Figure 2. Naito et al.

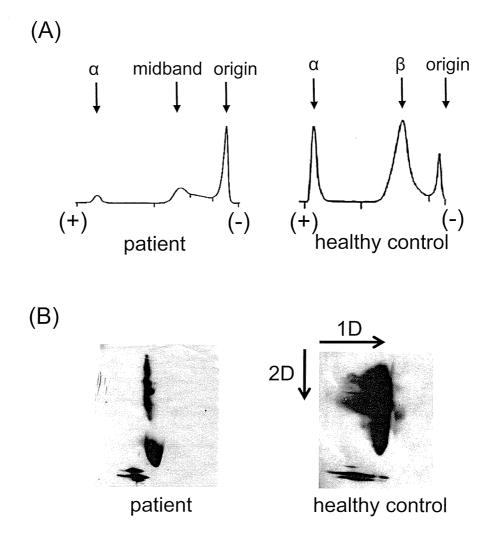
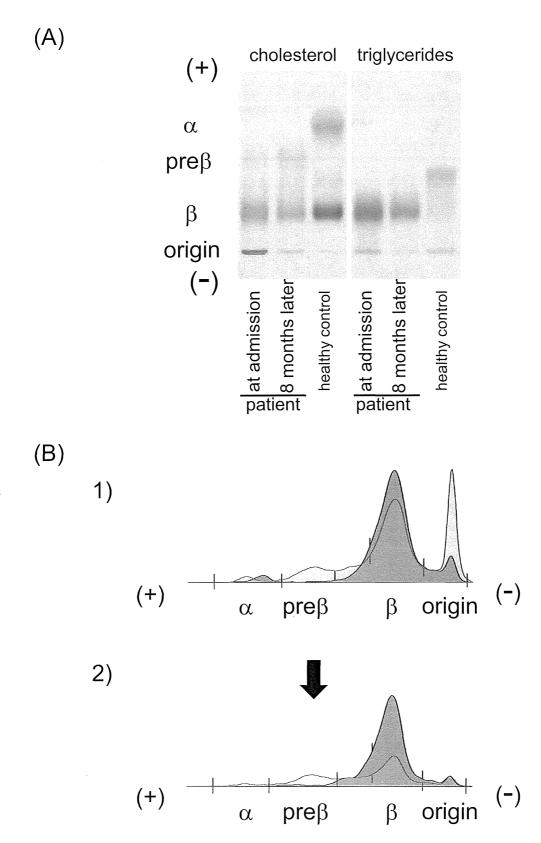


Figure 3. Naito et al.



| Lipid fraction | | Normal value | At admission | At 8 months of treatment |
|------------------------|---------|--------------|--------------|--------------------------|
| total cholesterol | (mg/dl) | 120-220 | 235 | 80 |
| triglyceride | (mg/dl) | 30-150 | 235 | 142 |
| LDL-cholesterol | (mg/dL) | 70-139 | 39 | 33 |
| HDL-cholesterol | (mg/dL) | 40- 96 | 22 | 19 |
| free cholesterol | (mg/dL) | 30- 65 | 205 | 71 |
| cholesterol ester | (mg/dL) | 90-200 | 30 | 9 |
| free/total cholesterol | (%) | 70-80 | 87 | 88 |

Table 1.

Lipid profiles in a patient with LCAT deficiency following a fat-restriction diet and administration of losartan for 8 months

Lipid profiles at admission and after adoption of a fat-restriction diet consisting of 10 g fat, 45 g protein and 1570 kcal energy per day and administration of losartan 50 mg for 8 months on lipid profile in a patient with LCAT deficiency.

| Apolipopro | tein fraction | Normal values | At admission | After 8 months |
|------------|---------------|---------------|--------------|----------------|
| | | | | of treatment |
| apoA-I | (mg/dL) | 126 - 165 | 39 | 34 |
| apoA-II | (mg/dL) | 24 - 33.3 | 5.1 | 3.3 |
| ароВ | (mg/dL) | 66 - 101 | 63 | 55 |
| apoC-II | (mg/dL) | 1.5 - 3.8 | 5.6 | 1.3 |
| apoC-III | (mg/dL) | 5.4 - 9.0 | 8.6 | 3.5 |
| apoE | (mg/dL) | 2.8 - 4.6 | 10.8 | 5.4 |

Table 2. Apolipoprotein profile in a patient with LCAT deficiency before and after treatment with a fat-restriction diet and administration of losartan for 8 months Apolipoprotein profile at admission, and effect of a fat-restriction diet consisting of 10 g fat, 45 g protein, and 1570 kcal energy per day for 8 months on apolipoproteins in a patient with LCAT deficiency.

Platelet-rich plasma inhibits the apoptosis of highly adipogenic homogeneous preadipocytes in an *in vitro* culture system

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Abbreviation: BIM, Bcl-2-interacting mediator of cell death

Abstract

Auto-transplantation of adipose tissue is commonly used for the treatment of tissue defects in plastic surgery. The survival of the transplanted adipose tissue is not always constant, and one of reasons is the accelerated apoptosis of the implanted preadipocytes. We have recently established highly homogeneous preadipocytes, named ccdPAs. The aim of the current study was to evaluate the regulation of the potency of platelet-rich plasma (PRP) on the apoptosis of ccdPAs *in vitro*. PRP stimulated the proliferation of the preadipocytes in a dose-dependent manner, and the stimulatory activity of 2% PRP was significantly higher than that of 2% FBS or 2% platelet-poor plasma (PPP). The

presence of 2% PRP significantly inhibited serum starvation- or TNF-α/cycloheximide-induced apoptosis in comparison to 2% FBS or 2% PPP. DAPK1 and Bcl-2-interacting mediator of cell death (BIM) mRNAs were reduced in the preadipocytes cultured with 2% PRP in comparison to those cultured in 2% FBS. The gene expression levels were significantly higher in cells cultured without serum in comparison to cells cultured with 2% FBS, and the levels in the cells with 2% PRP were reduced to 5-10% of those in the cells without serum. These results indicated that ccdPAs exhibit anti-apoptotic activities, in addition to increased proliferation, when cultured in 2% PRP in comparison to the same concentration of FBS, and that this was accompanied with reduced levels of DAPK1 and BIM mRNA expression in in vitro culture. PRP may improve the outcome of transplantation of adipose tissue by enhancing the anti-apoptotic activities of the implanted preadipocytes.

Keywords: adipocytes; apoptosis; Bcl-2-like protein 11; death-associated protein kinase; platelet-rich plasma; tissue transplantation

Introduction

Aspirated fat is a common source of autologous tissue transplantation for the correction of tissue defects in plastic and reconstructive surgery (Billings and May, 1989; Patrick, 2000, 2001). Aspirated fat contains multipotential preadipocytes and progenitor cells, which have been utilized as a source of cell-based regenerative medicine (Stashower et al., 1999; Zuk et al., 2001; Gimble et al., 2007; Yoshimura et al., 2009; Bauer-Kreisel et al., 2010; Sterodimas et al., 2010). Although several different techniques of fat grafting have been developed, the outcomes of the transplantation vary widely. The most important factor required for successful grafting is to optimize the survival of the transplanted preadipocytes and other cells in the graft. In previous studies, we and others have shown that various cytokines are involved in the efficient cell survival of the implants (Kimura et al., 2003;

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Yamaguchi et al., 2005; Cho et al., 2006; Torio-Padron et al., 2007; Kuramochi et al., 2008; Ning et al., 2009).

Platelet rich plasma (PRP) (Eppley et al., 2006; Foster et al., 2009; Redler et al., 2011) has been widely applied for practical medicine, such as aesthetic plastic surgery and the treatment of soft-tissue ulcers (Welsh, 2000; Man et al., 2001; Margolis et al., 2001; Bhanot and Alex, 2002; Martinez-Zapata et al., 2009; Sclafani, 2009). Once activated, platelets secrete various bioactive cytokines, including platelet-derived growth factor (PDGF) and transforming growth factor beta 1 (TGF-β1), which increase angiogenesis and cell proliferation relevant to soft tissue regeneration. PRP has been applied for fat grafting, and in fact, has been shown to improve the survival of implanted adipose tissue in patients (Abuzeni and Alexander, 2001; Sadati et al., 2006; Cervelli et al., 2009). Thus, the use of PRP has been broadened to the tissue-engineering field using adipose tissue-derived multi-potential cells (Anitua et al., 2006; Muller et al., 2009). PRP is also expected to function as an autologous fibrin-based scaffold for transplanted cells (Anitua et al., 2006; Wu et al., 2009; Kang et al., 2011). In fact, recent our study showed that fibrin-based scaffold decreased the apoptotic cell death of murine ccdPAs in mice transplantation model (Aoyagi et al., 2011).

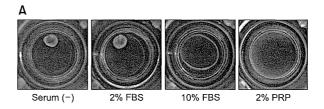
We have recently identified proliferative preadipocytes, ceiling culture-derived proliferative adipocytes (ccdPAs), as homogeneous cells suitable for ex vivo gene therapy applications via autologous transplantation (Asada et al., 2011; Kuroda et al., 2011). The ccdPAs are characterized by their high proliferative capacity with spontaneous adipogenic potential in scaffold fibrin gel culture (Aoyagi et al., 2012). The establishment of a highly homogenous preadipocyte line made it possible to perform examinations to identify the optimal scaffolds and cytokines that can be used to improve the survival of transplanted preadipocytes. We herein studied the effects of PRP, and an autologous cytokine cocktail, on the apoptotic properties of preadipocytes using the ccdPAs.

Results

PRP inhibits fibrin scaffold gel shrinkage and improves the viability of ccdPAs in 3-dimensional culture

We have recently established a 3-dimensional (3-D) culture system for ccdPAs using fibrin gel (FG) (Aoyagi et al., 2012). Using the 3-D culture system, the effects of PRP on the gel shrinkage and cell viability were analyzed in comparison to FBS. The FG/ccdPAs were formed and maintained in culture medium containing 10% FBS for 16 hr. The culture medium was replaced with fresh medium containing 2% PRP, 2% FBS or 10% FBS, or with medium without serum, and cells were subsequently incubated for an additional 24 hr.

The resulting gel sizes varied among the cultures grown in each type of medium. The gels without serum or with 2% FBS showed a drastic volume reduction, while the volumes of the gels cultured with 10% FBS or 2% PRP were not obviously reduced (Figure 1A). The culture supernatants were collected from each well and LDH activity was measured to evaluate the viability of cells. The LDH activity significantly decreased in the culture medium with 2% PRP in comparison to the medium with 2% or 10% FBS (Figure 1B). TUNEL staining of the gel sections showed the number of apoptotic cells to significantly decrease in the medium with 2% PRP in comparison to the medium with 2% FBS (1.5 \pm 1.1% vs 9.8 \pm 1.9%, P < 0.05). These results suggested that 2% PRP inhibits the shrinkage of FG/ccdPAs gels, and improves the cell viability in comparison to the same concentration of FBS.



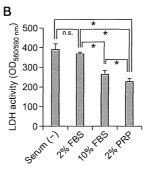


Figure 1. The effects of platelet-rich plasma (PRP) on the 3-dimensional culture of ccdPAs. 100 μ l of fibrin gels containing 1 \times 10' cells/ml of ccdPAs (FG/ccdPAs) were formed in cell culture insert and incubated in DMEM/HAM with 10% FBS for 16 hrs. The medium was replaced by DMEM/HAM in the presence or absence of different concentrations of FBS or PRP. (A) Photographs of FG/ccdPAs in the inserts were taken after 24 hr of culture. (B) The culture supernatant was collected from each well and the LDH activities expressed by the fluorescence of resorufin generated by coupled enzymatic reaction were examined. *P < 0.05.

PRP has a high proliferation-inducing potential for ccdPAs in plate culture

In order to evaluate the function of PRP on cell survival in the gel, we next examined the effects of PRP on the proliferation of ccdPAs in comparison to FBS. The cells (2.5×10^5 cells) were seeded and incubated with DMEM/HAM containing 20% FBS in 10 cm dishes for 16 hr. The media was replaced with medium containing 2% PRP, 2% FBS, or 10% FBS, and the cells were then cultured for 3 days. The cell appearance was not apparently changed among the ccdPAs cultured for 3 days in plates with media containing 2% PRP, 2% FBS, or 10% FBS (Figure 2A). To examine the cell proliferation, 2×10^3 cells of ccdPAs were seeded onto 96 well plates and incubated at 37°C for 24 hr. The media was replaced with medium with or without 2% PRP, 2% FBS, or 10% FBS (Day 0), and the cells were cultured for 3 days. The number of cells in each well was evaluated by measuring the DNA content. In contrast to the observation that the cell numbers on Day 3 were not significantly changed in comparison to those at Day 0 in the cultures incubated in medium containing 2% FBS. the cell numbers were significantly increased in cells cultured in the medium with 10% FBS or 2% PRP, and notably, the number of cells on Day 3 in the medium containing 2% PRP was significantly increased in comparison to the cells cultured with 10% FBS (Figure 1B). The cell numbers in the media with various concentrations of PRP showed a dose-dependent increase up to 5% PRP; the number of cells present in the media with 0.5-1% PRP was almost equivalent to that of the cells cultured with 5-10% FBS (Figure 2C). These results indicated that the proliferation-inducing potential of PRP for ccdPAs was higher in comparison to that of FBS.

PRP inhibits the apoptosis of ccdPAs

The high proliferation-inducing property of PRP for ccdPAs in culture prompted us to further analyze PRP for protective effects against apoptosis in ccdPAs, since PRP is rich in cytokines and proteinases involved not only in proliferation, but also in regulating apoptosis (Eppley et al., 2004, 2006; Foster et al., 2009; Redler et al., 2011). The protection of the cells from death may contribute to their longer survival after transplantation, together with a high potential for proliferation. To investigate the possibility, the ccdPAs (1 \times 10 6 cells) were seeded and incubated in a 10 cm dish with DMEM/HAM medium containing 20% FBS for 16 hr, and subsequently incubated with the medium with or without 2% FBS, 2% PRP, or 2% PPP. After

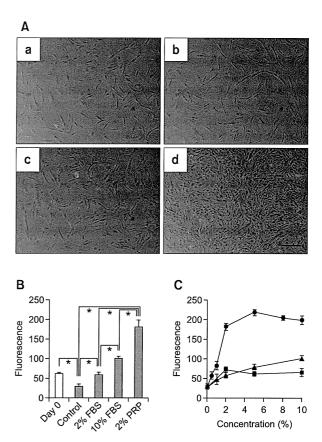


Figure 2. Platelet-rich plasma (PRP) promotes the proliferation of ccdPAs. (A) Photographs of ccdPAs were taken after 3 days in culture containing DMEM/F12-HAM in the absence of serum (a) or the presence of 2% (b) or 10% (c) FBS or 2% (d) PRP. The scale bar indicates 200 um. (B) Cells were seeded into 96 well plates and incubated in DMEM/F12-HAM containing 20% FBS for 24 hr. The culture medium was then replaced with DMEM/F12-HAM in the absence of serum (control) or presence of 2% FBS or 10% FBS or 2% PRP. After 3 days in CO2 incubator, the cell number in each well was examined by DNA content in comparison to those on day 0 (open bar). The values for the serum (-), 10% FBS, and 2% PRP groups were significantly different compared with those on Day 0 (*P < 0.05). (C) The cell numbers were examined in wells cultured in DMEM/F12-HAM containing various concentrations of PRP (circle), FBS (triangle), and PPP (square) after 3 days of culture similarly as Figure 2B. The growth stimulatory effect was not significantly different between 10% and 20% FBS and PPP (data not shown).

incubation for 8 hr, the cells were collected and stained with Annexin V-FITC. The flow cytometric analysis showed that 5.5% of cells were identified as Annexin V positive in the medium without serum (Figure 3A). The number of apoptotic cells was significantly decreased in the media with 2% FBS, 2% PRP, or 2% PPP in comparison to that in the cells cultured in serum-free medium. Among the various supplements, 2% PRP drastically reduced the number of apoptotic cells in comparison to 2% FBS or 2% PPP. ERK1/2 phosphorylation was examined to further analyze the protective effect of PRP against apoptosis, because the activation of the

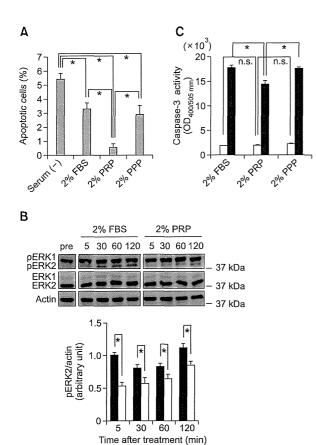


Figure 3. PRP decreased the apoptotic cell death and caspase 3 activity induced by TNF- α and cycloheximide in ccdPAs. (A) ccdPAs were seeded and incubated for 16 hr with medium containing 20% FBS, and the medium was then replaced with fresh medium without serum (Serum (-)) or with media containing 2% PRP, FBS, or PPP, and the cells were subsequently incubated at 37°C for 8 hr. The cells were then collected, stained by Annexin V-FITC and propidium iodide (PI), and analyzed using a Tall Image Based Cytometer (Life technologies). FITC-positive/ PI-negative cells were considered to be apoptotic cells. *P < 0.05. (B) After incubation for 16 hr with medium containing 20% FBS, ccdPAs were pretreated for 2 hr with the medium containing 2% PRP or FBS. The cells were treated with TNF- α and cycloheximide for 5, 30, 60, and 120 min in the medium with 2% FBS (closed bar) or 2% PRP (open bar). Cell lysates were prepared at each time point as well as pretreatment (pre) and then were subjected to an immunoblot analysis of phosphorylated or unphosphorylated form of ERK1/2, and Actin. Results of densitometric analysis of phosphorylated form of ERK2 (pERK2) is shown below. After normalization of signals of pERK2 by Actin, each value of pERK2 was expressed as the fold increase of that at 5 min with 2% FBS. $^{*}P < 0.05$. (C) After pretreatment for 2 hr with the medium containing 2% PRP, FBS, or PPP, the cells were incubated for 3 hr in the absence (open bars) or presence (closed bars) of TNF- α and cycloheximide, which induce apoptotic cell death. The caspase-3 activity in the lysates of collected cells were measured. *P < 0.05.

cascade is important for apoptosis via various intracellular signals including TNF- α (Cawthorn and Sethi, 2008; Mebratu and Tesfaigzi, 2009; Cagnol and Chambard, 2010). The cells were incubated with 2% PRP, FBS, or PPP for 2 hr, and apoptosis was induced by TNF- α and cycloheximide. Phosphorylation was detected following treatment with TNF- α and cycloheximide for 5 min in the cells cultured with 2% FBS. A densitometric analysis showed the amount of phosphorylated ERK2, and not phosphorylated ERK1, to significantly decrease in the medium with 2% PRP in comparison to the medium with 2% FBS (Figure 3B). The caspase-3 activity induced by TNF- α and cycloheximide for 3 hr were also significantly decreased in ccdPAs in the medium with 2% PRP in comparison to the cells cultured with 2% FBS or 2% PPP (Figure 3C). Thus, the apoptosis of ccdPAs was inhibited by culturing them in the medium with 2% PRP in vitro.

PRP almost completely inhibits the expression of the pro-apoptotic genes, DAPK1 and BIM, in ccdPAs after serum starvation

In order to identify the molecules involved in the anti-apoptotic effects of PRP on ccdPAs in culture, the expression profiles of representative apoptosisrelated genes were examined using a PCR array profiler. The cells $(2.5 \times 10^5 \text{ cells})$ were seeded into 10 cm dishes and incubated in DMEM/HAM containing 20% FBS for 16 hr. The media was replaced with DMEM/HAM containing 2% PRP or FBS, the cells were incubated for 3 days, and the total RNA was isolated from the cultured cells to analyze the expression of apoptosis-related genes. Two independent experiments showed that, among the 84 genes examined, there were 8 genes with a more than 2-fold increase in expression, and 9 genes with a more than 2-fold decrease in expression in the cells cultured in the medium with 2% PRP compared with those cultured in the medium with 2% FBS (Table 1). We focused our interest on two genes, DAPK1 (reduced to 7.4% of the expression level observed with FBS) and BCL2L11 (also called BIM, reduced to 18.9% of the level observed with FBS), as representative genes with the obvious downregulation in the medium with 2% PRP (Figure 4). DAPK1 and BIM have been shown to be one of master regulators of cell death (Gozuacik and Kimchi, 2006), and is essential for BAXdependent cell death (Kim et al., 2009; Ren et al., 2010), respectively.

The role of DAPK1 and BIM genes in apoptosis of preadipocytes was investigated by examining the effect of serum starvation of cells incubated with PRP on the expressions of these genes. The ccdPAs (2.5×10^5 cells) were seeded into 10 cm dishes and incubated in DMEM/HAM containing 20% FBS for 16 hr. The medium was replaced by medium containing 10% FBS (control), 2% FBS, 2% PRP, or 2% PPP, the cells were cultured for 3 days and the expression of DAPK1 and BIM were

Table 1. Apoptosis-related genes affected by PRP

| Unigene | Refseq | Symbol | Description | Fold change |
|---------------|-----------|-----------|---|-------------|
| Downregulated | | | | |
| Hs.380277 | NM_004938 | DAPK1 | Death-associated protein kinase 1 | 13.5803 ↓ |
| Hs.469658 | NM_006538 | BCL2L11 | BCL2-like 11 (apoptosis facilitator) | 5.2596 ↓ |
| Hs.5353 | NM_001230 | CASP10 | Caspase 10, apoptosis-related cysteine peptidase | 4.0726 ↓ |
| Hs.591834 | NM_003844 | TNFRSF10A | Tumor necrosis factor receptor superfamily, member 10a | 3.967 ↓ |
| Hs.513667 | NM_003946 | NOL3 | Nucleolar protein 3 (apoptosis repressor with CARD domain) | 2.8887 ↓ |
| Hs.501497 | NM_001252 | CD70 | CD70 molecule | 2.8129 ↓ |
| Hs.87247 | NM_003806 | HRK | Harakiri, BCL2 interacting protein (contains only BH3 domain) | 2.5816 ↓ |
| Hs.710305 | NM_004536 | NAIP | NLR family, apoptosis inhibitory protein | 2.3876 ↓ |
| Hs.643120 | NM_000875 | IGF1R | Insulin-like growth factor 1 receptor | 2.1732 ↓ |
| Upregulated | | | | |
| Hs.127799 | NM_001165 | BIRC3 | Baculoviral IAP repeat-containing 3 | 10.851 ↑ |
| Hs.462529 | NM_003790 | TNFRSF25 | Tumor necrosis factor receptor superfamily, member 25 | 4.0981 ↑ |
| Hs.478275 | NM_003810 | TNFSF10 | Tumor necrosis factor (ligand) superfamily, member 10 | 4.0907 ↑ |
| Hs.654459 | NM_001561 | TNFRSF9 | Tumor necrosis factor receptor superfamily, member 9 | 2.9875 ↑ |
| Hs.522506 | NM_021138 | TRAF2 | TNF receptor-associated factor 2 | 2.8331 ↑ |
| Hs.9216 | NM_001227 | CASP7 | Caspase 7, apoptosis-related cysteine peptidase | 2.2033 ↑ |
| Hs.145726 | NM_001205 | BNIP1 | BCL2/adenovirus E1B 19kDa interacting protein 1 | 2.0258 ↑ |
| Hs.194726 | NM_004874 | BAG4 | BCL2-associated athanogene 4 | 2.0241 ↑ |

Genes identified as having a change in expression > 2-fold induced by the addition of PRP in comparison to 2% FBS are shown.

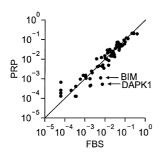


Figure 4. The results of the analysis of the expression of apoptosis-related genes affected by PRP. Total RNA was extracted from the cells cultured in the presence of 2% FBS or 2% PRP for 72 hr. The total RNA was subjected to cDNA synthesis and subsequent quantification of the mRNA expression for various apoptosis-related genes. The fold-changes in the quantified mRNA amounts compared to the average value of house-keeping genes were plotted for each gene (x-axis; cultured in 2% FBS, y-axis; cultured in 2% PRP).

analyzed. The DAPK1 mRNA level was increased 10.6-fold by serum starvation in comparison to the level in the cells cultured with 10% FBS, and the mRNA level was decreased to that of 10% FBS by the presence of 2% PRP. It is worth noting that, although the mRNA levels of DAPK1 in the cells cultured with 2% FBS and 2% PPP significantly decreased in comparison to those cultured without serum, the reductions were by 20.4% and 11.9%, respectively, which were less than that (93.6%) induced by culture in 2% PRP. The BIM mRNA levels were also drastically increased in the cells cultured in serum free medium in comparison to

those cultured in the medium with 10% FBS (Figure 2C). The mRNA levels were reduced to those observed in the cells cultured with 10% FBS by the addition of 2% PRP. Again, the potential of 2% PRP to inhibit the mRNA expression of the target gene (by 87.2%) was significantly higher than that of the 2% FBS (54.1%) or 2% PPP (72.2%). Thus, PRP almost completely inhibited the expression of apoptosis-related genes induced by serum starvation.

Discussion

PRP inhibited the volume reduction of the 3D gels embedded with ccdPAs, the homogeneous preadipocytes, in comparison to the same concentration of FBS, and this was accompanied by increased cell viability in the gel. These observations prompted us to analyze the effects of PRP on the apoptosis and proliferation of the ccdPAs. The results showed that 2% PRP had a higher inhibitory effect on the apoptotic cell death of ccdPAs than 2% FBS or 2% PPP (Figure 3). A comparison between 2% PRP and 2% FBS by a gene expression profile analysis revealed that PRP downregulated 11% of the 84 representative apoptosis-related genes and upregulated 10% of the 84 representative apoptosis-related genes (Figure 4 and Table 1). The most drastically reduced genes were DAPK1, the protein product of which plays important roles in a wide range of signal transduction pathways with diverse outcomes, such as apoptosis, autoph-

agy and immune responses (Lin et al., 2010), and BIM, encoding one of the BH3-only proteins, which is a critical regulator of apoptosis in many cell types (Ramesh et al., 2009). The induction of these genes by apoptotic stimuli was almost completely prevented in the presence of PRP (Figure 5).

PRP, a concentrate of physiological cytokines, has been widely utilized as an injectable material in the clinic since the 1970s to enhance soft and hard tissue healing (Andia et al., 2010; Lopez-Vidriero et al., 2010; Redler et al., 2011; Yu et al., 2011), mainly by stimulating cell proliferation and angiogenesis in the injured tissues. PRP promotes the growth of various cells, including tissue-derived progenitor cells (Liu et al., 2002; Lucarelli et al., 2003; Doucet et al., 2005; Frechette et al., 2005; Vogel et al., 2006; Kakudo et al., 2008; Kurita et al., 2008; Cervelli et al., 2009; Chieregato et al., 2011), and increases the revascularization of the transplanted tissues (Bir et al., 2009). Based on these findings, the clinical applications of PRP have been broadened to recommend its use as an additive to tissue/cell transplantation therapies in plastic and reconstructive surgeries, and more recently in regenerative medicine. In fact, PRP has been shown to improve the fat graft survival (Abuzeni and Alexander, 2001; Sadati et al., 2006; Cervelli et al., 2009; Nakamura et al., 2010; Pires Fraga et al., 2010; Oh et al., 2011) and bone and periodontal regenerations via cell transplantation (Tobita et al., 2008; Chen et al., 2010; Yamada et al., 2010; Arvidson et al., 2011).

In order to apply PRP for clinical transplantation therapy using preadipocytes cultured in vitro, it is necessary to elucidate the effects of PRP on cell survival in the grafts. However, the mechanisms by which PRP increases graft survival have not been well-characterized so far. The current study showed that PRP strongly induces the proliferation of ccdPAs, preadipocytes which were previously shown to be more adipogenic than ASCs (Asada et al., 2011), compared with FBS at an equivalent concentration. Vogel et al. (2006) described that, because the addition of 2% PRP did not result in sufficient thrombocyte-clot formation to maintain a clot in the medium, a higher concentration of PRP, 3%, was evaluated for the stimulation of the MSC proliferation. In this study, to evaluate the efficacy of lower concentrations of PRP, the PRP was activated by thrombin to release cytokines (Aiba-Kojima et al., 2007) prior to the experiments. As a result, 2% PRP showed almost the same effects on proliferation as 10% PRP, indicating its usability as a substitute for FBS in the expansion of preadipocytes for clinical applications. Finally, 2% PRP showed anti-apoptotic activities on the

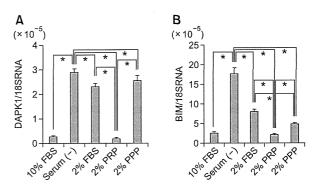


Figure 5. Serum starvation induced the expression of the DAPK1 and BIM genes, which was prevented by culture with 2% PRP. The ccdPAs were seeded and incubated for 16 hr in DMEM/HAM containing 20% FBS, and the culture medium was then replaced with medium without serum (Serum (-)), or with 2% or 10% FBS, 2% PRP, or 2% PPP, followed by incubation for an additional 72 hr. Quantitative reverse transcription-polymerase chain reaction (RT-PCR) was performed to evaluate the mRNA expression levels of DAPK1 (A) and BIM (B). The quantification of the given genes was expressed as relative mRNA level compared with a control after normalization to 18S RNA. *P < 0.05.

preadipocytes, providing evidence that it can be used as an efficacious additive in the cell transplantation cocktail.

We observed that the expression of the DAPK1 and BIM genes was substantially upregulated by serum starvation in ccdPAs. However, the addition of PRP in the growth media effectively inhibited the apoptosis and downregulated the expression of these genes. TGF-B has been shown to induce the expression of DAPK1 and BIM, and to lead to subsequent apoptosis in other cell types (Jang et al., 2002; Wildey et al., 2003; Ramjaun et al., 2007; Yu et al., 2008). PRP may therefore inhibit the TGF-β-induced apoptosis cascade(s) during serum starvation in ccdPAs. Further analyses are needed to elucidate the mechanism(s) underlying the inhibitory potential of PRP on the expression levels of the representative apoptotic genes. The gene expression analysis also showed that PRP regulated the expression levels of genes involved in TNF signaling (TNFRSF10A, TNFRSF25, TNFSF10, TNFRSF9, and TRAF2), and of the Bcl protein superfamily, with its related proteins (HRK, BNIP1, and BAG4) (Table 1). The changes in the expression of these genes may also improve the survival of ccdPAs by modulating the apoptotic stimuli, considering that TNF-α signaling plays an important role in the regulation of the adipose tissue mass (Warne, 2003).

In conclusion, PRP inhibits cell apoptosis as well as or better than FBS, and also promotes the proliferation of the ccdPAs. The gene expression analyses identified that the DAPK1 and BIM genes were the most highly downregulated apoptosis-related genes by PRP treatment in the preadipocytes. The identified characteristics of PRP with regard to the preadipocytes have advantages including increases in the cell number and improved cell survival in the transplanted grafts. Together with our findings for the efficacies of fibrin scaffold in transplantation of ccdPAs (Aoyagi *et al.*, 2011), the use of PRP for cell preparation and implantation of fat tissues and/or propagated cells may provide the graft with stable long-term survival after auto-transplantation.

Methods

Cell culture

Subcutaneous adipose tissues were obtained from healthy donors after informed consent was obtained, with approval from the ethics committee of Chiba University School of Medicine, and all studies were performed according to the guidelines of the Declaration of Helsinki. The preparation of the ceiling culture-derived proliferative adipocytes (ccdPAs) was performed as described previously (Kuroda *et al.*, 2011). Dulbecco's modified Eagle's medium/F12-HAM (DMEM/HAM, Sigma-Aldrich, St. Louis, MO) supplemented with 20% fetal bovine serum (FBS, SAFC Biosciences, Lenexa, KS) and 40 $\mu g/ml$ gentamicin (GENTACIN, Schering-Plough Co., Kenilworth, NJ) was used as the culture media, unless otherwise noted in the text.

Preparation of PRP

Human PRP and PPP were prepared from healthy donors as follows; 52 ml of blood was obtained from the donors and mixed with 8 ml of Anticoagulant Citrate Dextrose Solution Formula A (ACD-A, TERUMO, Tokyo, Japan) solution, and transferred to 15 ml tubes. The tubes were centrifuged at 300 \times g for 15 min at 20°C. The plasma and the buffy coat below the plasma were collected and transferred to new tubes. Secondary centrifugation was performed at $2000 \times g$ for 15 min at 20° C. The clear supernatant (plasma) was decanted off until 6 ml was left and the middle portion of supernatant (plasma) was taken to be used as PPP. Finally, the remaining supernatant including the buffy coat was taken to be used as PRP. The platelet number of each product was automatically measured (XS 800i, sysmex Japan). The PRP utilized in this study contained 8.6×10^6 platelets/µl, which was approximately 7-fold concentrated from the original concentration in whole human plasma. Preparations of serum lysates containing platelet-released growth factors were essentially performed according to the method described by Aiba-Kojima et al. (2007). In brief, 2 U/ml of thrombin (Astellas Pharma Inc. Tokyo, Japan) was added to PRP and PPP, and the samples were agitated for 1 hr at 37°C and then incubated overnight at 4°C. Platelet bodies and any remaining fibrin were eliminated by centrifugation (2000 \times g for 10 min), and the supernatants were obtained for the PRP and PPP. The serum samples were frozen at -20°C and thawed at 37°C before use. The growth medium was supplemented with 2 U/ml of heparin (Novo-Heparin, 5,000 units/5 ml for

Injection, Mochida Pharm. Co. Tokyo, Japan).

Culture on fibrin scaffolds

Bolheal (The Chemo-Sero-Therapeutic Research Institute, Kumamoto, Japan) was used as a clinically available material to generate the fibrin gel. Fibrinogen and thrombin solutions were diluted with Ringer's Solution (Fuso Pharmaceutical Industries, Osaka, Japan) containing 0.5% human serum albumin (Mitsubishi Tanabe Pharma., Tokyo, Japan). The ccdPAs were suspended at 1×10^7 cells/ml by the diluted fibrinogen and thrombin solution. The final concentration of fibrinogen was 4 mg/ml and the thrombin solution was used at 1 U/ml. To form fibrin clots, 50 μ l of the cell-fibrinogen suspension was added to each cell culture insert (Falcon 3104; Becton Dickinson, Franklin Lakes, NJ), then shortly thereafter, 50 µl of the cell-thrombin suspension was added into the insert, mixed by pipetting, and incubated at room temperature for 2 h. The inserts with fibrin clots were put on 12 well culture plates, and culture media were added to the inserts and wells. The plates were incubated at 37°C for 12 h in a 5% CO2 incubator, and the media were replaced by fresh media containing FBS or PRP.

LDH assay

LDH released into the culture supernatant from the FG/ccdPA was measured using the CytoTox-One Homogeneous Membrane Integrity Assay kit (Promega, Madison, WI). A 100 μl sample of each culture supernatant was collected and added into to a 96-well plate. An equal volume of CytoTox-One Reagent was added and incubated for 10 min. Fifty μl of Stop Solution was added and the sample fluorescence was measured on a fluorescence microplate reader (SPECTRA max GEMINI XPS, Molecular Devices, Carlsbad, CA) using a wavelength of 560 nm/590 nm for excitation/emission. The original culture medium before the serum concentration was changed served as a pre-treatment control sample and the control value was subtracted from the value obtained after incubation with the medium containing different concentrations of serum.

Cell proliferation assay

The cell proliferation was examined using the CyQUANTR Cell Proliferation Assay Kit (Life Technologies, Carlsbad, CA). Cells were seeded into 96 well plates at a density of 2 imes 10 3 cells per well with DMEM/HAM/20% FBS. After 24 h, the culture medium was removed and changed to fresh DMEM/HAM without serum, or with FBS, PRP or PPP. After 3 days, the microplates were gently inverted and blotted onto paper towels to remove the medium from the wells. The microplates were then frozen and stored at -80°C and thawed at room temperature prior to analysis. CyQUANT GR dye/cell-lysis buffer was added to each well. Cells were incubated at room temperature for 5 min and the sample fluorescence was measured on a fluorescence microplate reader (SPECTRA max GEMINI XPS, Molecular Devices) using wavelength of 480 nm/520 nm for excitation/ emission

Induction of apoptosis, and the annexin V binding and caspase 3 activity assays

The cells were seeded into 10 cm dishes at a density of 1 \times 10⁶ cells per well with DMEM/HAM/20%FBS. After 24 h, the culture medium was removed and changed to fresh DMEM/HAM with 2% FBS, 2% PRP or 2%PPP. After 2 h, apoptosis was induced by the addition of 100 ng/ml TNF- α (Peprotech, Rocky Hill, NJ) and 100 µg/ml cycloheximide (CHX, Sigma-Aldrich). After 3 h, the culture supernatant was collected, and the cells were detached by TrypZean treatment. The detached cells were suspended in the collected culture supernatant. Subsequently, the cells were stained with Annexin V-FITC using a TaliTM Apoptosis kit (Life Technologies). Stained cells were analyzed by a Tali™ Image Based Cytometer (Life technologies). Cell lysates at the concentration of 1×10^4 cells/µl were prepared from the cells treated to induce apoptosis, and the caspase 3 activity levels were measured by a caspase-3/CPP32 Fluorometric Assay Kit (Biovision, Mountain View, CA). To examine the phosphorylation status of ERK1/2, the cells were scraped off at each time point in PBS and washed. The cells were pelleted and lysed by RIPA buffer (Wako Pure Chemical Industries, Ltd. Osaka, Japan), and the protein concentration was determined by Quant-iT Protein Assay Kit (Life technologies), and 5 μg of protein were analyzed by Western blotting using anti-ERK1 and anti-ERK1/2 (pT202/pY204) as primary antibodies (BD Biosciences, Franklin Lakes, NJ). Mouse TrueBlot ULTRA HRP-conjugated Anti-Mouse IgG (eBioscience, Inc. San Diego, CA) was used as a secondary antibody, and the signals were detected by SuperSignal® West Femto Maximum Sensitivity Substrate (Thermo Fisher Scientific Inc.) with LAS1000 apparatus (FUJI film, Tokyo, Japan). ERK signals were normalized using Actin signals detected by Anti-Actin monoclonal antibody (clone AC-40, Sigma-Aldrich).

Gene expression analysis

Cells (2.5×10^5 cells) were seeded into 10 cm dish with DMEM/HAM/20% FBS and cultured for 16 h. The culture medium was changed to fresh DMEM/HAM supplemented with 2% FBS or 2% PRP, and the cells were further incubated for 72 h. The total RNA from cultured cells was extracted using a RT² RNA Isolation Kit (SA Bioscience, Frederick, MD). Complementary DNA was generated from 1 μg of total RNA using the RT 2 First Strand Kit. An Apoptosis Reverse Transcriptase RT² profiler PCR array and RT2 Real-Time SYBR Green/ROX PCR Mix (SA Bioscience, Frederick, MD) were used to identify the genes affected by PRP according to manufacturer's instruction. The data were analyzed by web-based data analysis software provided by the manufacturer. The probe and primer sets used to quantify the mRNA for the DAPK1 and BIM genes were purchased from Applied Biosystems (Life Technologies). The quantification of given genes was expressed as the relative mRNA level compared with a control after normalization to 18S RNA. All the real-time PCR were performed using an ABI 7500 real-time PCR apparatus.

Statistical analysis

The data are presented as the means \pm S.D. Statistical comparisons were made by Student's t-test or an ANOVA followed by the post-hoc Tukey test using the SPSS software program. In all cases, P-values < 0.05 were considered to be significant.

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Arteriosclerosis, Thrombosis, and Vascular Biology



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Liver-Specific Deletion of 3-Hydroxy-3-Methylglutaryl Coenzyme A Reductase Causes Hepatic Steatosis and Death

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Liver-Specific Deletion of 3-Hydroxy-3-Methylglutaryl Coenzyme A Reductase Causes Hepatic Steatosis and Death

Shuichi Nagashima, Hiroaki Yagyu, Ken Ohashi, Fumiko Tazoe, Manabu Takahashi, Taichi Ohshiro, Tumenbayar Bayasgalan, Kenta Okada, Motohiro Sekiya, Jun-ichi Osuga, Shun Ishibashi

Objective—3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGCR) catalyzes the rate-limiting step in cholesterol biosynthesis and has proven to be an effective target of lipid-lowering drugs, statins. The aim of this study was to understand the role of hepatic HMGCR in vivo.

Methods and Results—To disrupt the HMGCR gene in liver, we generated mice homozygous for a floxed HMGCR allele and heterozygous for a transgene encoding Cre recombinase under the control of the albumin promoter (liver-specific HMGCR knockout mice). Ninety-six percent of male and 71% of female mice died by 6 weeks of age, probably as a result of liver failure or hypoglycemia. At 5 weeks of age, liver-specific HMGCR knockout mice showed severe hepatic steatosis with apoptotic cells, hypercholesterolemia, and hypoglycemia. The hepatic steatosis and death were completely reversed by providing the animals with mevalonate, indicating its essential role in normal liver function. There was a modest decrease in hepatic cholesterol synthesis in liver-specific HMGCR knockout mice. Instead, they showed a robust increase in the fatty acid synthesis, independent of sterol regulatory element binding protein-1c.

Conclusion—Hepatocyte HMGCR is essential for the survival of mice, and its abrogation elicits hepatic steatosis with jaundice and hypoglycemia. (Arterioscler Thromb Vasc Biol. 2012;32:1824-1831.)

Key Words: cholesterol ■ liver ■ 3-hydroxy-3-methylglutaryl coenzyme A ■ fatty acids ■ knockout mouse

The mevalonate pathway produces isoprenoids that are essential for the diverse cellular functions ranging from cholesterol synthesis to growth control. The enzyme 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR) (EC 1.1.1.34), which catalyzes the conversion of HMG-coenzyme A to mevalonate, is the rate-limiting enzyme in the mevalonate pathway.1 Mammalian HMGCR is an integral high-mannose glycoprotein of the endoplasmic reticulum (ER).2 Structurally, it is divided into 2 major domains: a C-terminal cytosolfacing domain that tetramerizes to form the active site and an N-terminal hydrophobic region that spans the ER membrane 8× and bears a single N-glycan. This membrane region is dispensable for the enzymatic activity but necessary for the metabolically controlled stability of the enzyme and sufficient to cause sterol-accelerated degradation of heterologous proteins. Within this region, transmembrane spans 2 through 6 bear significant sequence homology to the corresponding transmembrane spans of sterol regulatory element binding protein (SREBP) cleavage-activating protein (SCAP).³

To ensure a steady supply of mevalonate, the nonsterol and sterol end products of the mevalonate metabolism exert feedback regulatory effects on the activity of this enzyme through multivalent mechanisms, including inhibition of the transcription of its RNA, blocking of translation, and acceleration of the

protein's degradation by a mechanism called ER-associated degradation, thereby regulating the amount of protein over a several hundred-fold range. ER-associated degradation of HMGCR requires the binding of Insig-1 to the sterol-sensing domain.⁴ Despite the critical role of HMGCR in cholesterol biosynthesis, little is known about its relevance to diseases. Only recently, HMGCR has been identified as a determinant of plasma cholesterol levels.⁵

Inhibitors of HMGCR, statins, are potent cholesterollowering agents that have been widely used to prevent the occurrence of coronary heart disease and other atherosclerotic diseases.6 The atheroprotective properties of statins are primarily because of the potent low-density lipoprotein (LDL)cholesterol-lowering effect. 7 Statins have also been reported to exert cholesterol-independent, or so-called pleiotropic, effects that involve improving endothelial function and decreasing oxidative stress and vascular inflammation.8 The benefits of statins extend beyond cardiovascular diseases and include a reduction in the risk of dementia, Alzheimer disease, ischemic stroke, osteoporosis, tumor growth, and viral infection. Most of these pleiotropic effects are mediated by an ability to block the synthesis of nonsterol isoprenoid intermediates. Statins have toxic effects in only a limited number of patients and are generally considered safe.

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To establish an animal model for investigating the mechanisms behind the effects, including toxicity of statins, we have generated HMGCR knockout (KO) mice lacking the enzyme throughout their bodies. These mice die in a relatively early stage of embryonic development (ie, before E8.5). Because mice lacking squalene synthase, the first committed enzyme in the sterol pathway, die in the embryonic stage with apparent anomalies of the development of the central nervous system, we took advantage of the tissue-specific gene targeting using the Cre-loxP system to generate mice lacking HMGCR in a liver-specific manner.

Materials and Methods

Liver-specific HMGCRKO (L-HMGCRKO) mice were generated by cross-breeding heterozygous floxed HMGCR (referred to as HMGCR+ff; f denotes floxed) mice with transgenic mice expressing Cre recombinase under the control of albumin gene promoter (Alb-Cre). 11.12 All animal experiments were performed with the approval of the Institutional Animal Care and Research Advisory Committee at Jichi Medical University. For detailed protocols for the generation of L-HMGCRKO mice and other experimental procedures, please refer to the online-only Data Supplement.

Results

Because there were no differences in growth curves or metabolic parameters, such as plasma lipid and glucose levels, among the HMGCR**/+ (wild-type), HMGCR**/+ Alb-Cre (CRE), and HMGCR*/f (fHMGCR) mice, we used fHMGCR mice as a control. To determine whether the expression of the HMGCR gene was abrogated in the liver, we performed a Southern blot (Figure 1A), Northern blot (Figure 1B), and real-time polymerase chain reaction (Figure 1C). The Southern blot

analysis shows that only the 6.3-kb wild-type allele and 7.7kb floxed allele were observed in the DNA from liver in wildtype and fHMGCR mice, respectively. In L-HMGCRKO mice at 3 weeks, the liver contained predominantly the 12.0-kb KO allele (70% based on PhosphorImager analysis [BAS 200, Fujifilm, Tokyo, Japan]) and some residual floxed allele (30%). The mRNA expression of HMGCR in the liver of L-HMGCRKO mice was decreased to 30% of the fHMGCR mice at 3 weeks of age and to <10% at 4 and 5 weeks upon Northern blot analysis. The time-dependent abrogation of the mRNA expression of HMGCR was also confirmed by realtime polymerase chain reaction. Based on this method, the mRNA levels were decreased to only 2% of the fHMGCR mice at 4 and 5 weeks, although there were no significant differences in other organs (Figure IIA in the online-only Data Supplement). Immunoblot analysis showed that the amount of HMGCR protein in the liver of L-HMGCRKO mice was 15% of that in fHMGCR mice (Figure 1D). Despite the profound reduction in HMGCR at both the mRNA and protein levels, the HMGCR activity in the liver of L-HMGCRKO mice was decreased by only 44% compared with that in fHMGCR mice (Figure 1E). To determine whether HMGCR is specifically abrogated in the liver parenchymal cells of L-HMGCRKO mice, we separated parenchymal and nonparenchymal cells from the liver at 3 weeks of age by density-gradient centrifugation after liver perfusion with collagenase. The mRNA expression of HMGCR in the parenchymal cells of L-HMGCRKO mice was decreased by 70.6% compared with that in fHMGCR mice, whereas the mRNA expression of HMGCR in the nonparenchymal cells was not different between the fHMGCR and L-HMGCRKO mice at 3 weeks of age (Figure IIC in the

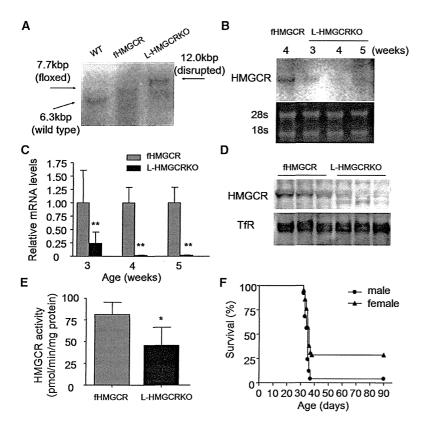


Figure 1. Conditional deletion of the 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR) gene in mice and their survival. A. Southern blot analysis of BamHI-digested DNA from the livers of wild-type (WT) floxed HMGCR (fHMGCR) and liver-specific HMGCR knockout (L-HMGCRKO) mice at 3 weeks of age as described in the online-only Data Supplement. B, Northern blot analysis of hepatic RNA from the livers of fHMGCR and L-HMGCRKO mice at 3, 4, and 5 weeks of age. Aliquots (20 µg) of total RNA from liver were subjected to electrophoresis and blot hybridization with 32P-labeled cDNA probes for mouse HMGCR as described in the online-only Data Supplement. C, Quantitative real-time polymerase chain reaction of HMGCR mRNA levels from the livers of mice indicated in B (n=5 in each group). D, Immunoblot analysis of HMGCR protein from the livers of control and L-HMGCRKO mice at 4 weeks of age (n=3 in each group). Aliquots (50 µg) of liver membrane fractions were subjected to SDS-PAGE and immunoblot analysis. The membrane protein transferrin receptor was used as a loading control. E, HMGCR activity in the liver microsomal fractions of fHMGCR and L-HMGCRKO mice at 4 weeks of age (n=5 in each group). F, The survival curves were generated by the Kaplan-Meier method, and differences among the survival rates were compared using the χ^2 method. Male (n=25) and female (n=42) L-HMGCRKO mice were followed for >100 days. Each value represents mean±SD. Significant differences compared with control mice: *P<0.05 and **P<0.001.

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Table. Liver Weight and Plasma Parameters of Control and L-HMGCRKO Mice

| Age (wks) | 3 | | 4 | | 5 | |
|-----------------------------------|--------------|-----------------|-----------------|-----------------|--------------|-----------------|
| Genotype | fHMGCR (n=5) | L-HMGCRKO (n=5) | fHMGCR (n=9) | L-HMGCRKO (n=7) | fHMGCR (n=6) | L-HMGCRKO (n=5) |
| Body weight (g) | 10.6±1.3 | 11.7±1.5 | 17.2±1.3 | 15.5±0.8* | 21.7±2.0 | 13.5±0.8*** |
| Liver weight (g) | 0.47±0.11 | 0.51±0.11 | 0.78±0.14 | 0.92±0.13 | 1.08±0.11 | 1.17±0.28 |
| Liver/body weight (%) | 4.4±0.4 | 4.2±0.4 | 4.4±0.4 | 6.1±0.8* | 5.0±0.12 | 8.7±2.1** |
| Total cholesterol (mg/dL) | 63.6±9.1 | 47.1±1.0** | 66.5±11.1 | 46.7±13.2** | 64.6±6.8 | 282.6±72.6*** |
| Free cholesterol (mg/dL) | 26.2±4.0 | 20.1±0.5* | 33.3±5.5 | 24.6±13.5 | 33.1±2.7 | 263.0±72.6*** |
| Cholesterol ester (mg/dL) | 37.4±5.5 | 27.0±1.4* | 33.1±5.7 | 22.1±4.6* | 31.5±4.9 | 19.6±10.3 |
| Triglyceride (mg/dL) | 62.5±13.3 | 51.1±9.9 | 78.5±25.4 | 24.9±6.9*** | 92.5±31.1 | 27.7±9.4** |
| Free fatty acids (mmol/L) | 0.34±0.10 | 0.40±0.06 | 0.63±0.20 | 0.51±0.19 | 0.55±0.09 | 1.70±0.92* |
| Phospholipids (mg/dL) | 132.2±20.2 | 106±2.7* | 143.5±22.8 | 117.3±31.7 | 150.9±12.3 | 601.1±133.5** |
| Aspartate aminotransferase (IU/L) | 76.1±10.2 | 95.7±45.5 | 92.7±39.3 | 343.1±602.8 | 55.9±18.6 | 1178.5±182.1*** |
| Alanine transaminase (IU/L) | 35.1±12.1 | 61.9±46.7 | 20.7±17.5 | 54.2±101.7 | 13.1±4.6 | 878.8±357.6** |
| Total bilirubin (mg/dL) | 0.31±0.09 | 0.31±0.09 | 0.30 ± 0.08 | 0.36±0.29 | 0.33±0.19 | 3.25±1.69* |
| Blood glucose (mg/dL) | 110.6±16.7 | 123.0±15.5 | 115.9±13.7 | 99.6±16.7 | 135.7±9.4 | 48.3±23.3* |

Blood samples were taken from male mice fed a normal chow diet ad libitum before the study. Each value represents the mean±SD. Significant differences compared with control mice: *P<0.05, **P<0.01, and ***P<0.001. HMGCR indicates 3-hydroxy-3-methylglutaryl-coenzyme A reductase; L-HMGCRKO, liver-specific HMGCR knockout mice; fHMGCR, floxed HMGCR.

online-only Data Supplement). HMGCR activity in the parenchymal cells of L-HMGCRKO mice was decreased by only 47% compared with that in fHMGCR mice (Figure IID in the online-only Data Supplement). The relative decreases in the mRNA and activity of HMGCR in the parencymal cells were similar to those observed in the whole liver of L-HMGCRKO mice (Figure 1C and E), supporting that HMGCR gene was specifically abrogated in the parenchymal cells of the liver and that there was no compensatory upregulation of HMGCR in the nonparenchymal cells of the L-HMGCRKO mice.

L-HMGCRKO mice were born at a rate in accordance with the rule of Mendelian inheritance. However, 96% of males died with a median survival time of 35 days, whereas 71% of females died with a median survival time of 36 days (Figure 1F), and the rest of them survived until 12 months of age. Therefore, the survival rate of females was significantly higher than males (P=0.025). The mRNA expression levels of HMGCR in the liver from the surviving HMGCRKO mice were as high as those from fHMGCR mice (Figure IIB in the online-only Data Supplement). Next, we compared body weight, liver weight, plasma lipid levels, liver functions, and blood glucose levels between fHMGCR and L-HMGCRKO mice (Table). Although the body weight of L-HMGCRKO mice was not different from that of fHMGCR mice at 3 weeks of age, it decreased by 10% at 4 weeks and by 38% at 5 weeks of age. Liver weight did not differ between the 2 groups. However, the ratio of liver weight to body weight was increased by 39% and 74% at 4 and 5 weeks of age, respectively. The livers of L-HMGCRKO mice were enlarged, paler, and whiter than those of fHMGCR mice at 5 weeks of age (Figure 2A and 2B). Consistent with the macroscopic abnormalities of the liver, plasma levels of aspartate aminotransferase, alanine transaminase, and bilirubin were markedly increased in the L-HMGCRKO mice compared with fHMGCR mice at 5 weeks of age. Total cholesterol levels in the plasma were decreased in the L-HMGCRKO mice by 26% at 3 weeks of age (Table). In parallel, plasma concentrations of LDL cholesterol and apolipoprotein (apo) B-100 protein were decreased (Figure IIIA and IIIE in the online-only Data Supplement). Despite the liver failure of L-HMGCRKO mice at 5 weeks of age, the plasma levels of cholesterol, free cholesterol, and phospholipids were increased 4.3-, 7.9-, and 4.0-fold, respectively. On the other hand, plasma cholesterol ester levels were decreased by 38% (Table). Therefore, calculated ratios of free cholesterol to cholesterol ester were increased 13-fold. Most of the increased cholesterol was distributed in the size of very low-density lipoprotein through LDL (Figure IIIC in the online-only Data Supplement). Although apoB-100 levels were decreased, apoB-48 levels were substantially increased in the plasma of L-HMGCRKO mice at 5 weeks of age (Figure IIIG in the online-only Data Supplement). These findings together with the results of agar gel electrophoresis of the plasma (Figure III-I in the online-only Data Supplement) strongly indicate that both lipoprotein X and apoB-48-containing lipoproteins were increased in the L-HMGCRKO mice. Hepatic LDL receptor protein levels were not altered between fHMGCR and L-HMGCRKO mice at 3 and 5 weeks of age (Figure IIIF and IIIH in the online-only Data Supplement), despite increased hepatic LDL receptor mRNA levels (Figure 4A). Plasma lipoprotein changes in L-HMGCRKO mice may not be influenced by LDL receptor protein levels. Plasma free fatty acid levels were also increased 3.1-fold at 5 weeks. In contrast, plasma triglyceride levels were decreased by 69% and 70% at 4 and 5 weeks of age, respectively. It is of note that L-HMRCRKO mice were moderately hypoglycemic at 5 weeks.

To determine the causes of the liver dysfunction associated with hepatomegaly, we performed a microscopic analysis of the liver (Figure 2). Hematoxylin and eosin staining revealed moderate to severe ballooning and unicellular necrosis of parenchymal cells at 5 weeks (Figure 2C and 2D). Oil-red O staining showed moderate to severe microvesicular steatosis of the parenchymal cells (Figure 2E and 2F). TdT-mediated dUTP-nick end labeling-positive (Figure 2G, 2H, and 2M) and Ki-67-positive parenchymal cells

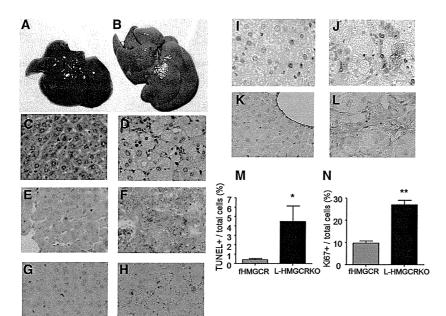


Figure 2. Gross appearance and histological analysis of the livers in male mice at 5 weeks. Gross appearance of the liver from control (A) and liver-specific HMGCR knockout (L-HMGCRKO) mice (B). Hematoxylin and eosin-stained liver sections from control (C) and L-HMGCRKO (D) mice. Frozen sections of liver stained with oil-red O from control (E) and L-HMGCRKO (F) mice. TdT-mediated dUTP-nick end labeling (TUNEL)-stained liver sections from control (G) and L-HMGCRKO (H) mice. Ki-67-stained liver sections from control (I) and L-HMGCRKO (J) mice. Type 4 collagen-stained liver sections from control (K) and L-HMGCRKO (L) mice. Bar graph shows the percentages of TUNEL-positive cells (M) and Ki-67-positive cells (N) relative to the total number of cells. Each value represents mean±SD. Significant differences compared with control mice: *P<0.01 and **P<0.001.

(Figure 2I, 2J, and 2N) were significantly increased 11- and 2.8fold in the liver of L-HMGCRKO mice compared with that in fHMGCR mice, respectively. The liver of L-HMGCRKO mice contained increased amounts of type 4 collagen (Figure 2K and 2L). Caspase 3 activity in the liver of L-HMGCRKO mice was also increased 1.8-fold compared with that of fHMGCR (Figure VA in the online-only Data Supplement). The mRNA levels of C/EBP-homologous protein were also significantly increased (Figure VD in the online-only Data Supplement). However, no significant differences were observed in either caspase 8 activity or H₂O₂ contents in the liver (Figure VB and VC in the online-only Data Supplement). The pathology of the liver from L-HMGCRKO mice at 4 weeks was milder (Figure IVB in the online-only Data Supplement) than that at 5 weeks. The liver of the mice which survived the lethal period still had hepatocyte ballooning (Figure IVD in the online-only Data Supplement).

To determine whether the liver-specific abrogation of HMGCR affected cholesterol metabolism in the liver, we measured the hepatic levels of cholesterol and triglycerides (Figure 3). The hepatic cholesterol content was decreased by only 22% in the L-HMGCRKO mice compared with the fHMGCR mice (Figure 3A). Unexpectedly, the hepatic contents of triglyceride were increased 2-fold (Figure 3B). These results indicate that the neutral lipids stained with oil-red O in the liver were primarily triglycerides. The reduction in the cholesterol contents of the liver was smaller than expected. We measured cholesterol synthesis in liver slices in culture (Figure 3C). The cholesterol synthesis was reduced by 45%. This reduction paralleled the degree of reduction in HMGCR activity in the liver (Figure 1E). We also measured the amounts of fatty acids synthesized in the liver (Figure 3D). Surprisingly, the synthesis of fatty acids from acetate was markedly increased 17-fold in the liver of L-HMGCRKO mice. Although total amounts of fatty acids were not different between the 2 mice (Figure 3E), the following fatty acid species were significantly increased in the liver of L-HMGCRKO mice: C18:0, C18:1n-9, C20:1n-9,

C20:3n–9, and C22:4n–6 (Figure 3F). Given the increased production of fatty acids and triglycerides in the liver, we measured other metabolites of fatty acids such as diglycerides and ceramides. The hepatic levels of diglycerides were increased 1.8-fold (Figure 3G), but those of ceramides were not increased significantly (Figure 3H).

To clarify the mechanisms behind the changes in fatty acid metabolism, we determined the changes in the levels of mRNA expression in various genes involved in cholesterol or fatty acid metabolism in the liver at 4 weeks of age by real-time polymerase chain reaction (Figure 4A). As to the genes involved in cholesterol metabolism, the mRNA levels of SREBP2, LDL receptor, proprotein convertase subtilisin/kexin type 9, and squalene synthase were increased 1.4-, 1.9-, 2.8-, and 3.9-fold, respectively. On the other hand, the mRNA levels of cholesterol 7α -hydroxylase, a rate-limiting enzyme for bile acid synthesis, were decreased by 60%. With regard to the genes involved in fatty acid metabolism, the mRNA levels of fatty acid synthase (FAS), acetyl-CoA carboxylase, and stearoyl-CoA desaturase 2 were increased 2.4-, 1.4-, and 22-fold, respectively. On the other hand, the mRNA expression of SREBP1c and acyl CoA:diacylglycerol acyltransferase 2 was decreased by 80% and 40%, respectively. There were no changes in either the mRNA expression of SREBP1a, a splice variant of SREBP1c, or liver X receptor α (LXR α), an important transcriptional activator of the SREBP1c gene. The mRNA expression of peroxisome proliferator–activated receptor α , a transcription regulator of genes for fatty acid oxidation, was not changed.

HMGCR catalyzes the formation of mevalonate, which is used as a substrate for the synthesis not only of cholesterol but also nonsterols such as isoprenoids, ubiquinone, heme A, and dolichol. To test the notion that death, likely because of severe liver failure, was caused by the alteration of a nonsterol pathway, we evaluated the isoprenylation of small GTP-binding proteins such as H-Ras and Rac1 by measuring the amount of membrane-bound forms (Figure 4B). The ratio of the

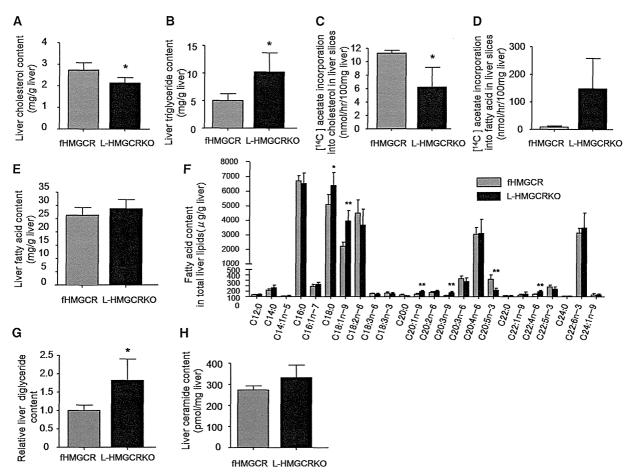


Figure 3. Hepatic lipid contents and lipid synthesis in the control and liver-specific HMGCR knockout (L-HMGCRKO) male mice. Hepatic total cholesterol (A), triglyceride (B), fatty acid levels (E), and fatty acid composition in total liver lipids (F) were determined in the livers from control and L-HMGCRKO mice at 4 weeks of age (n=5 in each group). C and D, In vitro hepatic lipid synthesis rate using the liver slices in culture (n=3 in control and n=4 in L-HMGCRKO). Liver slices (≈100 mg) were incubated with ¹⁴C-labeled acetate (8 mmol/L, 0.1 μCi/μπol) for 90 minutes. After incubation, the slices were removed for measurement of ¹⁴C-labeled cholesterol (C) and fatty acids (D). Hepatic diglyceride (G) and ceramide (H) contents were measured in the livers of control and L-HMGCRKO mice at 4 weeks of age (n=5 in each group) by the diglyceride kinase method as described in the online-only Data Supplement. Each value represents mean±SD. Significant differences compared with control mice: *P<0.05 and **P<0.01.

membrane-bound form to the cytosolic form of H-Ras or Rac1 was decreased to 0.05 to 0.2 compared with control. These results indicate that the deficiency of HMGCR affected the nonsterol pathway more severely than the sterol pathway. We also estimated changes in intracellular signaling molecules (Figure 4C). p-Akt and c-Met were decreased by 72% and 81%, respectively, whereas phospho-signal transducer and activator of transcription 3 was increased 7.6-fold.

If the lethal phenotype of HMGCR deficiency is because of the deficiency of mevalonate, supplementation with mevalonate could theoretically rescue the lethal phenotype. In fact, providing the male mice with water containing mevalonate significantly attenuated the liver dysfunction and hypercholesterolemia (Figure 5A–5C). The pathological abnormalities observed in the male L-HMGCRKO mice were almost normalized by the supplementation with mevalonate (Figure 5D–5G). Consistently, the amounts of the membrane-bound form of H-Ras or Rac 1 were restored to normal levels (Figure 5H). Similar improvements were found in female L-HMGCRKO

mice (data not shown). No death occurred until 40 days of age in L-HMGCRKO mice supplemented with mevalonate.

Because L-HMGCRKO mice were hypoglycemic (Table), it is possible that hypoglycemia is the direct cause of death. To test this hypothesis, we allowed mice free access to drinking water containing 20% (w/v) glucose. Glucose feeding significantly increased plasma glucose levels $(43.5\pm16.2\,\text{mg/dL} [\text{n=}10] \text{ versus } 79.5\pm40.6\,\text{mg/dL} [\text{n=}13] [P=0.01] \text{ in males}; 36.6\pm13.3\,\text{mg/dL} [\text{n=}4] \text{ versus } 65.2\pm35.6\,\text{mg/dL} [\text{n=}11] [P=0.04] \text{ in females})$. Concurrently, it dramatically improved the mortality of L-HMGCRKO mice (96% versus 13% in males and 71% versus 15% in females) (Figure VI in the online-only Data Supplement).

Discussion

Nearly all the male L-HMGCRKO mice died before 40 days of age, whereas 30% of females survived until 12 months of age. Before their death, the mice developed severe hepatic damage with hepatomegaly, steatosis, and hypoglycemia. Thus, we ascribe the lethal effect of the liver-specific deficiency of HMGCR