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なし

肝炎ウイルス感染の肝外病変の基礎的及び臨床的包括研究
分担研究報告書

HCV陽性者における末梢血Bリンパ球のclonality解析

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研究要旨

HCV陽性者とコントロール群において、末梢血中に clonal（単一な、つまり腫瘍性の）な B リンパ球が存在する頻度をフローサイトメトリー（FCM）を用いて解析し、その細胞の特性について検討した。結果、clonal な B リンパ球のみられる症例は HCV 陽性者に有意に多く存在することが示され、HCV がリンパ球を clonal に（腫瘍性に）増殖させる作用があることが示唆された。Clonal に増殖する B リンパ球の CD5 発現は均一ではなく、これらの細胞はクローン内の多様性（intraclonal diversity）をもつ細胞集団であると考えられる。

A. 研究目的

HCV 陽性者における末梢血 B リンパ球の clonality（単一性、つまり腫瘍性）をフローサイトメトリー（FCM）を用いて解析する。さらに、clonal な増殖を示す B 細胞の性状について精査することにより、HCV とリンパ増殖性疾患との関連について検討する。

B. 研究方法

HCV(+)患者 240 例（インターフェロン治療、化学療法、免疫療法を施行中、また、リンパ系腫瘍、血液疾患を有する患者は除く）とコントロール（HCV(-)肝疾患患者）150 例の末梢血リンパ球を CD19、 κ 、 λ の 3 種の抗体を用いて染色し、B リンパ球の κ 、 λ の発現比率を解析し、clonality の有無を検討した。clonality 陽性例では、CD5、CD20 染色を追加し、免疫グロブリン重鎖遺伝子の再構成（IgH rearrangement）と Bcl-2/IgH(t(14;18))転座の有無に関して

PCR 法を用いて検討した。

【検査内容、方法】

- ① 静脈採血（ヘパリン採血約 5cc）を行い、適量を取り、洗浄して血漿を十分に除去する。CD19（B リンパ球特異的マーカー）、 κ 、 λ の 3 種類の抗体を用いて染色した後、溶血剤により赤血球を除去する。十分に洗浄した後 FCM を施行する。リンパ球領域を gating し、CD19 陽性集団内での κ 鎖、 λ 鎖の比率（ κ/λ 比）を算定する。 κ/λ 比 3 以上、1/2 以下を clonality 陽性とする。
- ② Clonality 陽性例に関しては、CD19、CD5、CD20 の 3 種類の抗体を用いて上記と同様の方法で染色する。FCM でリンパ球領域を gating し、CD19 陽性集団内での CD5、CD20 の発現を評価する。
- ③ 免疫グロブリン重鎖遺伝子の再構成に関しては、末梢血より単核球分離後、

DNA 採取を行い、primer を用いて semi-nested PCR を行い判定する。

- ④ Bcl-2/IgH (t(14;18))キメラ遺伝子に関しては、末梢血より単核球分離後、DNA 採取を行い、PCR を施行し、その有無を判定する。Bcl-2 には major breakpoint region (MBR) と minor cluster region (mcr) があり、それぞれに対して primer を作成し、PCR を行う。

(倫理面への配慮)

本研究は当大学の倫理委員会における承認を得ており、また、末梢血の提供者である患者には研究の意図を十分に説明し、文書で同意を得たうえで研究に参加していただいた。また、検体提供者の個人情報は確実に保護され、検体は上記検査目的のみに使用された。

C. 研究結果

HCV(+)患者 240 例中 7 例に clonal な B リンパ球の増殖がみられたのに対し、コントロール (HCV(-)肝疾患患者) 150 例ではみられず、有意差あり ($p < 0.05$) の結果であった。7 例全てに IgH の monoclonal rearrangement が確認され、Bcl-2/IgH(t(14;18))転座は 7 例中 1 例で陽性であった。Clonal に増殖した B リンパ球の CD5 発現強度は均一ではなく、正常の B リンパ球と比較して有意差は認めなかった。7 例中 2 例がインターフェロン治療を受けたが、2 例ともに clonal な B リンパ球の消失がみられた。

D. 考察

本研究では、clonal な B リンパ球の増殖がコントロール患者と比較して HCV(+)患者の末梢血において有意に多くみられることが示された。この事実は、HCV がリンパ球を clonal に (腫瘍性に) 増殖させる作用があることを示唆する。さらに、HCV の消失と出現が clonal な B リンパ球の消失と再燃に並行する事実は、HCV とリンパ増殖性疾患との関係を強く示唆するものである。海外の論文では PCR 法を用いて HCV(+)患者の末梢血に clonal な B リンパ球が存在することは示されているが、その集団が B リンパ球集団全体の中でどの程度を占めているかは検討されていない。われわれはフローサイトメトリー (FCM) を用いて同内容を検討した。結果、B リンパ球数は正常範囲を維持しつつ、その中で clonal な腫瘍性 B リンパ球が大多数を占めていることが示された。

また HCV 感染に伴う CD5 陽性 B リンパ球の増減に関しては以前よりいくつかの報告があるが、見解は一致していない。そこで本研究では、HCV 陽性者において clonal に増殖することが確認された B リンパ球の CD5 発現に関して、正常リンパ球と比較しつつ検討した。結果、HCV 関連の clonal な B リンパ球は正常 B リンパ球と同様、個々の細胞によりその CD5 発現強度が異なり、また、CD5 陽性細胞の占める割合も正常 B リンパ球と比較して有意差はないという事実が示された。これは、末梢血で増殖する HCV 関連 clonal B リンパ球細胞は、'慢性リンパ性白血病細胞' (末梢血で clonal に増殖する、CD5 陽性細胞のみから構成される均一な細胞) とは異なる phenotype の細胞であることを示している。同じ clonal

なB細胞であっても分化段階において細胞表面形質 (immunophenotype) が変化するという報告がある。本研究においてHCV関連 clonal Bリンパ球細胞のCD5発現が均一でない点を考えると、これらの clonal なBリンパ球集団は分化段階の異なる種々の細胞の集合体である可能性が考えられる。

これらのHCV関連 clonal Bリンパ球細胞が将来、悪性リンパ腫、クリオグロブリン血症などのリンパ増殖性疾患へと進展していくか否かに関して、今後の経時的観察が必要と考えられる。

E. 結論

HCV(+)患者では末梢血Bリンパ球の clonal な(腫瘍性の)増殖がみられる症例が有意に多く存在する。そのCD5発現は均一ではなく、HCVにより増殖するBリンパ球はクローン内の多様性 (intraclonal diversity)をもつ細胞集団であると考えられる。これらの細胞集団がリンパ増殖性疾患へと進展していくか否かについて今後の経時的研究が必要である。

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PPAR α activation is essential for HCV core protein–induced hepatic steatosis and hepatocellular carcinoma in mice

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Transgenic mice expressing HCV core protein develop hepatic steatosis and hepatocellular carcinoma (HCC), but the mechanism underlying this process remains unclear. Because PPAR α is a central regulator of triglyceride homeostasis and mediates hepatocarcinogenesis in rodents, we determined whether PPAR α contributes to HCV core protein–induced diseases. We generated PPAR α -homozygous, -heterozygous, and -null mice with liver-specific transgenic expression of the core protein gene (*Ppara*^{+/+}:HCVcpTg, *Ppara*^{+/-}:HCVcpTg, and *Ppara*^{-/-}:HCVcpTg mice). Severe steatosis was unexpectedly observed only in *Ppara*^{+/-}:HCVcpTg mice, which resulted from enhanced fatty acid uptake and decreased mitochondrial β -oxidation due to breakdown of mitochondrial outer membranes. Interestingly, HCC developed in approximately 35% of 24-month-old *Ppara*^{+/-}:HCVcpTg mice, but tumors were not observed in the other genotypes. These phenomena were found to be closely associated with sustained PPAR α activation. In *Ppara*^{+/-}:HCVcpTg mice, PPAR α activation and the related changes did not occur despite the presence of a functional *Ppara* allele. However, long-term treatment of these mice with clofibrate, a PPAR α activator, induced HCC with mitochondrial abnormalities and hepatic steatosis. Thus, our results indicate that persistent activation of PPAR α is essential for the pathogenesis of hepatic steatosis and HCC induced by HCV infection.

Introduction

HCV is one of the major causes of chronic hepatitis, whereas patients with persistent HCV infection have a high incidence of hepatocellular carcinoma (HCC) (1, 2). Occurrence of HCC associated with chronic HCV infection has increased over the past 2 decades (3–5), and chronic HCV infection is recognized as a serious debilitating disease. However, the mechanism in which chronic HCV infection mediates hepatocarcinogenesis remains unclear.

HCV core protein was shown to have oncogenic potential (6). To examine how HCV core protein participates in HCV-related hepatocarcinogenesis, transgenic mouse lines were established in which HCV core protein is expressed constitutively in liver at cellular levels similar to those found in chronic HCV-infected patients (7). These mice exhibited hepatic steatosis (7) and insulin resistance (8) as early as 3 months of age; on further aging, these symptoms worsened and hepatic adenomas developed in approximately 30% of mice between 16 and 18 months of age (9). Finally, HCC was found within hepatic adenomas in a classic “nodule-in-nodule” pathology (9). Interestingly, no hepatic inflammation or fibrosis was found in these mice throughout

the course of HCC development (9), which suggested that the HCV core protein itself induces hepatic steatosis and HCC independently of hepatitis.

Several studies support the contention that hepatic steatosis promotes the development of HCC (10). Epidemiologic data have identified hepatic steatosis as a major accelerating factor of hepatocarcinogenesis in chronic HCV-infected patients (11). Moreover, increases in ROS production that can cause oxidative DNA damage, mitochondrial abnormalities, and accelerated hepatocyte proliferation were observed in the steatotic livers (12–14). Thus, an intriguing possibility has emerged that alteration of fatty acid metabolism in hepatocytes may be central to the pathogenesis of HCC induced by HCV core protein.

PPARs are ligand-activated nuclear receptors belonging to the steroid/thyroid hormone receptor superfamily; 3 isoforms designated as α , β/δ , and γ exist, all of which are involved in lipid homeostasis (15). PPAR α regulates constitutive transcription of genes encoding fatty acid–metabolizing enzymes (16) and is associated with the maintenance of fatty acid transport and metabolism, primarily in liver, kidney, and heart. Administration of PPAR α agonists, such as the widely prescribed fibrate drugs clofibrate, gemfibrozil, and fenofibrate, ameliorate hyperlipidemia in humans (17) and hepatic steatosis in mice (18).

On the other hand, long-term administration of PPAR α ligands to rodents causes accelerated hepatocyte proliferation, increased ROS generation, and development of HCC (19, 20). Disruption of the PPAR α gene was shown to prevent the development of HCC caused by long-term exposure to PPAR α activators (21). Interestingly, accumulation of fatty acids/triglycerides in hepatocytes

Nonstandard abbreviations used: ACC, acetyl-CoA carboxylase; AOX, acyl-CoA oxidase; CDK, cyclin-dependent kinase; CYP4A1, cytochrome P450 4A1; FAS, fatty acid synthase; FAT, fatty acid translocase; FATP, fatty acid transport protein; HCC, hepatocellular carcinoma; HCVcpTg, HCV core protein–expressing transgenic; L-FABP, liver fatty acid-binding protein; MCAD, medium-chain acyl-CoA dehydrogenase; MTP, microsomal transfer protein; 8-OHdG, 8-hydroxy-2'-deoxyguanosine; PCNA, proliferating cell nuclear antigen; RXR α , retinoid X receptor α .

Conflict of interest: The authors have declared that no conflict of interest exists.

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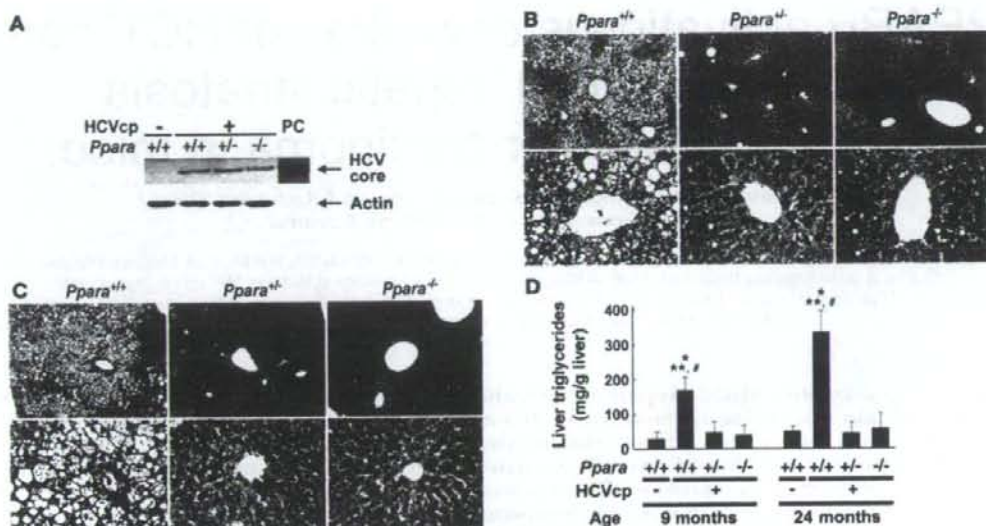


Figure 1

Phenotype changes in transgenic mouse liver. (A) Immunoblot analysis of HCV core protein expression in livers of 9-month-old mice. Because no significant individual differences in the same mouse group were found in the preliminary experiments, 10 mg of liver prepared from each mouse ($n = 6$ /group) was mixed and homogenized. Whole-liver lysate (50 μ g protein) was loaded in each well. The band of actin was used as the loading control. Results are representative of 4 independent experiments. PC, lysate prepared from COS-1 cells overexpressing HCV core protein as a positive control. (B) Histological appearance of hematoxylin- and eosin-stained liver sections from 9-month-old HCVcpTg mice. Upper and lower rows show a lower ($\times 40$) and higher ($\times 400$) magnification, respectively. Microvesicular and macrovesicular steatosis was found only in $Ppara^{+/-}$:HCVcpTg mice. No inflammation or hepatocyte degeneration was evident in any of the genotypes. (C) Histological appearance of hematoxylin- and eosin-stained liver sections from 24-month-old HCVcpTg mice. Upper and lower rows show a lower ($\times 40$) and higher ($\times 400$) magnification, respectively. Hepatic steatosis was marked in $Ppara^{+/-}$:HCVcpTg mice, but not in other mice. Hepatic inflammation, fibrosis, and hepatocyte degeneration were not observed. In $Ppara^{+/-}$:HCVcpTg and $Ppara^{+/-}$:HCVcpTg mice, dysplastic hepatocytes and precancerous lesions were not detected throughout the entire liver. (D) Content of liver triglycerides. Results are expressed as the mean \pm SD ($n = 6$ /group) and compared between genotypes at the same age. * $P < 0.05$ compared with $Ppara^{+/+}$ nontransgenic mice; ** $P < 0.05$ compared with $Ppara^{+/-}$:HCVcpTg mice; # $P < 0.05$ compared with $Ppara^{+/-}$:HCVcpTg mice.

could lead to continuous PPAR α activation because of the presence of fatty acid metabolites that serve as natural PPAR α ligands. For example, mice lacking expression of the peroxisomal acyl-CoA oxidase (AOX) gene showed massive accumulation of very-long-chain fatty acids in hepatocytes, severe microvesicular steatosis, chronic PPAR α activation, and development of hepatic adenoma and HCC by 15 months of age (22). These results suggest a strong contribution of activated PPAR α to liver tumorigenesis.

On the basis of several lines of evidence, we hypothesized that PPAR α might contribute to hepatocarcinogenesis in HCV core protein-expressing transgenic (HCVcpTg) mice. To explore this possibility, PPAR α -homozygous ($Ppara^{+/+}$), PPAR α -heterozygous ($Ppara^{+/-}$), and PPAR α -null ($Ppara^{-/-}$) mice bearing the HCV core protein gene, designated $Ppara^{+/+}$:HCVcpTg, $Ppara^{+/-}$:HCVcpTg, and $Ppara^{-/-}$:HCVcpTg mice, were generated, and phenotypic changes were examined. Surprisingly, we found that severe hepatic steatosis and HCC induced by HCV core protein developed only in $Ppara^{+/-}$ mice, which were related to persistent PPAR α activation.

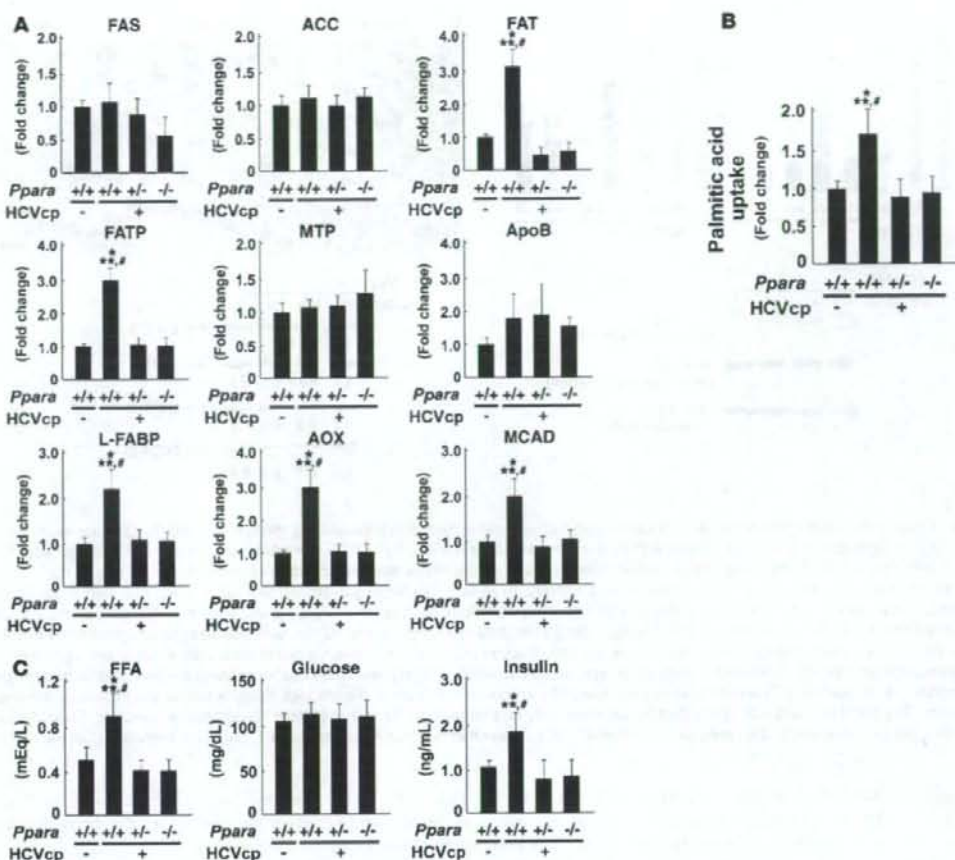
Results

Expression of HCV core protein in transgenic mice. $Ppara^{+/-}$:HCVcpTg and $Ppara^{+/-}$:HCVcpTg mice appeared healthy, and body weight in both genotypes was similar to that of $Ppara^{+/+}$:HCVcpTg and $Ppara^{+/+}$ mice

without the transgene. When hepatic expression of HCV core protein in 9-month-old transgenic mice was examined by immunoblot analysis, it was similar among $Ppara^{+/+}$:HCVcpTg, $Ppara^{+/-}$:HCVcpTg, and $Ppara^{-/-}$:HCVcpTg mice (Figure 1A) and was also similar to expression in HCVcpTg mice reported previously (7, 9). Age and sex had only a minor influence on the hepatic expression of HCV core protein.

Requirement of homozygous PPAR α for the development of hepatic steatosis in transgenic mice. Livers of 9-month-old male HCVcpTg mice with or without the $Ppara$ allele were examined. Those of $Ppara^{+/-}$:HCVcpTg mice were soft, slightly enlarged, and light in color and histologically showed macrovesicular and microvesicular steatosis with no apparent inflammation or hepatocyte necrosis (Figure 1B), in agreement with previous reports (7, 9). Biochemical analysis of liver extracts showed marked hepatic accumulation of triglycerides (Figure 1D). In contrast, livers of 9-month-old $Ppara^{+/+}$:HCVcpTg and $Ppara^{-/-}$:HCVcpTg mice showed neither histological abnormalities nor accumulation of triglycerides (Figure 1, B and D). Hepatic levels of free fatty acids in $Ppara^{+/-}$:HCVcpTg mice were approximately 3 times those in $Ppara^{+/+}$:HCVcpTg and $Ppara^{-/-}$:HCVcpTg mice or $Ppara^{+/+}$ mice not expressing the HCV core protein.

In 24-month-old $Ppara^{+/-}$:HCVcpTg mice, hepatic steatosis was found (Figure 1C), and the hepatic levels of triglycerides were further increased (Figure 1D). Apparent inflammation, hepatocyte

**Figure 2**

Analyses of factors associated with hepatic fatty acid and triglyceride metabolism. (A) Expression of genes associated with fatty acid and triglyceride metabolism in 9-month-old mouse livers. Total RNA was extracted from each mouse liver, and mRNA levels were determined by RT-PCR. mRNA levels were normalized by those of GAPDH and subsequently normalized by those in *Ppara*^{+/+} nontransgenic mice. Results are expressed as the mean \pm SD ($n = 6$ /group). * $P < 0.05$ compared with *Ppara*^{+/+} nontransgenic mice; ** $P < 0.05$ compared with *Ppara*^{+/-}:HCVcpTg mice; # $P < 0.05$ compared with *Ppara*^{-/-}:HCVcpTg mice. (B) Uptake of fatty acids in 9-month-old mouse livers. Liver slices obtained from 3 mice in each group were incubated in medium containing 0.8 mM [¹⁻¹⁴C]palmitic acid for 7 h. Fatty acid uptake ability was estimated by the sum of palmitic acid converted to CO₂ and ketone bodies with that incorporated into total cellular lipids after incubation. The experiment was repeated 3 times. Results were normalized by those of *Ppara*^{+/+} nontransgenic mice and expressed as the mean \pm SD. (C) Plasma concentrations of free fatty acids, glucose, and insulin. After an overnight fast, blood was obtained from each mouse and the above variables were determined. Results are expressed as the mean \pm SD ($n = 6$ /group).

degeneration and necrosis, and fibrosis were not detected. On the other hand, *Ppara*^{-/-}:HCVcpTg and *Ppara*^{+/-}:HCVcpTg mice showed no steatosis (Figure 1, C and D). These results indicate that hepatic steatosis develops in *Ppara*^{+/-}:HCVcpTg mice, but not in *Ppara*^{-/-}:HCVcpTg and *Ppara*^{+/-}:HCVcpTg mice.

Hepatic fatty acid and triglyceride metabolism in transgenic mice. To investigate the mechanism responsible for the development of severe steatosis in *Ppara*^{+/-}:HCVcpTg mice, the expression of genes associated with fatty acid and triglyceride metabolism in the livers of 9-month-old mice was analyzed using the quantitative RT-PCR method. As shown in Figure 2A, the mRNA levels of genes related

to de novo lipogenesis (fatty acid synthase [FAS] and acetyl-CoA carboxylase [ACC]) and secretion of VLDL (microsomal transfer protein [MTP] and apoB) were constant in all groups. The mRNA levels of fatty acid translocase (FAT) and fatty acid transport protein (FATP), which are associated with the uptake of fatty acids into hepatocytes, were significantly increased only in *Ppara*^{+/-}:HCVcpTg mice, but the mRNA levels of hepatic triglyceride lipase, another contributor to fatty acid uptake, remained unchanged (data not shown). The mRNA levels of liver fatty acid binding protein (L-FABP) were also elevated only in *Ppara*^{+/-}:HCVcpTg mice. Surprisingly, the mRNA levels of AOX and medium-chain acyl-CoA

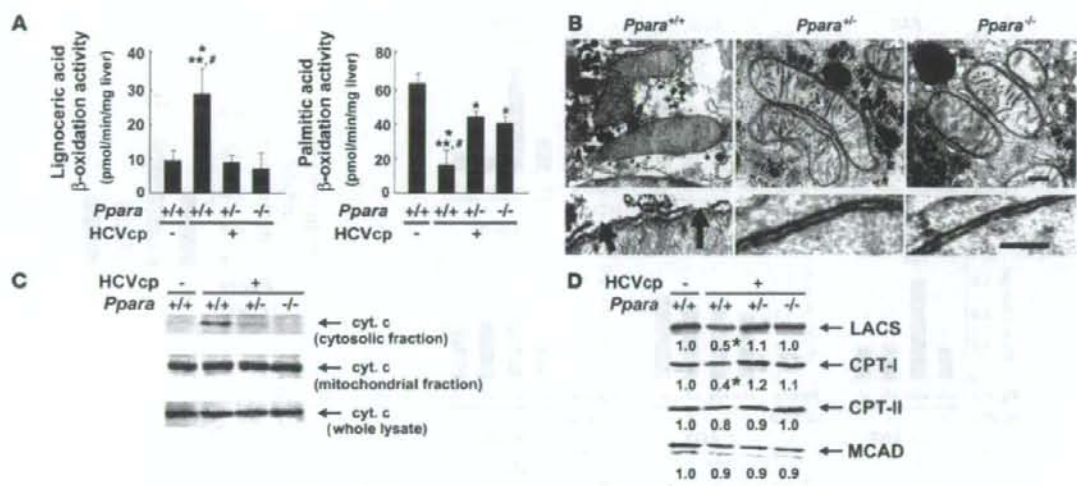


Figure 3 Analyses of mitochondrial abnormalities. (A) Lignoceric and palmitic acid β -oxidation activities in 9-month-old mice. Results are expressed as the mean \pm SD ($n = 6$ /group). * $P < 0.05$ compared with *Ppara*^{+/+} nontransgenic mice; ** $P < 0.05$ compared with *Ppara*^{-/-}:HCVcpTg mice; # $P < 0.05$ compared with *Ppara*^{+/-}:HCVcpTg mice. (B) Electron microscopic features of hepatic mitochondria of 9-month-old HCVcpTg mice. Upper and lower rows show a lower and higher magnification, respectively. In *Ppara*^{+/+}:HCVcpTg mice, some mitochondria showing discontinuance of outer membranes (arrows) and amorphous inner structures were observed. In *Ppara*^{-/-}:HCVcpTg and *Ppara*^{+/-}:HCVcpTg mice, mitochondria appeared normal; the scale bars represent 200 nm (top) and 30 nm (bottom), respectively. (C) Immunoblot analysis of cytochrome *c* in 9-month-old mice. Whole-liver lysate, mitochondrial fraction, or cytosolic fraction (50 μ g protein) was loaded in each well. Results are representative of 4 independent experiments. (D) Immunoblot analysis of representative mitochondrial β -oxidation enzymes using a mitochondrial fraction prepared from 9-month-old mouse livers. The mitochondrial fraction (20 μ g protein) was loaded in each well. Results are representative of 4 independent experiments. The band intensity was quantified densitometrically and normalized by that in *Ppara*^{+/+} nontransgenic mouse. The mean value of the fold changes is shown under the representative band. LACS, long-chain acyl-CoA synthase; CPT, carnitine palmitoyl-CoA transferase.

dehydrogenase (MCAD), a rate-limiting enzymes in the peroxisomal and mitochondrial β -oxidation pathways, respectively, were significantly increased in *Ppara*^{+/-}:HCVcpTg mice. When fatty acid uptake ability was measured in fresh liver slices, it was significantly enhanced only in *Ppara*^{+/-}:HCVcpTg mice (Figure 2B). Additionally, plasma free fatty acid levels were higher in these mice than in mice in the other groups. Although there were no differences in fasting plasma glucose levels between the groups, hyperinsulinemia was observed only in *Ppara*^{+/-}:HCVcpTg mice (Figure 2C), in agreement with the previous observation that significant insulin resistance developed in these mice (8). Similar results were obtained from 24-month-old mice (data not shown). These results combined show that the increased plasma fatty acid levels, which were likely due to enhanced peripheral fatty acid release caused by insulin resistance, and the increase in fatty acid uptake ability are consistent with steatogenesis in *Ppara*^{+/-}:HCVcpTg mice.

Decreased mitochondrial β -oxidation in transgenic mice. Although the transcriptional activities of major β -oxidation enzymes were markedly increased, *Ppara*^{+/-}:HCVcpTg mice had severe steatosis. To explore this discrepant result, peroxisomal and mitochondrial β -oxidation activities were measured using lignoceric and palmitic acids as substrates, respectively. The lignoceric acid-degrading capacity was increased only in *Ppara*^{+/-}:HCVcpTg mice, where it corresponded to an increase in AOX expression. However, the capacity for palmitic acid degradation, which occurs particularly in mitochondria, was significantly lower in *Ppara*^{+/-}:HCVcpTg mice than in *Ppara*^{-/-}:HCVcpTg and *Ppara*^{+/+}:HCVcpTg mice (Figure 3A).

Thus, decreased mitochondrial β -oxidation ability was considered to be another important mechanism for the development of steatosis induced by the core protein.

We further evaluated mitochondrial abnormalities. In electron microscopic examination, discontinuous outer membranes (Figure 3B, arrows) and lack of an internal structure were observed in some mitochondria of *Ppara*^{+/-}:HCVcpTg mouse livers, in agreement with the previous report (9). However, these abnormalities were not seen in *Ppara*^{-/-}:HCVcpTg and *Ppara*^{+/+}:HCVcpTg mice (Figure 3B). Immunoblot analysis showed that cytochrome *c*, which is usually localized in the mitochondrial intermembrane space, was present in the cytosolic fractions of *Ppara*^{+/-}:HCVcpTg mice (Figure 3C). Moreover, immunoblot analysis using mitochondrial fractions showed that the expression levels of long-chain acyl-CoA synthase and carnitine palmitoyl-CoA transferase-I, which are enzymes indispensable to the initial step of mitochondrial β -oxidation and are localized mainly in mitochondrial outer membranes, were significantly decreased only in *Ppara*^{+/-}:HCVcpTg mice (Figure 3D).

Overall, these results suggest that homozygous PPAR α is essential to the pathogenesis of hepatic steatosis induced by the HCV core protein, which results from a decrease in mitochondrial fatty acid degradation capacity caused by the breakdown of mitochondrial outer membranes and a disproportionate increase in the uptake of fatty acids. Interestingly, steatosis and the related changes did not occur in *Ppara*^{-/-} and *Ppara*^{+/+} mice expressing the HCV core protein, which suggested that these changes were not caused by the core protein itself.

Table 1
Incidence of HCC in 24-month-old mice

HCV core protein	<i>Ppara</i>	Mice (n)	Mice with HCC (n)	Incidence (%)
-	+/+	20	0	0
-	+/-	18	0	0
-	-/-	20	0	0
+	+/+	17	6	35.3 ^A
+	+/-	16	0	0
+	-/-	14	0	0

Mice were killed at 24 months of age for analysis. HCC was diagnosed according to histological findings. ^A*P* < 0.05 compared with *Ppara*^{+/-} nontransgenic mice, *P* < 0.05 compared with *Ppara*^{+/-}:HCVcpTg mice, *P* < 0.05 compared with *Ppara*^{-/-}:HCVcpTg mice.

Requirement of homozygous PPAR α for hepatic tumor development in transgenic mice. At 9 months of age, hepatic nodules were not observed at all in transgenic mice, whereas, at 24 months, approximately 35% of *Ppara*^{+/-}:HCVcpTg mice had macroscopically evident hepatic nodules (Table 1). Microscopically, these nodules had the appearance of well-differentiated HCC with trabecular features, which was consistent with the previous report (9). Surprisingly, *Ppara*^{+/-}:HCVcpTg and *Ppara*^{-/-}:HCVcpTg mice of the same ages developed no evidence of hepatic tumors, despite the expression of HCV core protein at similar levels to those found in *Ppara*^{+/-}:HCVcpTg mice (Table 1). Microscopic examination showed that there were no dysplastic cells

or precancerous lesions throughout the livers in *Ppara*^{+/-}:HCVcpTg and *Ppara*^{-/-}:HCVcpTg mice (Figure 1C). These results provide strong evidence that homozygous PPAR α is essential for hepatic tumorigenesis induced by HCV core protein.

Increased hepatocyte proliferation only in *Ppara*^{+/-}:HCVcpTg mice. Because sustained acceleration of hepatocyte proliferation relative to apoptosis may promote the development of HCC, these opposing processes were quantified in the livers of 24-month-old mice. Both the liver-to-body weight ratio and the number of hepatocytes expressing proliferating cell nuclear antigen (PCNA) were increased only in *Ppara*^{+/-}:HCVcpTg mice (Figure 4, A and B). In contrast, the number of TUNEL-positive hepatocytes and the hepatic caspase 3 activity, indicators of hepatocyte apoptosis, remained similar among the 3 mouse strains (Figure 4, C and D). Interestingly, despite the presence of HCV core protein, the amounts of these proliferative and apoptotic markers in *Ppara*^{+/-}:HCVcpTg and *Ppara*^{-/-}:HCVcpTg mice were similar to those in *Ppara*^{+/-} nontransgenic mice. Expression levels of several proteins, such as protooncogenes (*c-Fos* and *c-Myc*), cell-cycle regulators (cyclin D1, cyclin-dependent kinase [CDK] 4, and PCNA), and phosphorylated ERK 1 and 2, all of which are associated with hepatocyte proliferation, were elevated in *Ppara*^{+/-}:HCVcpTg mice but not in other genotypes (Figure 4, E and F).

Increased oxidative stress and DNA damage only in *Ppara*^{+/-}:HCVcpTg mice. HCV core protein is associated with increased production of ROS (23). Enhanced ROS production induces nuclear DNA damage, which results in the initiation of hepatocarcinogenesis, and can also injure organelles, which can result in disorders in their

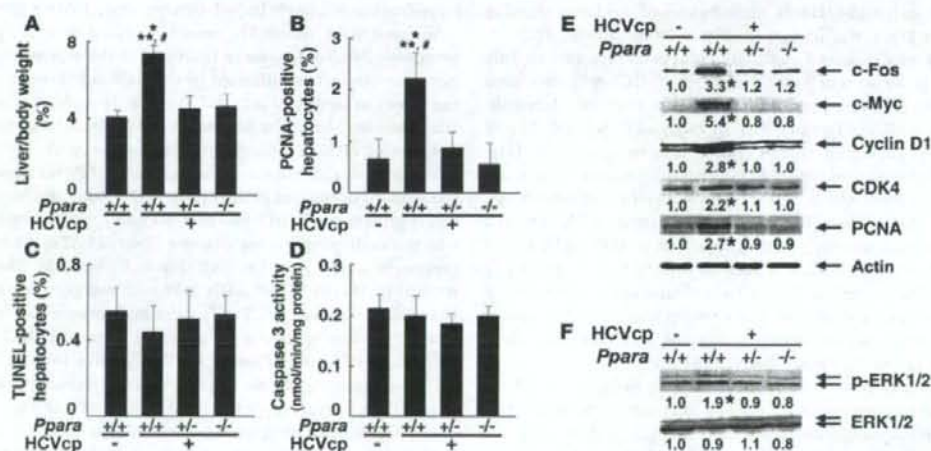
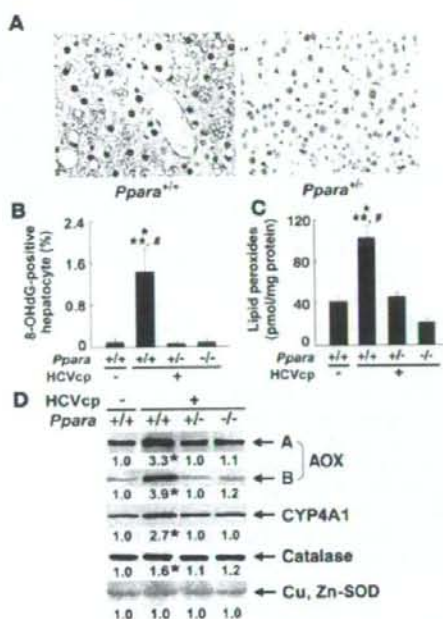


Figure 4

Increased hepatocyte proliferation in *Ppara*^{+/-}:HCVcpTg mice at 24 months of age. (A) Liver-to-body-weight ratio. Results are expressed as the mean \pm SD (*n* = 6/group). (B) Numbers of proliferating hepatocytes. Two thousand hepatocytes were examined in each mouse, and hepatocyte nuclei positive for anti-PCNA antibody were counted. Results are expressed as the mean \pm SD (*n* = 6/group). For A and B, comparisons are designated as follows: **P* < 0.05 compared with *Ppara*^{+/-} nontransgenic mice; ***P* < 0.05 compared with *Ppara*^{+/-}:HCVcpTg mice; **P* < 0.05 compared with *Ppara*^{-/-}:HCVcpTg mice. (C) Numbers of apoptotic hepatocytes. Liver sections were subjected to TUNEL staining, and TUNEL-positive hepatocyte nuclei were counted in 2,000 hepatocytes from each mouse. Results are expressed as the mean \pm SD (*n* = 6/group). (D) Caspase 3 activity. Results are expressed as the mean \pm SD (*n* = 6/group). (E) Immunoblot analysis of oncogene products and cell cycle regulators. The same sample used in Figure 1A (whole-liver lysate, 50 μ g protein) was loaded in each well. The band of actin was used as the loading control. Results are representative of 4 independent experiments. The band intensity was quantified densitometrically, normalized by that of actin, and subsequently normalized by that in *Ppara*^{+/-} nontransgenic mice. The mean value of the fold changes is expressed under each band. (F) Immunoblot analysis of phosphorylated ERK1/2 and total ERK1/2. The same samples in Figure 4E (50 μ g protein) were used.

**Figure 5**

Increased oxidative stress and DNA damage in *Ppara*^{+/-}:HCVcpTg mice at 24 months of age. (A) Immunohistochemical staining using antibody against 8-OHdG. In *Ppara*^{+/-}:HCVcpTg mice, some steatotic hepatocytes were positive for 8-OHdG. Original magnification, $\times 400$. (B) Numbers of 8-OHdG-positive hepatocytes. Hepatocyte nuclei stained with anti-8-OHdG antibody were counted in 2,000 hepatocytes of each mouse. Results are expressed as the mean \pm SD ($n = 6$ /group). (C) Hepatic content of lipid peroxides. Results are expressed as the mean \pm SD ($n = 6$ /group). * $P < 0.05$ compared with *Ppara*^{+/-} nontransgenic mice; ** $P < 0.05$ compared with *Ppara*^{+/-}:HCVcpTg mice; # $P < 0.05$ compared with *Ppara*^{+/-}:HCVcpTg mice. (D) Immunoblot analysis of AOX, CYP4A1, catalase, and Cu, Zn-SOD. The whole-liver lysate used in the experiment in Figure 4E (20 μ g protein for AOX and CYP4A1 and 50 μ g for others) was loaded in each lane. The band of actin was used as the loading control. Results are representative of 4 independent experiments. A and B indicate full-length and truncated AOX, respectively. The band intensity was quantified densitometrically, normalized by that of actin, and subsequently normalized by that in *Ppara*^{+/-} nontransgenic mice. The mean value of the fold changes is expressed under each band. * $P < 0.05$ compared with *Ppara*^{+/-} nontransgenic mice.

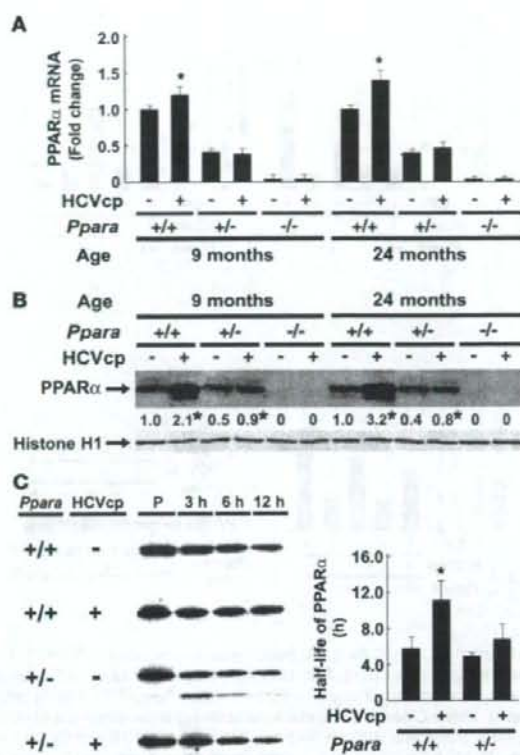
function. The number of hepatocytes positive for 8-hydroxy-2'-deoxyguanosine (8-OHdG), an indicator of oxidative damage to nuclear DNA, was increased only in 24-month-old *Ppara*^{+/-}:HCVcpTg mice (Figure 5, A and B). Lipid peroxides were slightly increased in the livers of 9-month-old *Ppara*^{+/-}:HCVcpTg mice (data not shown) and were more abundant in the livers of 24-month-old *Ppara*^{+/-}:HCVcpTg mice than in those of *Ppara*^{+/-}:HCVcpTg and *Ppara*^{+/-}:HCVcpTg mice or *Ppara*^{+/-} nontransgenic mice (Figure 5C). Expression of typical ROS-generating enzymes (AOX and cytochrome P450 4A1 [CYP4A1]) and ROS-eliminating enzymes (catalase and Cu, Zn-SOD) was examined. Immunoblot analysis showed marked increases in the expression of AOX and CYP4A1 and mild increases in that of catalase only in *Ppara*^{+/-}:HCVcpTg mice. No changes in Cu, Zn-SOD were found in the subgroups of transgenic mice (Figure 5D). These results suggest that enhanced oxidative stress causes damage in nuclear DNA and probably in mitochondria in the *Ppara*^{+/-}:HCVcpTg mice.

Persistent and spontaneous PPAR α activation in *Ppara*^{+/-}:HCVcpTg mice. Liver tumorigenesis induced by long-term exposure to peroxisome proliferators and the related changes, such as sustained hepatocyte proliferation and increased oxidative stress, are associated with persistent PPAR α activation (19–21). To examine the activation of PPAR α , we quantified the level of PPAR α mRNA, which is induced by PPAR α activation (24, 25). PPAR α mRNA levels were higher in 9-month-old *Ppara*^{+/-}:HCVcpTg mice than in *Ppara*^{+/-} nontransgenic mice (Figure 6A). These increases were more pronounced at 24 months of age. However, there were no differences in PPAR α mRNA levels between *Ppara*^{+/-}:HCVcpTg and *Ppara*^{+/-} nontransgenic mice at either 9 or 24 months of age. The expression levels of typical PPAR α target genes (16, 25, 26) – such as FAT, FATP, L-FABP, AOX, and MCAD (Figure 2); c-Myc, cyclin D1, CDK4, and PCNA (Figure 4); and CYP4A1 (Figure 5)

– were simultaneously and synchronously increased in *Ppara*^{+/-}:HCVcpTg mice, but not in *Ppara*^{+/-}:HCVcpTg or *Ppara*^{+/-}:HCVcpTg mice. These results confirm that persistent activation of PPAR α occurs only in *Ppara*^{+/-}:HCVcpTg mice. Various changes observed in *Ppara*^{+/-}:HCVcpTg mice, i.e., increased fatty acid uptake, mitochondrial abnormalities, steatosis, ROS overproduction, accelerated hepatocyte proliferation, and hepatocarcinogenesis, were considered to be closely linked with sustained PPAR α activation.

Nuclear PPAR α content. The results described above suggest that persistent PPAR α activation is critical to the steatogenesis and hepatocarcinogenesis induced by the HCV core protein. A question arises as to why *Ppara*^{+/-}:HCVcpTg mice with an active *Ppara* allele do not exhibit the hallmarks of PPAR α activation and do not develop HCC. To address this issue, the nuclear PPAR α content was analyzed. Immunoblot analysis for PPAR α showed that the amount of nuclear PPAR α protein in *Ppara*^{+/-}:HCVcpTg mice was approximately 2- to 3-fold that of *Ppara*^{+/-} nontransgenic mice, which was disproportionate to the higher PPAR α mRNA levels (approximately 1.2- to 1.6-fold) (Figure 6, A and B). The level of nuclear PPAR α in *Ppara*^{+/-}:HCVcpTg mice was significantly lower than that in *Ppara*^{+/-}:HCVcpTg mice and was similar to that in *Ppara*^{+/-} nontransgenic mice (Figure 6B). Thus, the lower amount of nuclear PPAR α in *Ppara*^{+/-}:HCVcpTg mice than in *Ppara*^{+/-}:HCVcpTg mice might have heightened the threshold of expression required for long-term spontaneous PPAR α activation.

The degree of an increase in nuclear PPAR α levels was evidently higher than the degree of an increase in PPAR α mRNA levels in HCVcpTg mice (Figure 6, A and B). To investigate this disparity, the stability of nuclear PPAR α was evaluated by pulse-chase experiments using isolated hepatocytes obtained from these mice. The half-life of nuclear PPAR α was significantly longer ($P < 0.05$) in *Ppara*^{+/-}:HCVcpTg mice (11.5 ± 2.3 h) than in *Ppara*^{+/-} nontransgenic mice (5.8 ± 1.4 h) (Figure 6C). The half-life of nuclear PPAR α in *Ppara*^{+/-}:HCVcpTg mice tended to be prolonged compared with that in *Ppara*^{+/-} nontransgenic mice (Figure 6C). These results suggest that the stability of nuclear PPAR α was increased as a result of HCV core protein expression. Because it is known that the core protein interacts with retinoid X receptor α (RXR α) (27) and that



PPAR α influences the stability of RXR α (28), it is plausible that the core protein would affect its action in nuclei through an interaction with the PPAR α -RXR α heterodimer and stabilization of PPAR α .

Development of hepatic steatosis and HCC with long-term clofibrate treatment in *Ppara*^{+/-}:HCVcpTg mice. To further confirm the significance of persistent PPAR α activation on core protein-induced pathological changes, *Ppara*^{+/-} and *Ppara*^{+/-}:HCVcpTg mice were fed a standard diet containing 0.05% clofibrate for 24 months. Interestingly, hepatic steatosis appeared in the clofibrate-treated *Ppara*^{+/-}:HCVcpTg mice, but not in the *Ppara*^{+/-} mice under the same treatment conditions (Figure 7, A and B). Similar to our observations in *Ppara*^{+/-}:HCVcpTg mice not treated with clofibrate, aberrant mitochondria with discontinuous outer membranes and decreased palmitic acid β -oxidation activity were found only in the clofibrate-treated *Ppara*^{+/-}:HCVcpTg mice (Figure 7, A and C). In addition, levels of MCAD mRNA; AOX, and CYP4A1 proteins; PPAR α mRNA; and nuclear PPAR α protein were higher in the clofibrate-treated *Ppara*^{+/-}:HCVcpTg mice than in the clofibrate-treated *Ppara*^{+/-} mice (Figure 7, D-F), which suggests that the degree of PPAR α activation in the former group was greater than that in the latter group and similar to that in *Ppara*^{+/-}:HCVcpTg mice not treated with clofibrate. Finally, the incidence of HCC after clofibrate treatment was higher in *Ppara*^{+/-}:HCVcpTg mice (25%; 5 in 20 mice) than in *Ppara*^{+/-} mice (5%; 1 in 20 mice). Therefore, these results corroborate the importance of constant PPAR α activation to the pathogenesis of hepatic steatosis and HCC in the transgenic mice.

Figure 6

Persistent PPAR α activation in *Ppara*^{+/-}:HCVcpTg mice. (A) PPAR α mRNA levels. Total RNA was prepared from each mouse, and PPAR α mRNA levels were determined by RT-PCR, normalized by those of GAPDH, and subsequently normalized by those of 9-month-old *Ppara*^{+/-} nontransgenic mice. Results are expressed as the mean \pm SD ($n = 6$ /group). (B) Immunoblot analysis of nuclear PPAR α . The nuclear fraction obtained from each mouse (100 μ g protein) was loaded in each well. The band of histone H1 was used as the loading control. Results are representative of 6 independent experiments. The band intensity was quantified densitometrically, normalized by that of histone H1, and subsequently normalized by that in 9-month-old *Ppara*^{+/-} nontransgenic mice. The mean value is expressed under each band. * $P < 0.05$ compared with nontransgenic mice of the same age and *Ppara* genotype. (C) Pulse-chase experiments for 3, 6, and 12 h and pulse-label (P) experiments for nuclear PPAR α using isolated mouse hepatocytes. Left: labeled PPAR α bands on x-ray film. Pulse-label and pulse-chase experiments were performed as described in Methods. Results are representative of 4 independent experiments. Right: half-life of PPAR α . The band intensity was measured densitometrically and subsequently normalized by that of the pulse-label experiments. The percentage of the band intensity was plotted, and the half-life of PPAR α was calculated. Results obtained from 4 independent experiments are expressed as the mean \pm SD. * $P < 0.05$ compared with nontransgenic mice in the same *Ppara* genotype.

Discussion

A novel and striking finding in this study is the absolute requirement of persistent PPAR α activation for the development of HCV core protein-induced steatosis and HCC. Our data also show that the HCV core protein alone cannot induce steatosis and HCC in transgenic mice.

Mechanisms of development of steatosis in HCVcpTg mice were previously explained as an enhancement of de novo synthesis of fatty acids (29) and a decrease in MTP expression, the latter of which results in insufficient VLDL secretion from hepatocytes (30). In the present study, we revealed 2 novel mechanisms of steatogenesis in the transgenic mice, i.e., an impairment of mitochondrial β -oxidation due to the breakdown of mitochondrial outer membranes and an increase in fatty acid uptake into hepatocytes, associated with PPAR α activation. PPAR α activation, mitochondrial dysfunction, and hepatic steatosis appeared in 9-month-old *Ppara*^{+/-}:HCVcpTg mice and continued until 24 months of age, clearly preceding development of HCC. These findings thereby indicate a correlation between PPAR α activation, hepatic steatosis, and HCC.

We obtained the novel and rather paradoxical finding that significant PPAR α activation, which generally is expected to reduce hepatic triglyceride levels, is essential for the development of severe steatosis induced by HCV core protein. According to the results of this study, the following hypothesis concerning the development of steatosis in *Ppara*^{+/-}:HCVcpTg mice is proposed. First, the HCV core protein localizes partly in mitochondria (9). A recent study