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Phosphodiesterase 3B Is Localized in Caveolae and Smooth ER in Mouse Hepatocytes and Is Important in the Regulation of Glucose and Lipid Metabolism

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Abstract

Cyclic nucleotide phosphodiesterases (PDEs) are important regulators of signal transduction processes mediated by cAMP and cGMP. One PDE family member, PDE3B, plays an important role in the regulation of a variety of metabolic processes such as lipolysis and insulin secretion. In this study, the cellular localization and the role of PDE3B in the regulation of triglyceride, cholesterol and glucose metabolism in hepatocytes were investigated. PDE3B was identified in caveolae, specific regions in the plasma membrane, and smooth endoplasmic reticulum. In caveolin-1 knock out mice, which lack caveolae, the amount of PDE3B protein and activity were reduced indicating a role of caveolin-1/caveolae in the stabilization of enzyme protein. Hepatocytes from PDE3B knock out mice displayed increased glucose, triglyceride and cholesterol levels, which was associated with increased expression of gluconeogenic and lipogenic genes/enzymes including, phosphoenolpyruvate carboxykinase, peroxisome proliferator-activated receptor γ, sterol regulatory element-binding protein 1c and hydroxyl-3-methylglutaryl coenzyme A reductase. In conclusion, hepatocyte PDE3B is localized in caveolae and smooth endoplasmic reticulum and plays important roles in the regulation of glucose, triglyceride and cholesterol metabolism. Dysregulation of PDE3B could have a role in the development of fatty liver, a condition highly relevant in the context of type 2 diabetes.

Introduction

Cyclic nucleotide phosphodiesterases (PDEs) are important regulators of signal transduction processes mediated by cAMP and cGMP. The PDE family contains eleven structurally related and functionally distinct subfamilies (PDE1-11) that differ in their primary structures, affinities for cAMP and cGMP, responses to specific effectors and inhibitors, as well as mechanisms through which they are regulated [1]. PDE3 isoforms are encoded by two similarly organized genes, PDE3A and PDE3B. These enzymes hydrolyze cAMP and cGMP with high affinity in a mutually competitive manner and are inhibited by compounds such as cilostamide, cilastazol and milrinone [2,3]. The structural organization of PDE3A and PDE3B proteins is identical with the catalytic domain found in all PDEs located in the C-terminal portions of the molecules [2,3]. The catalytic domains of PDE3A and B are highly conserved, except for an insertion of 44 unique amino acids that is not found in the catalytic domains of other PDE families and that also differs in, and thus distinguishes, PDE3A and B isoforms [2,3]. Their N-terminal regulatory domains are quite divergent, consisting of two hydrophobic regions important for membrane association of these enzymes. Full-length PDE3s (Mw 135 kDa) are found in association with membranes; smaller PDE3A forms are found in cytosolic fractions [4]. Furthermore, PDE3B has been shown to be localized to the endoplasmic reticulum (ER) and to specific detergent-resistant parts of the plasma membrane, caveolae [5,6]. Caveolae are special forms of lipid rafts observed as small flask-shaped 50–100 nM invaginations of the plasma membranes and are particularly abundant in adipocytes. They have a high content of sphingolipids, cholesterol and are stabilized by one or more isoforms of caveolin. Caveolae are believed to be important in the organization of signal transduction events, particularly insulin and cAMP signalling [7]. The exact intracellular location of the hepatocyte PDE3B has not been elucidated. The N-terminal region of PDE3B contains regulatory phosphorylation sites [2,3]. Multisite phosphorylation of PDE3s has, for example, been demonstrated in adipocytes, hepatocytes and HeLa cells [8,9] which is believed to be important in the regulation of PDE3 activity and in interaction with other proteins [2,3].
PDE3A and PDE3B exhibit cell-specific differences in expression. PDE3A is highly expressed primarily in the cardiovascular system, for example in platelets, smooth muscle cells and cardiac myocytes [2,3]. PDE3B on the other hand is relatively highly expressed in cells important in energy metabolism, such as white and brown adipocytes, pancreatic β-cells and liver [2,3] indicating a role for this enzyme in the regulation of metabolism.

Recent results from PDE3B transgenic mouse models do indicate that PDE3B plays an important role in overall regulation of energy metabolism [10,11]. For example, mice that specifically overexpress PDE3B in pancreatic β-cells demonstrate glucose intolerance and impaired insulin response to glucose and glucagon-like peptide-1 (GLP-1) [10]. The phenotype of PDE3B knock out (KO) mice is complex. Hence, on one hand PDE3B KO mice are lean and have improved insulin secretion but they also exhibit glucose intolerance, insulin resistance and increased lipolysis [11]. The role of hepatocyte PDE3B in the regulation of lipid and glucose metabolism remains unknown. However, clamp studies in PDE3B KO mice show increased glucose production and reduced ability of insulin to suppress glucose production indicating multiple roles for this enzyme in hepatocytes [11].

In this study we demonstrate that, in hepatocytes, PDE3B is localized to caveolae and smooth ER and that the enzyme has an important role in the regulation of triglyceride, cholesterol and glucose metabolism in these cells.

**Materials and Methods**

**Ethics statement**

All animals were handled in strict accordance with good animal practice as defined by the national and local animal welfare bodies, and all animal work was approved by the Ethics Committee at Lund University, Lund, Sweden.

**Materials**

C57BL/6 male mice were purchased from Taconic (Skensved, Denmark). Caveolin-1 KO mice on the C57BL/6 background, obtained from the Jackson Laboratory (Bar Harbor, Maine, USA), were further backcrossed on the same background and genotyped as described by Razani et al [12]. PDE3B deficient mice were generated and characterized as previously described in [11] (a fragment containing exon 1 of the mouse Pde3b gene was cloned into the pBluescript and used to construct the targeting vector).

Antibodies against caveolin-1 (rabbit polyclonal) and adenyl cyclase (AC) V were obtained from Santa Cruz Biotechnology (Santa Cruz, CA, USA); flotillin-1, Na+K+-ATPase, nucelopin p62 and BiP from BD Transduction Laboratories. Antibodies against phosphoenolpyruvate carboxylase [PEPCK (PCK1)] were obtained from Abgent (San Diego, CA, USA). Anti-PDE3B antibodies used for immunoblot analysis were raised in rabbits against the peptide CQGGYGSGKMFRRPSPLP and affinity purified. For electron microscopy affinity purified antibodies against the C-terminal (CT) part of PDE3B were generated in rabbit using the peptide NASLQDAEIQVIEEA. As secondary antibody, HRP-goat anti-rabbit antibody (BioSource, Invitrogen, Carlsbad, CA, USA) was used. If not otherwise stated, reagents and chemicals were obtained from Sigma-Aldrich (Stockholm, Sweden).

**Subcellular fractionation**

Hepatocyte subcellular fractions were prepared according to Fleisher and Kervina [13] with a few modifications based on a study by Tuma et al [14]. Isolated and washed hepatocytes (35–100 x 10⁶ cells) from C57BL/6 mice or washed whole livers from 10–12 weeks old caveolin-1 KO and wild type (WT) mice were homogenized with a Dounce homogenizer (10–15 strokes) in 10 ml buffer A (10 mM HEPES pH 7.5, 0.25 M sucrose, 1 mM EDTA, 1 mM NaF, 0.2 mM sodium orthovanadate, 1 μg/ml pepstatin A, 10 μg/ml leupeptin and 10 μg/ml antipain). The homogenate was centrifuged (280 xg, 5 min). The supernatant was saved and the pellet rehomogenized in 2.5 ml buffer A and centrifuged as above (280 xg, 5 min). The first and second supernatants were combined and further centrifuged (1 500 xg for 10 min). The resulting supernatant (sup 1) was further centrifuged as described below and the pellet was homogenized in 2 ml buffer B (10 mM Tris pH 7.4, 0.25 M sucrose, 0.5 mM MgCl₂, 3 mM NaF, 0.6 mM sodium orthovanadate, 3 μg/ml pepstatin A, 30 μg/ml leupeptin and 30 μg/ml antipain). The homogenate was supplemented with 6.75 ml of a sucrose rich buffer (2 M sucrose, 10 mM Tris (pH 7–8) and 0.5 mM MgCl₂ in order to yield a final concentration of 1.6 M sucrose. The suspension was transferred into a rotor tube, overlayed with 2 ml buffer B and centrifuged (SW41, 70 900 xg, 70 min). The interphase with plasma membranes was collected and the pellet containing nuclei was rehomogenized in buffer A supplemented with sucrose to a final concentration of 2 M, and centrifuged (70 900 xg, 60 min). The pellet, referred to as the nuclei fraction, was suspended in 1 ml buffer C (50 mM TES pH 7.4, 50 mM sucrose, 1 mM EDTA, 0.1 mM EGTA, 1 μg/ml pepstatin A, 10 μg/ml leupeptin and 10 μg/ml antipain). The interphase containing plasma membranes was resuspended in 6 ml buffer A and centrifuged (1 700 xg, 10 min). The pellet was used for caveolae enrichment as described in the next section, or further purified with regard to the plasma membrane on a 1.45 M sucrose gradient according to Fleisher and Kervina [13]. The purified plasma membrane fraction was finally suspended in 1 ml buffer C. The supernatant from the first centrifugation step (sup 1) was centrifuged twice (8 000 xg, 15 min) to isolate mitochondria. The combined pellets were resuspended in buffer A and centrifuged (25 000 xg, 10 min), the lower brown part of the pellet was resuspended in 1 ml buffer C and is referred to as the mitochondria fraction. The supernatant from the 8 000 xg centrifugation was further centrifuged (124 000 xg, 60 min) and the pellet referred to as internal membranes were suspended in 1 ml buffer C. Each step was performed at 4°C.

**Caveolae enrichment**

Plasma membranes (originating from 50–115 x 10⁶ isolated hepatocytes) prepared as described above were resuspended in 1 ml 0.5 M Na₂CO₃ pH 11 with 1 μg/ml pepstatin A, 10 μg/ml leupeptin and 10 μg/ml antipain and sonicated with a probe-type sonifier (soniprep 150) 3 x 20 sec according to previously well described procedures [15–17]. The sonicated plasma membranes were thereafter placed in the bottom of a tube and mixed with 1 ml 90% sucrose in 25 mM MES and 0.15 M NaCl to yield a final concentration of 250 mM Na₂CO₃ and 45% sucrose. On top of this solution, 4 ml 35% sucrose in 25 mM MES, 0.15 M NaCl and 250 mM Na₂CO₃ pH 11 was added. Finally, 4 ml of 5% sucrose in 25 mM MES, 0.15 M NaCl and 250 mM Na₂CO₃ pH 11 was layered on top. The gradient was centrifuged using a SW41 Beckman rotor at 39 000 xg for 18–19 hrs at 4°C. From the top of the tube, 1 ml fractions were collected. Before measuring PDE3 activity, pH was neutralized (pH 7–8) using approximately 30 μl of 5.0 M HCl per ml sample. Each step was performed at 4°C.

**Preparation of detergent resistant membranes and Superose-6 chromatography**

Isolated mouse hepatocytes (20–100 x 10⁶) were homogenized in 1 ml buffer A and centrifuged (280 xg, 10 min). The supernatant
was further centrifuged (175 000 xg, 40 min) to obtain a pellet containing total membranes. The pellet was homogenized in 1.5 ml of detergent containing buffer, buffer D (25 mM HEPES pH 7.4, 150 mM NaCl, 1 mM EDTA, 10 mM Na3VO4, 1% NP-40, 5 mM NaF, 1 mM PMSE, 1 mM NaN3VO4, 1 μg/ml pepstatin A, 5 μg/ml leupeptin and 5 μg/ml antipain). Half of the homogenized pellet was immediately subjected to centrifugation (10 000 xg for 10 min, 4°C). The supernatant was filtrated (0.2 μm pore size) and thereafter subjected to gel filtration chromatography on a Superose-6 (10/300) column with a separation range of 5–40 000 kDa (Amersham Pharmacia Biotech AB, Uppsala, Sweden) in a fast protein liquid chromatography system. The remaining part of the homogenized pellet from the 175 000 xg centrifugation was incubated for 1 h at 4°C and then re-centrifuged (175 000 xg for 50 min, 4°C). The subsequent supernatant contained solubilized membranes and the pellet detergent resistant membranes (DRM). The pellet was homogenized in 0.75 ml buffer D and thereafter subjected to centrifugation (10 000 xg for 10 min, 4°C). The supernatants containing either solubilized membranes or DRM were filtered (0.2 μm pore size) and thereafter subjected to gel filtration chromatography on a Superose-6 (10/300) column. The column was equilibrated and eluted with buffer D and the flow rate was set to 0.5 ml/min and 0.4 ml fractions were collected. Absorbance at 280 nm was monitored on-line and gel filtration standards (Bio-Rad, Hercules, CA, USA) ranging from 1–670 kDa was used.

**Immunoelectron microscopy**

Livers from C57BL/6 mice were perfused in situ with 50 ml 37°C phosphate buffered saline (PBS) followed by 100 ml 1.5% paraformaldehyde, 0.5% gluteraldehyde in 0.1 M phosphate buffer, pH 7.2. Liver pieces were dissected and left in fixative for 1 h. The tissue pieces were washed in 0.1 M phosphate buffer pH 7.2, dehydrated in gradient ethanol concentrations to 100% ethanol and embedded in Lowicryl HM120 (TAAB, Reading, UK) as previously described [18,19]. Ultrathin sections were cut and placed on gold grids. Sections were blocked with PBS (pH 7.2) containing 0.5% bovine serum albumin (BSA) and incubated over night at 4°C with primary antiserum (PDE3B-CT diluted 1:50 in PBS containing 0.25% BSA and 0.25% Triton X-100) or PBS containing 0.25% BSA and 0.25% Triton X-100 (as negative control). The sections were washed thoroughly in PBS and thereafter incubated for 1 h with gold-conjugated (10 nm diameter gold particles) goat-anti-rabbit IgG (diluted 1:20, Amersham Pharmacia Biotech AB, Uppsala, Sweden) and washed again in PBS. All sections were contrasted with 0.5% lead citrate and 4% uranyl acetate before examination in a Philips CM10 transmission electron microscope.

**PDE-assay**

PDE activity was measured in duplicate in the presence or absence of 3 μM of the specific PDE3 inhibitor OPC3911 [20] (Otsuka Pharmaceuticals Co., Tokyo, Japan), as described previously [10]. The assay was performed at 30°C in a total volume of 300 μl containing 50 mM TES pH 7.4, 250 mM sucrose, 1 mM EDTA, 0.1 mM EGTA, 8.3 mM MgCl2, 0.5 μM cAMP, 1 μCi/ml 3H-cAMP and 0.6 μg/ml ovalbumin.

**Immunoblot analysis**

Different hepatocyte fractions were mixed with Laemmli sample buffer and subjected to SDS-polyacrylamide gel electrophoresis (PAGE) (9–12% acrylamide) before electrophoresis of the proteins to hybond-C extra (Amersham Biosciences, Buckinghamshire, UK) (fractions from subcellular fractionation) or PVDF mem-
frozen in −80°C until use or total RNA was immediately isolated using RNeasy kit (Qiagen, Solna, Sweden). Primers were designed on the basis of the sequences available at the NCBI gene bank and produced by DNA technologies (Aarhus, Denmark). Primer sequences and accession numbers are presented in Table 1. The real-time RT-PCR analyses were performed on a MiniOpticon Thermal Cycler (BioRad, Hercules, CA, USA) and the software MJ Opticon Monitor (BioRad) was used for analysis. SYBR Green I was used as the source of fluorescence and cyclophilin A (CypA) was used as reference gene. The concentration of primers was 400 nM and 250 ng of template was used under the following conditions: 25°C for 5 min, 50°C for 10 min, 95°C for 5 min and then 55 cycles of 94°C for 10 sec, 53°C for 10 sec and 72°C for 1 min. The specificities of the PCR products were confirmed by single dissociation curves. The mRNA expression was calculated using the 2−ΔΔCt-formula and expressed as arbitrary units in relation to cyclophilin A mRNA expression.

Glucose production

Hepatocytes were cultured overnight in 6-well plates, washed twice with PBS, and thereafter incubated in Krebs-Ringer bicarbonate buffer (120 mM NaCl, 5 mM NaHCO3, 5 mM KCl, 1.2 mM KH2PO4, 2.5 mM CaCl2, 1.2 mM MgSO4, 0.2% BSA, 10 mM HEPES, pH 7.2–7.4) supplemented with 5 mM Na-pyruvate and 5 mM Na-lactate as gluconeogenic substrate. The cells were incubated for 4 h after which the culture medium was collected and centrifuged and glucose concentration was determined as protein content using Bradford protein assay.

Hepatocyte triglyceride content

Non-cultured hepatocytes (about 2×10⁶ cells) were homogenized in 200 μl William’s E medium supplemented with Complete protease inhibitor cocktail (Roche, Bromma, Sweden), 5 mM NaF and 1% Triton X-100. The homogenate (25 or 50 μl) was transferred to a glass tube containing 3 ml chloroform/methanol (2:1) solution and stored in a N2 environment at 4°C overnight. Water (1.5 ml) was added and the tubes were centrifuged at 2000×g for 10 min. After removal of the upper layer the wash step was repeated once. The samples were dried under N2 and reuspended in chloroform. Aliquots were transferred into Eppendorf tubes and air-dried. The Thesit (Bio Chemika, Sigma-Aldrich, Stockholm, Sweden; 20%, v/w, in chloroform) was added and thereafter the sample was sonicated in high concentration of Na2CO3 and put on a membrane of isolated mouse hepatocytes. The plasma membranes were extracted with methanol:chloroform (2:1) as described in the section “Hepatocyte triglyceride content”. Lipids were extracted with methanol:chloroform (2:1) as described in the section “Hepatocyte triglyceride content”. Cholesterol levels were determined by measuring the amount of H2O2 produced by cholesterol oxidase using Infinity™ Cholesterol Liquid Stable Reagent (Thermo Electron, Melbourne, Australia). This assay was optimized for measuring cholesterol in tissue samples. Protein was measured using a bicinchoninic acid (BCA) protein reagent kit from Pierce (Rockford, USA).

Statistics

Data are presented as mean±standard error of the mean (SEM) from the indicated number of experiments. Data was analyzed using a two-tailed paired student’s t-test (hepatocyte stimulation and glucose output) or a two-tailed non-parametric Mann-Whitney test (triglyceride and cholesterol content and mRNA expression). Differences with a p<0.05 were considered significant. *p<0.05, **p<0.01 and ***p<0.001.

Results

Hepatocyte PDE3B is distributed in plasma membrane and internal membrane fractions

To examine the intracellular localization of PDE3B in mouse hepatocytes, we performed subcellular fractionation of isolated mouse hepatocytes, as described in Materials and Methods. Subcellular fractions were first analyzed with regard to subcellular markers; Na+K+ -ATPase for plasma membrane, BiP (an ER chaperone) for ER and Nucleoporin p62 (nucl) for the nucleus (Figure 1b). As seen in Figures 1a and 1b, PDE3B was found in the plasma membranes and internal membranes, the latter consisting to a large extent, of ER. According to Figure 1a, the proportion of PDE3B in the plasma membrane and internal membrane fraction is 1:5. When PDE3B activity in subcellular fractions was expressed per mg protein the following results were obtained for plasma membranes, internal membranes, mitochondria and nucleus, respectively: 5.5±1.7, 10.2±3.2, 4.4±1.2 and 2.9±0.83 pmol PDE3B/mg protein (n=3, mean±SEM). The subcellular fractions were also analyzed for the caveolae marker caveolin-1 and the lipid-raft marker flotillin-1. Both these proteins were present selectively in the plasma membrane (Figure 1b). PDE4, another major hepatocyte PDE, was mainly found in the cytosolic fraction (data not shown).

Plasma membrane PDE3B is associated with caveolae in hepatocytes

In order to investigate the possibility that PDE3B is localized to caveolae in hepatocytes, we isolated caveolae from the plasma membrane of isolated mouse hepatocytes. The plasma membranes were sonicated in high concentration of Na2CO3 and put on a

Table 1. Primer sequences used for quantitative real-time RT-PCR.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer fwd</th>
<th>Primer rev</th>
<th>Accession nr</th>
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<tr>
<td>Phosphoenolpyruvate carboxy kinase (PEPCK)</td>
<td>tatcggaggacaggtcaaa</td>
<td>tagatcctagccagtcgctg</td>
<td>NM_011044</td>
</tr>
<tr>
<td>Peroxisome proliferator activated receptor gamma (PPARγ)</td>
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<td>tgaaggctctagctgcttcc</td>
<td>NM_011146</td>
</tr>
<tr>
<td>Hydroxy-3-methylglutaryl coenzyme A reductase (HMGCR)</td>
<td>gcagttcaggaatgctcaga</td>
<td>cggtctacaaaaacccagtcgt</td>
<td>NM_008255</td>
</tr>
<tr>
<td>Sterol regulatory element binding transcription factor 1 (SREBF-1)</td>
<td>ggagccatgtgattgcacatt</td>
<td>ggaagtctgctgtgtgttgatga</td>
<td>NM_011480</td>
</tr>
</tbody>
</table>

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sucrose gradient to separate caveolae and lipid rafts from other components of the plasma membrane fraction. After sucrose gradient fractionation of the sonicated plasma membrane a milky band was detected at the interface of 5 and 35% sucrose. All of the PDE3B activity appeared together with flotillin-1, caveolin-1 and cholesterol in the caveolae/raft enriched fraction (Figures 2a and 2c). This fraction (fraction 6) contained 33% of total proteins whereas factions 7–8 contained 20% and fractions 9–13 contained 42% of total proteins (Figure 2b). When caveolae were enriched from detergent resistant plasma membrane of hepatocytes the same results were obtained (data not shown).

The importance of caveolin-1 for PDE3B expression was studied using caveolin-1 KO mice. The lack of caveolin-1 results in the absence of caveolae [12]. Thus, we isolated plasma membranes from livers from caveolin-1 KO mice and measured the level of PDE3B protein and activity. As seen in Figure 3, PDE3 protein and activity were significantly lower in plasma membranes from the caveolin-1 KO mice compared to WT mice. In total homogenates from caveolin-1 KO mice PDE3 activity was slightly lower (3.88±0.22) compared to WT mice (4.40±0.65) (n = 3, not significant). These results show that caveolin-1 and caveolae are important for determining the amount of PDE3B protein in the plasma membrane of hepatocytes.

To further study the possible association of PDE3B with caveolae, we took advantage of the fact that caveolae are detergent resistant. Total membranes, solubilized membranes and detergent resistant membranes (DRM) were prepared from mouse hepatocytes. The solubilized membranes and DRM fractions were subjected to superose-6 gel filtration chromatography. PDE3 activity in the total membrane fraction (detergent-treated, 10 000 g supernatant) eluted in two peaks, one with a Mw slightly above 670 kDa (elution volume 10–12 ml) and one corresponding to the void volume (7–8 ml) (Figure 4). PDE3 from the solubilized membranes (detergent-treated, 100 000 g supernatant) eluted with the “10–12 ml peak” whereas PDE3 in the DRM (detergent-treated, 100 000 g pellet) eluted primarily with the void volume which may represent PDE3 associated with caveolae and/or lipid rafts.
Basal glucose production is elevated in PDE3B KO mice

PDE3B is associated with smooth endoplasmic reticulum

In order to study PDE3B localization in internal membranes at the ultrastructural level, transmission electron microscopy (TEM) with immunogold labeling for PDE3B was employed. Thorough examination of several liver sections from different mouse livers revealed that the majority of the labeling for PDE3B was localized to smooth ER (Figure 5). In addition, weak PDE3B labeling was detected in rough ER as well as in mitochondria (Figure 5). Plasma membranes displayed weak labeling only (data not shown). Control sections displayed randomly scattered labeling only. Smooth ER has previously been shown to be in close association with glycogen particles [22–24]. As seen in Figure 5, PDE3B is located in close proximity to the glycogen particles which appear as pale areas among the smooth ER.

Basal glucose production is elevated in PDE3B KO mice

Hepatocytes isolated from C57BL/6 mice were cultured over night and thereafter stimulated without or with insulin or glucagon for 15 minutes. Cell homogenates were analyzed for PDE3 activity. As seen in Figure 6a, stimulation of hepatocytes with either insulin or glucagon induced activation of PDE3 by 33 and 45%, respectively, in agreement with previous results from rat hepatocytes [25–26]. Activation of PDE3B by insulin and glucagon has previously been suggested to play a role in hormone-mediated regulation of rat hepatocyte glucose production [27]. Indeed, as shown in Figure 6b, PDE3B KO mouse hepatocytes showed increased glucose production as compared to WT hepatocytes which is in agreement with previously performed clamp studies in these mice [11]. Furthermore, PDE3B KO hepatocytes showed increased mRNA (Figure 6c) and protein levels (Figure 6d) of the key gluconeogenic enzyme phosphoenolpyruvate carboxykinase (PEPCK).

Triglyceride- and cholesterol contents are increased in hepatocytes isolated from PDE3B KO mice

Triglycerides (Figure 7a) and cholesterol (Figure 7b) were analyzed in isolated hepatocytes. Both triglycerides and cholesterol were increased in PDE3B KO hepatocytes. The increments were associated with elevated levels of peroxisome proliferator-activated receptor γ (PPARγ) and sterol regulatory element-binding protein 1c (SREBP1c) mRNAs, both key lipogenic transcriptional factors (Figures 7c and 7d), as well as mRNA for hydroxyl-3-methylglutaryl coenzyme A (HMG CoA) reductase, a rate-limiting enzyme in cholesterol synthesis (Figure 7e).

Discussion

In this study we demonstrate that PDE3B is localized to caveolea/lipid raft regions in the plasma membrane as well as in smooth ER. Further, we show that PDE3B plays important roles in the regulation of glucose, triglyceride and cholesterol metabolism in hepatocytes.

The localization of PDE3B to caveolae is highly interesting, since caveolae have been suggested to be important in the organization of cellular signalling as well as in lipid synthesis and cholesterol homeostasis [7]. The presence of caveolae in hepatocytes has previously been demonstrated using different approaches. Plasma membranes of isolated rat hepatocytes has been shown to contain sphingolipid-enriched microdomains with high amounts of cholesterol and caveolin-1 [28], and the presence of caveolae in the hepatocyte plasma membrane has been shown directly using rapid-freeze, deep-etching electron microscopy [29]. In agreement with the presence of caveolae in hepatocyte plasma membranes, in this study we detect caveolin-1 and flotillin-1, markers for caveolae and lipid rafts, respectively, specifically in the plasma membrane of isolated mouse hepatocytes and fractionation of sonicated plasma membranes in a sucrose gradient resulted in co-migration of caveolin-1, flotillin-1 and cholesterol. Furthermore, results from caveolin-1 KO mice suggest an important role of caveolin-1 in hepatocyte lipid droplet formation and liver regeneration [30–32]. The finding that caveolin-1 KO livers show reduced levels of both PDE3B activity and protein expression indicates a role of caveolin-1/caveolae in the stabilization of the PDE3B protein which has also been demonstrated for the adipocyte PDE3B [5]. Our results demonstrating that PDE3B in hepatocytes is localized to distinct cellular locations, plasma membrane/caveolae as well as smooth ER, is in agreement with recent results in adipocytes [5,6]. Exactly which is the role for PDE3B at these cellular locations needs to be further investigated.

In this study, we demonstrate increased glucose production and increased level of PEPCK mRNA and protein in hepatocytes from PDE3B KO mice, which is in agreement with previous studies in
Figure 4. PDE3B is in large size complexes after gelfiltration. Total membranes were prepared from isolated mouse hepatocytes (20–100 × 10^6) and treated with detergent. A portion was used to isolate non-solubilized detergent resistant membranes (DRM) and solubilized membranes. The different membranes were subjected to Superose-6 chromatography. Fractions were collected and analyzed for PDE3 activity. One representative experiment is shown (n = 4).
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Figure 5. Transmission electron micrographs of mouse hepatocytes; PDE3B is localized to the smooth ER. Sections of lowicryl embedded mouse livers with immunogold labeling for PDE3B (A and C). B and D: negative control with omission of the primary antibody. C and D are higher magnifications of the indicated areas in A and B, respectively. Arrows show examples of gold labeling. Representative micrographs are shown (n = 4). G; Glycogen storage M; Mitochondria, NucI; nucleus, rER; rough endoplasmic reticulum, sER; smooth ER.
doi:10.1371/journal.pone.0004671.g005
these mice (clamp studies in vivo and PEPCK expression in intact liver) and with studies using PDE3 inhibitors [11,27]. The increase in glucose production observed in isolated hepatocytes is not extensive and whether this increase can fully explain the increased production of glucose seen in vivo in PDE3B KO mice is difficult to know. Although we culture the hepatocytes on Primaria™ dishes to keep as much as possible of the original properties of the cells [33], the hepatocytes most likely have reduced biological responsiveness compared to the in vivo situation in PDE3B KO mice. Furthermore, a number of defects related to the storage of triglycerides and cholesterol were identified in hepatocytes from PDE3B KO mice. Thus, we found up-regulation of triglyceride levels in hepatocytes as was the case in PDE3B KO livers [11] and of SREBP1c, one of two transcriptional factors encoded by SREBF1 [34]. The expression of SREBP1c predominates in the liver and has previously been shown to be regulated by insulin and increased intracellular cAMP [34]. In this study we demonstrate a specific role of PDE3B in cAMP mediated regulation of SREBP1c. Nuclear SREBPs is known to interact with cAMP response element binding protein (CREBP)-binding protein (CBP) and PPARγ-regulated coactivator-1β (PGC-1β) which leads to upregulation of fatty acid synthase and suppression of PEPCK gene expression in liver in response to insulin [34]. Cyclic AMP has also been shown to contribute to the regulation of HMG CoA reductase [35], however, little is known regarding involvement of specific PDEs, such as PDE3B, in this process and in the regulation of cholesterol homeostasis. In this study we show that indeed PDE3B seems to be important in this context but the exact signalling pathways in the regulation of HMG CoA reductase and cholesterol synthesis needs to be further evaluated. Thus, in hepatocytes from PDE3B KO mice, increased triglyceride and cholesterol biosynthesis occurred in parallel with elevated gluconeogenesis. At this point we can not completely exclude that decreased breakdown and/or release of triglycerides and cholesterol contribute to the increased levels of the lipids in the PDE3B KO hepatocytes. However, the increased expression of PPARγ, SREBP1c and HMG CoA reductase together with previous results [11] showing increased expression of fatty acid synthase (FAS) in PDE3B KO liver, indicate that increased biosynthesis contribute to the fatty liver phenotype. Indeed increased accumulation of fat in the liver is highly relevant in the context of type 2 diabetes (T2D) and the metabolic syndrome [36,37]. It has been estimated that 70-80% of T2D patients have non alcoholic fatty liver disease. This disease covers a spectrum of liver diseases from steatosis to nonalcoholic steatohepatitis and cirrhosis. Indeed, increased fat accumulation in the liver appears to be a marker of hepatic insulin resistance and a close correlate of all components of the metabolic syndrome independent of obesity. The role of defective/dysregulated PDE3B in fatty liver development needs to be further investigated.

In summary, we demonstrate that, in mouse hepatocytes, PDE3B is localized in caveolae/raft regions in the plasma membrane.

Figure 6. Hormonal regulation and glucose production in mouse hepatocytes. Hepatocytes were isolated from C57BL/6 mice and cultured on Primaria plates. After 18 hours the hepatocytes were incubated for 10 min with 10 nM insulin, 10 nM glucagon or without stimuli (Ctrl). PDE3 activity was measured in total homogenates (a). Values represent mean±SEM (p<0.032 for Insulin, p<0.024 for Glucagon, n = 5). Hepatocytes were isolated from PDE3B KO and WT mice. For glucose production (b) and Western blot analysis of PEPCK (d), the hepatocytes were cultured on Primaria plates over night before the experiment. RNA for PEPCK mRNA expression analysis (c) was isolated from non-cultured hepatocytes. Values are means±SEM. Glucose production: p<0.006, n = 7. PEPCK mRNA: p<0.02, analyzed in duplicate in two independent experiments from two mice of each genotype. PEPCK western blot: one representative experiment is shown, n = 4.

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liver (b) from PDE3B KO and WT mice were analyzed with regard to triglyceride (a) and cholesterol (b) content. Furthermore, PPARy mRNA (c), SREBP1c mRNA (d) and HMG CoA reductase mRNA (e) were analyzed in hepatocytes. Values are means±SEM. Triglyceride content was analyzed as duplicate lipid extractions from four animals of each genotype, p<0.03. Cholesterol content was measured in duplicate in six mice of each genotype, p<0.03. mRNA expressions were analyzed in duplicate in two independent experiments from two mice of each genotype.

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membrane as well as in smooth ER and that the enzyme has an important role in the regulation of triglyceride, cholesterol and glucose metabolism in these cells.

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Author Contributions

Conceived and designed the experiments: KB RL NW EZT AL VM ED. Performed the experiments: KB RL NW EZT AL VM ED. Analyzed the data: KB RL NW EZT AL VM ED. Contributed reagents/materials/analysis tools: KB RL NW EZT AL VM ED. Wrote the paper: KB RL NW EZT AL VM ED.

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