclusion, mice lacking AT1R are resistant to the development of hepatic steatosis with up-regulation of PPAR $\alpha$  in MCD diet-induced steatohepatitis model. Accordingly, the levels of TBARS, a marker of oxidative stress, as well as aminotransferases, indicators of liver damage were significantly attenuated in *AT1a*<sup>-/-</sup> mice. In addition, an *in vitro* experiment of hepatocellular steatosis revealed that blockade of AT1R by telmisartan and specific siRNA knockdown markedly decreased cellular lipid accumulation. Up-regulation of PPAR $\alpha$  was also confirmed by transient AT1R knockdown. These data provide strong evidence that, in addition to pharmacological effect of ARBs on PPAR $\gamma$  activation, AT1R signaling is involved in hepatic lipid metabolism.

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