A 15-ketosterol is a liver X receptor ligand that suppresses sterol-responsive element binding protein-2 activity¹

Robert J. Schmidt,* James V. Ficorilli,* Youyan Zhang,* Kelli S. Bramlett,* Thomas P. Beyer,* Kristen Borchert,* Michele S. Dowless,* Keith A. Houck,* Thomas P. Burris,* Patrick I. Eacho,* Guosheng Liang,* Li-wei Guo,[†] William K. Wilson,[†] Laura F. Michael,* and Guoqing Cao^{*,2}

Lilly Research Laboratories,* Eli Lilly & Company, Indianapolis, IN 46285; and Department of Biochemistry and Cell Biology,[†] Rice University, Houston, TX 77005

Abstract Hypercholesterolemia is a major risk factor for coronary artery disease. Oxysterols are known to inhibit cholesterol biosynthesis and have been explored as potential antihypercholesterolemic agents. The ability of 3βhydroxy-5a-cholest-8(14)-en-15-one (15-ketosterol) to lower non-HDL cholesterol has been demonstrated in rodent and primate models, but the mechanisms of action remain poorly understood. Here we show in a coactivator recruitment assay and cotransfection assays that the 15-ketosterol is a partial agonist for liver X receptor- α and - β (LXR α and LXR β). The binding affinity for the LXRs was comparable to those of native oxysterols. In a macrophage cell line of human origin, the 15-ketosterol elevated ATP binding cassette transporter ABCA1 mRNA in a concentrationdependent fashion with a potency similar to those of other oxysterols. We further found that in human embryonic kidney HEK 293 cells, the 15-ketosterol suppressed sterolresponsive element binding protein processing activity and thus inhibited mRNA expression of 3-hydroxy-3-methylglutaryl-coenzyme A reductase, LDL receptor, and PCSK9. Our data thus provide a molecular basis for the hypocholesterolemic activity of the 15-ketosterol and further suggest its potential antiatherosclerotic benefit as an LXR agonist.-Schmidt, R. J., J. V. Ficorilli, Y. Zhang, K. S. Bramlett, T. P. Beyer, K. Borchert, M. S. Dowless, K. A. Houck, T. P. Burris, P. I. Eacho, G. Liang, L-w. Guo, W. K. Wilson, L. F. Michael, and G. Cao. A 15-ketosterol is a liver X receptor ligand that suppresses sterol-responsive element binding protein-2 activity. J. Lipid Res. 2006. 47: 1037-1044.

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Hypercholesterolemia is a major risk factor for coronary artery disease. In recent years, success has been recorded with the development of the statin class of drugs, which

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inhibit 3-hydroxy-3-methyl glutaryl-CoA reductase (HMG-CoA reductase), resulting in inhibition of hepatic cholesterol biosynthesis, upregulation of LDL receptor (LDLR), and accordingly, the reduction of plasma LDL cholesterol (1). However, even with the widespread clinical utilization of statins, there is still an unmet medical need for agents that would further reduce hypercholesterolemia by complementary mechanisms. Certain oxysterols are known to be potent inhibitors of cholesterol biosynthesis (2, 3). The mechanism of this inhibition was not well understood until the recent discovery of a pair of transcription factors, sterol-responsive element binding proteins 1 and 2 (SREBP1 and -2), which primarily control cholesterol and fatty acid biosynthesis and LDL uptake (4). SREBPs are members of the basic helix-loop-helix-leucine zipper family of transcription factors that are synthesized as inactive precursors. The inactive full-length protein, which is anchored to the endoplasmic reticulum by two transmem-

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Abbreviations: LDLR, LDL receptor; LXR, liver X receptor; SPA, scintillation proximity assay; SREBP, sterol-responsive element bind-

ing protein. This work is dedicated to the memory of George J. Schroepfer, Jr., a pioneer in the development of oxysterols as antihypercholesterolemic agents. Dr. Schroepfer showed that the 15-ketosterol lowers LDL- and raises HDL-cholesterol in primates, but his many efforts in the 1980s to elucidate the mechanisms of action were doomed because the regulation of cholesterol metabolism was only partially understood. Dr. Schroepfer followed subsequent developments in genomics and proteomics and demonstrated that oxysterols activate LXRa [Forman et al. (1997) Proc. Natl. Acad. Sci. 94, 10588]. He also tested the 15ketosterol, but did not publish the results before his untimely death on December 11, 1998, just as the "promised land" was coming into view. Soon afterwards, (a) the big picture of cholesterol homeostasis was recognized as the sum of many processes, notably involving LXR, ABC transporters, and SREBP, and (b) Guoqing Cao (Lilly Research Laboratories) contacted Schroepfer's laboratory to initiate a collaboration on the 15-ketosterol. William K. Wilson (Rice University) helped facilitate the collaboration between Rice and Lilly as an obvious extension of research plans laid out by G. J. Schroepfer, Jr. This collaboration was inspired by the vision and perseverance of Dr. Schroepfer, to whom we are grateful.

To whom correspondence should be addressed.

e-mail: guoqing_cao@lilly.com

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brane domains, contains an N-terminal transcription factor and a carboxyl-terminal domain. Under sterol-depleted conditions, the protein is escorted to the trans-Golgi complex and undergoes sequential proteolytic cleavages by two proteases, S1P and S2P. This process results in the release of the N-terminal transcription factor, which enters the nucleus and activates the biosynthesis of cholesterol and upregulates LDLR expression (4). Oxysterols hinder the escort of SREBPs to the trans-Golgi apparatus, thus preventing the activation of cholesterol biosynthesis. Exactly how oxysterols exert their role in this process is not yet clear.

In recent years, certain oxysterols have been identified as liver X receptor (LXR) ligands (5, 6). LXRa and LXRB were initially isolated as orphan nuclear receptors and are now recognized to play critical roles in multiple physiological processes, including cholesterol catabolism (7). LXRs regulate the expression of several ATP binding cassette (ABC) transporters (8-10), HDL modifying enzymes (11, 12), and apolipoproteins (13-15) that are involved in cholesterol homeostasis. Synthetic LXR agonists have been shown to elevate HDL cholesterol in rodent models and to exert antiatherogenic properties (12, 16-18). However, LXR agonists also activate SREBP1c expression, which controls the entire fatty acid biosynthetic pathway and promotes hypertriglyceridemia and hepatic steatosis (16). Thus, selective LXR modulators have potential pharmacological benefits. The mechanism of oxysterol regulation of cholesterol metabolism was not known in late 1970s, when Schroepfer and colleagues (19, 20) pioneered the effort to develop synthetic oxysterols as hypocholesterolemic agents. One promising candidate, 3β -hydroxy- 5α -cholest-8(14)-en-15-one (15-ketosterol, referred to as compound 1 in the following text), was studied extensively and was demonstrated to have hypocholesterolemic efficacy in rodent and



Compound 1: 3\beta-hydroxy-5a-cholest-8(14)-en-15-one



primate models (20–24). However, the mechanisms for the observed hypocholesterolemic effects were not clearly defined. In this report, we present evidence that compound 1 interferes with SREBP processing and is a partial agonist for LXR α and LXR β . These effects may explain the ability of compound 1 to lower LDL and raise HDL cholesterol in animal models.

METHODS

Materials

15-Ketosterol was prepared as described previously (25) and showed >99% purity by 500 MHz NMR. The LXR radioligand binding assay was performed using scintillation proximity assay (SPA) technology as previously described (26). We utilized 800 ng of baculovirus-expressed, His-tagged human LXRα ligand binding domain (LBD) protein (aa 162-447) or 600 ng of LXRβLBD protein (aa 202-461), 25 nM [³H]25-hydroxycholesterol (Amersham; Piscataway, NJ), 0.05 mg polylysine-coated yttrium silicate SPA beads (Amersham), and varying concentrations of competitor per well of a 96-well OptiPlate (Packard; Meriden, CT). Protein, radioligand, and competitor were added to the plate. SPA beads were then added to the assay plate, followed by 10 min of gentle shaking at room temperature protected from light. The plates were incubated in the dark at room temperature for 2 h prior to reading in a TopCount plate reader (Packard).

Coactivator interaction assay

Interaction between the LXR α /LXR β and the coactivator SRC-1 was assayed using AlphaScreenTM (amplified luminescent proximity homogenous assay) technology (PerkinElmer; Wellesley, MA). The assay was performed in white, low-volume, 384-well plates (Greiner Bio-One; Germany) utilizing a final volume of 10 µl containing final concentrations of 10 nM of affinity-purified, His-tagged, baculovirus-expressed human LXR α LBD or LXR β LBD

Fig. 1. Compound 1 is a liver X receptor (LXR) ligand as measured by a radiolabeled scintillation proximity assay (A) chemical structure of compound 1. (B) Radiolabeled 25-hydroxycholesterol was incubated with LXR ligand binding domain, and competition of compound 1. With radiolabel was assessed with the scintillation proximity assay as described in Methods.

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protein, 5 nM of GST-SRC-1 protein that contained the entire nuclear receptor interacting domain of SRC-1 fused to GST, and $10 \,\mu\text{g/ml}$ of both Ni²⁺ chelate AlphaScreen donor beads and anti-GST AlphaScreen acceptor beads. The assay buffer contained 25 mM HEPES (pH 7.0), 100 mM NaCl, 0.1% BSA, and 2 mM DTT. All manipulations involving assay beads were done in ambient light. Assay plates were covered with a clear seal and incubated in the dark for 4 h, after which the plates were read for 1 s/well in a Packard AlphaQuest microplate analyzer using the manufacturer's standard AlphaScreen detection protocol.

LXR cotransfection assay

For transient transfection of HEK 293 cells, 6×10^3 cells were plated into 96-well dishes. Each well was transfected with 25 ng $5 \times UAS$ -luciferase reporter (pG5*luc*) and 25 ng of pM human LXR α (AA 162-447) or LXR β (AA 153-461) LBD plasmid using Fugene 6 reagent (Roche; Indianapolis, IN). The chimeric protein was assessed for the ability to transactivate a Gal4-responsive luciferase reporter plasmid in a concentration-responsive manner to compound 1 (0.001–30 μ M). Luciferase activity at each dose concentration was measured in triplicate using standard substrate reagents (BD Biosciences; San Diego, CA), and data are expressed as relative light units.

ABCA1 branched-DNA assay

The branched-DNA assay was performed according to the manufacturer's protocol for the QuantiGene® High Volume Kit (Genospectra; Fremont, CA). After treatment of the cells with compounds, cells were lysed with QuantiGene® lysis buffer containing the ABCA1 mRNA oligonucleotides as described (27). After a 15 min incubation at 37°C, 100 µl of the lysis buffer from each well was transferred to the corresponding wells of the capture plate. The capture plate was incubated overnight at 53°C. The capture plate was then washed twice with QuantiGene[®] wash buffer, followed by the addition of 100 µl/well QuantiGene® amplifier working reagent. The plate was incubated for 60 min at 46°C, followed by two washes. The mRNA to be measured was then labeled by the addition of 100 µl QuantiGene® label probe working buffer, followed by a 60 min incubation at 46°C. The capture plate was then washed twice, followed by the addition of 100 µl/well QuantiGene® substrate plus QuantiGene® enhancer reagent. The plates were incubated at 37°C for up to 30 min and then read on a luminometer to detect the luminescent signal. The induction of ABCA1 mRNA expression was calculated as a ratio of compound-treated luminescent levels compared with untreated control levels.

Western blot

HEK 293 cells were seeded to 100 mm dishes and grown to confluency in 3:1 DMEM/F12 (Invitrogen) + 10% FBS supplemented with 20 mM HEPES, L-glutamine, and Penicillin/Streptomycin. The dishes were washed twice with 10 ml PBS- Mg^{2} Ca²⁺, and the cells were then incubated with media under different culture conditions (see Figure legends). After 48 h, the cells were washed once with PBS and nuclear extracts were prepared for Western blot analysis (28). Equal concentrations of protein (40 µg/lane) were run on a 4-20% SDS-PAGE gel. Proteins were then transferred to Nitrocellulose membranes (0.45 µm; Novex), which were blocked for 90 min in Odyssey Blocking Buffer (Li-Cor Biosciences). Anti-SREPB1 antibody 2A4 (abcam AB3259) or SREBP2 antibody 1C6 (BD Pharmingen 557037) or the antibody raised against human LDLR (RDI-PRO61099, Research Diagnostics) was then added at a concentration of $1 \,\mu g/ml$ (SREBPs) or 10 μ l/10 ml blotting solution (LDLR) and incubated overnight at 4°C in blocking buffer. The blots were quickly washed three



Fig. 2. Agonist activity of compound 1 in a coactivator recruitment assay. Agonist activity of compound 1 (A) and T0901317 (B) was examined using LXR ligand binding domain with GST-SRC fusion protein, and the interaction was measured by AlphaScreen technology as described in Methods.



Fig. 3. Agonist activity in a cotransfection assay. Gal-LXR fusion proteins were used in assessing compound 1 (A) or T0901317 (B) agonist activity. HEK 293 cells were cotransfected with DNA constructs encoding Gal-LXR fusion proteins and a reporter construct. Luciferase reporter activity was measured by standard methods as described.

times in PBS + 0.1% Tween 20 (PBST) followed by three 5 min washes in PBST. Goat anti-mouse IgG was added to a concentration of 0.5 μ g/ml in blocking buffer + Tween 20 (Molecular Probes Alexa Fluor 680 goat anti-mouse IgG, A-21057). After 1 h, the blot was quickly washed in PBST, followed by three 5 min washes in PBST. A final wash in PBS was performed, and the blots were visualized in the Li-Cor infrared imaging system.

Quantitative real-time PCR

Dishes treated similarly to those described for Western blot analysis were washed two times in PBS and lysed in Trizol (Invitrogen; 10 ml Trizol/100 mm dish), and RNA was isolated according to the manufacturer's specifications. Molecular biologygrade water (0.5 ml) was used to resuspend the isolated RNA, which was then subjected to an additional purification using a Qiagen RNAeasy kit. Five micrograms of total RNA was converted to cDNA using the ABI High Capacity cDNA kit (ABI# 4322171). This cDNA was then used for Taqman RT-PCR. ABI Assays on Demand supplied the human LDLR and HMG-CoA reductase primer pairs (LDLR-Hs00181192, HMG-CoA Red-Hs00168352). Taqman analysis was performed in an ABI Prism 7100HT system.

RESULTS

As a first step in determining whether compound 1 (**Fig. 1A**) is an LXR ligand, we performed a radioligand binding assay for both LXR α and LXR β in the format of a scintillation proximity assay. As shown in Fig. 1B, compound 1 effectively competed with radiolabeled 25-hydro-xycholesterol, which is a natural ligand of LXRs. The

binding affinity for compound 1 binding to LXR α [inhibition constant (Ki) 0.60 μ M] or LXR β (Ki 0.76 μ M) is slightly less potent than that of another natural oxysterol ligand, 22-(R)-hydroxycholesterol (Ki 0.25 μ M for LXR α and 0.49 μ M for LXR β) (26). To discriminate between agonist and antagonist activity, we first used a biochemical coactivator recruitment assay. The purified ligand binding domain of either LXR α or LXR β was used to examine the interaction of the protein with the coactivator SRC-1



Fig. 4. ABCA1 mRNA regulation by compound 1 in THP-1 cells. Monocytic THP-1 cells were induced to differentiate into macrophage cells, and the activity of compound 1 in regulating ABCA1 was assessed via the branched-DNA method as described.

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upon the addition of the compound. Compound 1 demonstrated concentration-dependent agonist activity (Fig. 2A) in the assay for both LXR α and LXR β . The EC₅₀ concentrations for activating LXRa or LXRB in this assay were 0.62 µM and 0.40 µM, respectively, with a maximum activation of 5.2-fold (LXR α) and 2.3-fold (LXR β) over the baseline. We considered compound 1 to be a weak agonist, compared with the prototypic agonist T0901317, which demonstrated approximately 8.8-fold activation over the baseline for both LXRa and LXRB (Fig. 2B). To further confirm its agonist activity, we then performed a cotransfection assay using Gal-human LXR fusion proteins and a 5×UAS-luciferase reporter. As expected, in both LXRa and LXRB cotransfection assays, compound 1 displayed concentration-dependent agonist activity, with EC₅₀ concentrations at 15.4 µM and 0.74 µM, respectively, with approximately 2-fold activation over the baseline (Fig. 3A). In the same assay, the prototypic LXR agonist T0901317

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demonstrated potent agonist activity (Fig. 3B). We also examined the possibility of antagonist activity of compound 1 in both the coactivator recruitment assay and cotransfection assays and found no antagonist activity (data not shown). To explore whether compound 1 could regulate endogenous gene expression by modulating LXR, we examined ABCA1 mRNA expression in human macrophage cell line THP-1 cells. Compound 1 elevated ABCA1 mRNA expression in a concentration-dependent manner more than 3-fold (**Fig. 4**). This finding was consistent with the results obtained in both coactivator recruitment assay and cotransfection assays.

We also reasoned that compound 1 may exert its hypocholesterolemic activity by inhibition of SREBP processing, and thus we explored its activity in SREBP regulation. Using the HEK 293 model, cells grown under suppressed conditions (with 25-hydroxycholesterol, lane 1, **Fig. 5**) had significantly diminished mature SREBP2 levels as mea-



Fig. 5. Inhibition of sterol-responsive element binding protein 2 (SREBP2) processing activity in cell culture models. A and B: HEK 293 cells were cultured under either induced conditions (lane 2, lipoprotein-deficient serum with 50 μ M compactin and 50 μ M mevalonate) or suppressed conditions (lane 1, induced conditions with 1 μ g/ml 25-hydroxycholesterol and 10 μ g/ml cholesterol) and treated with various concentrations of compound 1 (lanes 3–5). Twenty-four hours after the treatment, cells were collected and extracts were subjected to Western blot analysis to assess the extent of SREBP processing using 2A4 antibody for SREBP1 and 1C6 antibody for SREBP2. Lane 1, suppressed conditions. Lane 2, induced conditions. Lanes 3–5, induced conditions with increasing concentrations of compound 1 at 0.3, 1, and 10 μ M. C: HepG2 cells with transfected SRE-luciferase reporter were treated with various concentrations of compound 1, and the luciferase activity was measured as described in Methods. D: HEK 293 cells were cultured and treated similarly to those described in A, and RT-PCR quantitation was carried out as described in Methods. Similar results were obtained in two other experiments.

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Fig. 5. Continued.

sured by Western blot analysis using a monoclonal antibody against the C terminus of SREBP2 in comparison to cells grown under induced conditions (lipoprotein-deficient serum plus compactin, an inhibitor of HMG-CoA reductase) (Fig. 5A, lane 1 vs. lane 2). Addition of com-

1.8

1.6

1.4

1.2

1.0

0.8

0.6

0.4

0.2

0.0

1.6

1.4

1.2

1.0 0.8

0.6

0.4

0.2 0.0 2 3 4 5

3

4 5

0.3 1.0 10

2+15-Ketosterol (µM)

1

1 2

the of the second

pound 1 under induced conditions (lanes 3-5) led to a significant reduction of mature SREBP2 levels (Fig. 5A, lanes 2-5), whereas nuclear SREBP1 levels (detected by an antibody against the SREBP1 N-terminal) did not display any observable change (Fig. 5B), suggesting that com-



Fig. 6. Compound 1 regulates PCSK9 mRNA and LDL receptor (LDLR) protein in HEK 293 cells. HEK 293 cells were cultured and treated similarly to those described in A, and PCSK9 mRNA was quantified through RT-PCR. The LDLR protein was examined using Western blot analysis (B).

pound 1 specifically repressed SREBP2 processing in HEK 293 cells. To further confirm the repression of SREBP activities by compound 1, HepG2 cells with a 3×SREluciferase reporter were treated with compound 1 and the luciferase activity was measured. As shown in Fig. 5C, compound 1 significantly decreased SRE reporter activity in a concentration-dependent manner, with an IC_{50} of 1 μ M. Consistent with these observations, quantitative real-time PCR analysis of the genes regulated by SREBP2, including HMG-CoA reductase and LDLR, demonstrated expression changes that paralleled SREBP2 proteolytic processing (Fig. 5D). Compound 1 appeared to slightly repress SREBP2 mRNA expression and trend toward elevating SREBP1 mRNA. These data demonstrate that compound 1 effectively suppresses SREBP2 activity and its downstream target genes in cell culture models.

Recently, PCSK9 (proprotein convertase subtilisin/kexin type 9) has been reported as an SREBP2 target gene that intimately regulates LDLR levels through protease degradation of LDLR (29–31). Therefore, we further monitored PCSK9 mRNA regulation by 15-ketosterol. As anticipated, compound 1 dramatically reduced PCSK9 mRNA expression (**Fig. 6A**). Western blot analysis showed that compound 1 effectively suppressed LDLR protein levels (Fig. 6B), even with the dramatically reduced expression of PCSK9, thus suggesting a predominant regulation of LDLR at the transcription level by compound 1.

DISCUSSION

In previous studies, synthetic oxysterols, notably compound 1, showed potent hypocholesterolemic effects in animal models. To date, the mechanisms for the observed effects have remained unclear. Here we report that compound 1 is an LXR agonist and also effectively suppresses SREBP2 proteolytic processing and activity in cell culture models.

The sterol nature of compound 1, along with its similarity in binding affinity to natural oxysterols, suggests that compound 1 binds to both LXR α and LXR β in a fashion similar to the binding affinity of native oxysterols. The lack of any preferential binding to either isoform is also characteristic of natural sterol ligands (6). The agonist activity identified in both the coactivator recruitment assay and the cotransfection assay is modest compared with the prototypic potent synthetic LXR agonist T0901317 (Figs. 2, 3) (26). However, compound 1 effectively regulates ABCA1 mRNA in macrophage cells (Fig. 4), suggesting additional potential athero-protective effects.

Two SREBP isoforms, SREBP2 and SREBP1c, are present primarily in vivo (4). Their distinct roles in regulating lipid metabolism have been defined in recent years. SREBP1c has been identified as the master transcription factor regulating the entire fatty acid biosynthetic program, whereas SREBP2 is primarily responsible for mediating cholesterol homeostasis (4). Although fatty acids regulate SREBP1c by negative feedback, certain oxysterols specifically suppress SREBP2 processing activity (32). Our data indicate that compound 1, like natural oxysterols, also specifically represses SREBP2 proteolytic processing and thus its transcriptional activity.

Plasma LDL cholesterol is balanced by hepatic VLDL secretion and LDL cholesterol uptake through receptormediated endocytosis (33). Previously, it was not known whether inhibition of both cholesterol biosynthesis (and thus, accordingly, VLDL secretion) and LDLR expression by sterols would result in overall LDL cholesterol lowering. Recent genetic data have demonstrated that in S1P- or SREBP cleavage-activating protein-deficient mice, SREBP processing was severely impaired and both plasma triglyceride and cholesterol levels were reduced (34, 35). Thus, although the expression of the proteins of both cholesterol biosynthesis and LDL uptake is inhibited, the overall effect is a reduction in plasma lipid, owing primarily to a reduction in lipid synthesis. These results suggest that pharmacological inhibition of the SREBP pathway may represent an alternative path for further lipid lowering. Thus, if the hypocholesterolemic effect of compound 1 is a result of reduced SREBP processing, our data could be viewed as pharmacological validation for this approach.

In summary, our cell culture results point to regulatory mechanisms that may explain the beneficial effects of compound 1 on lipoprotein cholesterol in intact animals. Consistent with its reported lowering of LDL + VLDL cholesterol (20), compound 1 effectively suppressed SREBP2 cleavage and transcription of its target genes (encoding HMG-CoA reductase, PCSK9), with little effect on SREBP1. Compound 1 is a weak partial agonist for LXR α and LXR β and increases transcription for ABCA1 that may contribute to the observed HDL cholesterol elevation in primates (20).

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