Perhexiline activates KLF14 and reduces atherosclerosis by modulating ApoA-I production


Introduction
Atherosclerosis-related cardiovascular disease (CVD), including coronary heart disease (CHD), ischemic stroke, and peripheral arterial disease, is the most common cause of death and disability worldwide. Epidemiologic studies and experimental observations have consistently shown that decreased levels of HDL cholesterol (HDL-C) and apolipoprotein A-I (ApoA-I), the major protein component of HDL-C, are powerful, independent predictors of CHD risk (1–4). High levels of HDL-C and ApoA-I are strongly associated with a reduced cardiovascular risk, even among statin-treated patients achieving LDL cholesterol (LDL-C) levels of less than 50 mg/dl (5). Indeed, both HDL and ApoA-I have cardiovascular protective effects, including reverse cholesterol transport (RCT) and antiinflammatory and antioxidative effects. HDL-C efflux capacity, a new biomarker that characterizes a key step in RCT, is a strong inverse predictor of coronary disease events (6, 7). Recently, a population-based cohort study has demonstrated that a high HDL-C efflux capacity is associated with a decreased risk of coronary disease, even after adjustment for traditional cardiovascular risk factors, including HDL particle numbers and size (8).

As HDL particles and ApoA-I are the key acceptors of cholesterol efflux, it may be necessary to develop therapeutic strategies to raise functional HDL and/or ApoA-I levels and enhance their antiatherogenic functions. Most of the oral administration of HDL-raising agents, such as niacin, cholesteryl ester transfer protein (CETP) inhibitors, and fibrates, has yielded convincing results in increasing HDL-C levels, but the effects on reducing cardiovascular risk and enhancing RCT need to be further investigated (9–11). Turning on endogenous production of ApoA-I to facilitate new HDL particle formation is becoming one of the most attractive approaches, which is strongly supported by results from human ApoA-I transgenic mice and virus-mediated overexpression of ApoA-I in a mouse model of experimental atherosclerosis (11, 12). RVX-208, a bromodomain and extraterminal domain inhibitor, is an orally active small molecule that upregulates ApoA-I production (12–14). However, in patients with CHD, administration of RVX-208 did not statistically reduce cardiovascular events and the percentage of coronary atheroma volume due to its small effect on HDL-C levels and significant side effects in the ASSURE study (15, 16). Therefore, the identification of novel molecules that regulate ApoA-I

Recent genome-wide association studies have revealed that variations near the gene locus encoding the transcription factor Krüppel-like factor 14 (KLF14) are strongly associated with HDL cholesterol (HDL-C) levels, metabolic syndrome, and coronary heart disease. However, the precise mechanisms by which KLF14 regulates lipid metabolism and affects atherosclerosis remain largely unexplored. Here, we report that KLF14 is dysregulated in the liver of 2 dyslipidemia mouse models. We evaluated the effects of both KLF14 overexpression and genetic inactivation and determined that KLF14 regulates plasma HDL-C levels and cholesterol efflux capacity by modulating hepatic ApoA-I production. Hepatic-specific Klf14 deletion in mice resulted in decreased circulating HDL-C levels. In an attempt to pharmacologically target KLF14 as an experimental therapeutic approach, we identified perhexiline, an approved therapeutic small molecule presently in clinical use to treat angina and heart failure, as a KLF14 activator. Indeed, in WT mice, treatment with perhexiline increased HDL-C levels and cholesterol efflux capacity via KLF14-mediated upregulation of ApoA-I expression. Moreover, perhexiline administration reduced atherosclerotic lesion development in apolipoprotein E–deficient mice. Together, these results provide comprehensive insight into the KLF14-dependent regulation of HDL-C and subsequent atherosclerosis and indicate that interventions that target the KLF14 pathway should be further explored for the treatment of atherosclerosis.
production is essential for increasing ApoA-I and HDL production and conferring protection against atherosclerosis.

Large-scale GWAS have identified that a genetic variant on chromosome 7 is strongly associated with both HDL trait and CHD (17–21). This variant lies in a noncoding region in the vicinity of KLF14 and TSGA13, which encode Krüppel-like factor 14 and testis-specific gene A13, respectively. KLF14 is a member of a large family of zinc-finger transcription factors that have been widely studied in embryogenesis and cell proliferation, differentiation, and development. The 18 KLFs described in mammals possess highly conserved cysteine and histamine zinc fingers, critical for recognition and binding to CACCC or CGCCC DNA motifs (22). KLF14, a maternally expressed imprinted gene without introns, is robustly associated with HDL-C levels, CHD, type 2 diabetes, obesity, and cancer (17, 18, 20, 21, 23–28). In fact, KLF14 has been recently proposed as a master trans-regulator of multiple genes that are associated with metabolic phenotypes in adipose tissue (26), T regulatory cell differentiation (29), and lipid-mediated signaling through a distinct epigenetic mechanism (20), though its role in lipid metabolism and CVD remains to be determined. Fortunately, through a combination of animal models, genetic tools, and pharmacological screening, we have identified a mechanistic role, reported here, for KLF14 in regulating HDL metabolism and cholesterol efflux capacity by modulation of ApoA-I production. Moreover, we identify a small drug, perhexiline, as a KLF14 activator, administration of which reduces atherosclerosis development in apolipoprotein E-deficient (ApoE–/–) mice. Collectively, these findings demonstrate molecular mechanisms by which the KLF14 pathway could serve as a promising therapeutic target for the treatment of atherosclerosis.

**Results**

**Hepatic KLF14 expression is reduced in dyslipidemia mouse models.** In an attempt to identify genes that may play a critical role in regulation of lipid metabolism using real-time polymerase chain reaction (PCR) analysis, we first examined the expression profiles of 43 candidate genes that are associated with the HDL-C trait and CHD, as indicated by previous GWAS (17–19, 21), in the liver from 2 dyslipidemia mouse models. We found that Klf14 mRNA expression was significantly decreased, by approximately 70%, in the liver of C57BL/6 mice in response to a high-fat diet (HFD) (Supplemental Figure 1A, A and B; supplemental material available online with this article; doi:10.1172/JCI79048DS1). We next assessed Klf4 mRNA expression in the liver of the leptin-deficient (ob/ob) mouse. Collectively, these findings demonstrate molecular mechanisms by which the KLF14 pathway could serve as a promising therapeutic target for the treatment of atherosclerosis.

We detected that Klf14 mRNA expression was significantly decreased, by approximately 70%, in the liver of C57BL/6 mice in response to a high-fat diet (HFD) (Supplemental Figure 1A, A and B; supplemental material available online with this article; doi:10.1172/JCI79048DS1). We next assessed Klf4 mRNA expression in the liver of the leptin-deficient (ob/ob) mouse, a well-accepted model characterized by obesity, insulin resistance, and dyslipidemia, and found that the levels of this gene were reduced by 52% (Supplemental Figure 1C). Among the tissues of healthy adult C57BL/6 mice examined, KLF14 protein expression was detected in liver and kidney, while heart showed the highest level of KLF14 (Supplemental Figure 2). Consistent with mRNA expression, KLF14 protein levels were decreased in the livers from mice fed HFD and ob/ob mice compared with control animals (Supplemental Figure 1, D and E).

Sterol-response element–binding proteins (SREBPs), transcription factors that regulate the expression of genes involved in the synthesis of cholesterol, fatty acids, and triglycerides (TG) in mammalian cells, are upregulated in the liver of both the dyslipidemia mouse models (30, 31). We also observed a significant upregulation of SREBP1 in the liver from C57BL/6 mice fed a HFD (Supplemental Figure 3A). Next, to test the effects of SREBPs on KLF14 expression, we performed luciferase reporter gene assays using human KLF14 promoter (KLF14-luc, spanning −1567 to +65, relative to the transcription start site) construct. Fitting with the effects observed for endogenous Klf14 expression, SREBP1c and SREBP2 significantly repressed the transcription at the human KLF14 promoter (Supplemental Figure 3B). Since KLF14 expression is reduced in the liver of dyslipidemia models, we postulated that hepatic KLF14 might play an important role in lipid metabolism and performed additional experiments to test the validity of this idea.

Overexpression of KLF14 increases HDL-C levels and cholesterol efflux capacity. To investigate whether KLF14 contributes to lipid metabolism, as inferred from genotype-to-phenotype correlations previously made in humans, C57BL/6 mice were fed a HFD for 12 weeks and recombinant adenoviruses encoding human KLF14 (AdKLF14) or β-galactosidase (AdLacZ) were injected via tail vein. After 6 days, AdKLF14–treated animals showed a 29% increase in HDL-C compared with the AdLacZ–treated group (Figure 1A), whereas total cholesterol (TC), LDL-C levels, TG, and fasting blood glucose (Figure 1, B–E) were not affected. Fast protein liquid chromatography (FPLC) analysis of pooled sera from each experimental group confirmed that AdKLF14–treated mice had increased circulating levels of HDL-C (Figure 1F), but not TG (Figure 1G). We also observed an increase in ApoA-I protein levels in both the liver and serum of AdKLF14–treated mice (Figure 1, I–K). We detected that KLF14 induced marked mRNA increases in Klf14 and Apoa1 in livers from mice treated with AdKLF14 (Supplemental Figure 4, A and B). Although we observed a slight upregulation of ApoC3 mRNA (Supplemental Figure 4C), which is linked in a genetic cluster with Apoa1 (30), the circulation ApoC3 levels did not increase dramatically, as measured by ELISA (Supplemental Figure 4D). As expected, overexpression of human KLF14 did not affect mouse endogenous Klf14 expression (Supplemental Figure 4E). The expression of genes related to cholesterol metabolism, including ApoA-II, apoB, and 3-hydroxy-3-methylglutaryl-CoA reductase, did not change in livers from AdKLF14–treated mice (Supplemental Figure 4, D, F, and G). We also did tail vein injection with adenovirus containing human KLF11, which is a member of the same family of metabolic regulator KLF proteins, and found that treatment with AdKLF11 did not affect both HDL-C and LDL-C levels in C57BL/6 mice fed a HFD (Supplemental Figure 5). Conversely, efficient in vivo shRNA-based knockdown of KLF14 in the liver dramatically decreased plasma HDL-C levels, but had no effect on TG (Supplemental Figure 6, A, D, and E). We also observed a reduced circulating level of ApoA-I by Western blot (Supplemental Figure 6, B and C).

ApoA-I and HDL particles play critical roles in the process of RCT, in which cholesterol from nonhepatic peripheral tissues is transferred to HDL particles and returns to the liver for biliary excretion (6, 32). HDL functionality is critical for the assessment of HDL-mediated atheroprotective effects. Thus, subsequently, we quantified the ATP-binding cassette transporter ABCA1-mediated cholesterol efflux capacity of serum from AdKLF14– or AdLacZ–treated mice. We found that, concomitant with increased HDL-C and ApoA-I levels, cholesterol efflux capacity increased...
and −1943/−1938) displayed increased reporter activity relative to control vector. Interestingly, mutation of the nt −491/−486 site greatly reduced promoter activity, while a similar change in the nt 1943/−1938 site had no significant change (Figure 2D). ChIP assay revealed that KLF14 binds the promoter region that harbors the proximal CACCC box (−491/−486) (Figure 2E), demonstrating that this is a functional KLF14-binding site in the human APOA1 promoter. Similarly, adenovirus-mediated overexpression of KLF14 significantly upregulated ApoA1 mRNA expression and ChIP assay revealed that KLF14 was bound to the promoter region that harbors the CACCC boxes (−499/−494 and −451/−446) in mouse primary hepatocytes (Supplemental Figure 7, A and B).

Given the similar DNA-binding preferences of KLF family members (22), we considered whether other KLF transcription factors could regulate ApoA-I expression. While AdKLF14 cotransfection upregulated APOA1 promoter activity in HepG2 cells, adenoviral significantly in the KLF14-treated group (Figure 1H). Therefore, collectively, these data demonstrate that KLF14 regulates lipid metabolism and establish that KLF14 expression directly modulates the levels of ApoA-I and HDL-C in vivo.

KLF14 is a regulator of ApoA-I expression. In accordance with our in vivo observations, overexpression of KLF14 in HepG2 cells resulted in increased APOAI transcription, and this KLF14-induced APOAI upregulation was blocked by actinomycin D (Figure 2, A and B), a transcriptional inhibitor, suggesting that KLF14 regulates ApoA-I at the transcriptional level. These results led us to investigate whether KLF14 functions as a transcriptional regulator of this protein. Indeed, initial evidence derived from analysis of the 5′ flanking regions of human APOAI identified a sequence (CACCC box) similar to the recently described functional KLF14-binding site (20). As shown in Figure 2C, the region from the APOAI promoter containing these sites (located at nt −491/−486 and −1943/−1938) displayed increased reporter activity relative to control vector. Interestingly, mutation of the nt −491/−486 site greatly reduced promoter activity, while a similar change in the nt 1943/−1938 site had no significant change (Figure 2D). ChIP assay revealed that KLF14 binds the promoter region that harbors the proximal CACCC box (−491/−486) (Figure 2E), demonstrating that this is a functional KLF14-binding site in the human APOAI promoter. Similarly, adenovirus-mediated overexpression of KLF14 significantly upregulated Apoai1 mRNA expression and ChIP assay revealed that KLF14 was bound to the promoter region that harbors the CACCC boxes (−499/−494 and −451/−446) in mouse primary hepatocytes (Supplemental Figure 7, A and B).
vectors containing KLF2, KLF4, or KLF11 failed to increase APOA1 promoter reporter activity (Figure 2F), indicating that these effects are specific for KLF14.

Loss of hepatic KLF14 induces decreased HDL-C levels. To study the role of hepatic KLF14 in lipid metabolism, we generated liver-specific Klf14-KO (LKO) mice using the Cre-loxP strategy (Supplemental Figure 8A). We generated mice harboring floxed Klf14 alleles in which only 1 exon of Klf14 was flanked by loxP sites (Klf14<sup>fl/fl</sup>). To ablate Klf14 in the liver, we crossed the Klf14<sup>-cre</sup> mice. Deletion of Klf14 in the liver was confirmed at the genomic DNA (Supplemental Figure 8B), mRNA (Supplemental Figure 8C), and protein levels (Figure 3A). We found that deletion of Klf14 was specific to the liver, as its mRNA levels in other tissues were comparable to those in the control mice (Supplemental Figure 8C). As shown in Figure 3, TC and TG levels were comparable between WT and Klf14<sup>fl/fl</sup> (herein referred to as KLF14-LKO) mice at 8 weeks of age (Figure 3B, D, and F). However, deletion of Klf14 in the liver resulted in an approximately 14.9% decrease in HDL-C levels compared with those of Klf14<sup>-cre</sup> littermates (Figure 3C). In addition, we also detected a decrease in the levels of ApoA-I in both the liver and the circulation of the KLF14-LKO mice (Figure 3A and G). These results reveal that hepatic KLF14 contributes to HDL metabolism.

Drug screening identifies perhexiline as an inducer of KLF14 expression. The preceding data demonstrate that upregulation of KLF14 expression results in increased ApoA-I and HDL-C levels, underscoring a fundamental role for KLF14 in maintaining the homeostasis of lipid metabolism. Therefore, we initiated efforts toward identifying pharmacological interventions that can activate endogenous Klf14 and thereby increase ApoA-I and HDL-C levels. For this purpose, we designed a high-throughput screening using a human KLF14 promoter–driven luciferase reporter, KLF14-luc. From the primary screening of a chemical library of the NIH/JDRF Custom Collection including 1,040 compounds, 8 compounds were identified as activating KLF14<sup>-luc</sup> activity 2-fold or more (Supplemental Table 1). It is noteworthy that we confirmed that perhexiline significantly increased KLF14 promoter activity, but not APOAI promoter activity, after incubation for 12 hours (Figure 4, A–C). To investigate the effect of perhexiline on ApoA-I production, we detected the ApoA-I levels in the medium by ELISA and Western blot. Following treatment of HepG2 cells with perhexiline (10 μM) for 24 hours, the production of ApoA-I in the medium was increased by 28% compared with DMSO-treated cells (Supplemental Figure 9A). Efficient knockdown of KLF14 significantly decreased the production of ApoA-I induced by perhexiline, suggesting that this effect was largely dependent on the KLF14 in hepatocytes (Figure 4D and Supplemental Figure 9, B and C). Next, our experiments demonstrated that perhexiline induced ApoA-I production in time-dependent and dose-dependent manners (Figure 4, E and F). Previous pharmacological studies indicated that perhexiline is a potent inhibitor of mitochondrial carnitine palmitoyltransferase 1 (CPT-1). To identify whether the effect of perhexiline on ApoA-I production is dependent on the
perhexiline behaves as the first KLF14 activator having a beneficial impact on the regulation of ApoA-I and HDL-C levels and function. To determine whether hepatic KLF14 deficiency interferes with perhexiline-induced increase in HDL-C levels, KLF14-LKO and littermate control mice were administrated with perhexiline or DMSO as control via gavage for 5 days. We found a significant increase in HDL-C and ApoA-I levels in perhexiline-treated control mice, though not in the perhexiline-treated KLF14-LKO counterparts (Figure 5, H and I). Subsequently, using real-time qPCR, we measured Klf14 and Apoa1 mRNA levels in livers obtained from mice belonging to each of these groups. Perhexiline-treated control mice showed a significant upregulation of Klf14 and Apoa1 expression in the liver as compared with KLF14-LKO mice (Figure 5, J and K). Thus, the systemic administration of perhexiline increases HDL-C levels in a manner that is largely dependent on hepatic KLF14.

Administration of perhexiline reduces atherosclerosis development in Apoe–/– mice. We tested the effect of perhexiline-mediated activation of the KLF14 pathway on atherosclerosis in Apoe–/– mice. After 10-week challenge of a high-cholesterol diet (HCD), Apoe–/– mice were treated 3 times a week (Monday, Wednesday, and Friday) with either perhexiline (10 mg/kg) or DMSO for 6 weeks via gavage administration. The circulating HDL-C levels were significantly increased in perhexiline-treated group (Figure 6, A–D). Next, we quantified the ABCA1-mediated cholesterol efflux capacity of serum from DMSO- or perhexiline-treated mice and found that cholesterol efflux capacity markedly increased in the perhexiline-treated group (Figure 6E).
that perhexiline-treated mice had increased circulating HDL-C levels, but no changes in TG (Figure 6, F and G). We also detected an increase in ApoA-I protein levels in plasma from perhexiline-treated mice (Figure 6H). Most importantly, perhexiline treatment significantly inhibited atherosclerotic lesion formation, by 27.3%, as measured by the fraction of the surface area in en face aorta trees stained by oil red O (Figure 7, A and B). The cross-sectional plaque area in the aortic sinus was also attenuated by 30.2% in perhexiline-treated Apoe–/– mice compared with DMSO-treated animals (Figure 7, C and D). These findings indicate that perhexiline, the KLF14 activator, inhibited atherosclerosis development.

Discussion
Numerous epidemiological studies have demonstrated that HDL-C and ApoA-I levels are strong, independent, inverse predictors for CVD risk (1–5). In large cohort studies including patients hospitalized with CHD, a low HDL-C is the most prevalent lipoprotein abnormality, with more than half of patients having admission HDL-C levels of less than 40 mg/dl (34, 35). HDL-C efflux capacity, which is a marker of HDL function that measures RCT, has a strong inverse association with coronary disease events (6, 7).

In this study, we provide evidence that KLF14 and its activator contribute to lipid metabolism in a manner that contributes to the suppression of atherosclerosis. Using gain- and loss-of-function approaches, we demonstrate that KLF14 increases both HDL-C levels and cholesterol efflux capacity by the regulation of ApoA-I production. A screening for compounds that can activate the expression of KLF14 led us to identify perhexiline as a KLF14 activator that, when administered to animals, increases ApoA-I and HDL-C levels and enhances cholesterol efflux capacity in vivo. Notably, the treatment of ApoE-deficient mice with perhexiline attenuates atherosclerosis development.

HDL has been reported to exhibit many antiatherogenic properties, including its role in cholesterol efflux, inducing nitric oxide production, and antioxidant, antiinflammatory, and antiatherosclerotic effects. Recently, large cross-sectional studies have demonstrated that HDL-C cholesterol efflux capacity is decreased in CHD patients, which is independent of plasma HDL-C levels (6), suggesting that enhancing HDL functions may be the clinically relevant therapeutic target. Recent evidence has supported the concept that serum cholesterol efflux capacity is a strong predictor of cardiovascular risk, as cholesterol efflux capacity is an
integrated measurement of HDL quantity and quality and also reflects the important function of HDL particles (6–8). Both HDL particles and ApoA-I can serve as acceptors of cholesterol from peripheral cells to the liver. Recombinant HDL (ApoA-I Milano) or reconstituted HDL particle infusion causes significant reduction in aortic cholesterol content and plaque size in small clinical trials and in rabbits (36–41). Raising the level of ApoA-I also results in a quick and significant plaque regression in mice (42–44). Consequently, approaches aimed at turning on endogenous production of ApoA-I are becoming critical strategies for increasing the number of circulating HDL particles and thus improving HDL functionality (13, 15, 45). Our findings demonstrate that the activation of KLF14 enhanced ABCA1-mediated cholesterol efflux capacity of serum by increasing circulation ApoA-I and HDL-C levels. The effect of KLF14 was determined to be specific for the upregulation of ApoA-I and HDL-C levels, as KLF2, KLF4, and KLF11 induced neither ApoA-I expression in vitro nor HDL-C levels in vivo. Recently, KLF11 was found to play a critical role in regulating hepatic TG metabolism, but not in cholesterol metabolism (46), suggesting that, although belonging to the same subfamily of metabolic regulator KLF proteins, these 2 highly related members have distinct functions. It was shown previously that KLF14 is a master trans-regulator of multiple genes that are associated with metabolic phenotypes in adipose tissue (26). These findings suggest that the role of KLF14 could be a central regulator of lipid metabolism in health and disease.

Figure 5. Administration of perhexiline increased HDL-C levels in vivo. C57BL/6J mice placed on a HFD for 12 weeks were treated with DMSO or perhexiline maleate salt (10 mg/kg/d) for 5 consecutive days by gavage administration, and plasma samples were collected at day 7 (n = 10 per group). HDL-C (A), TC (B), LDL-C (C), and TG (D) levels were measured. *P < 0.05, Student’s t test. (E) The ABCA1-mediated cholesterol efflux capacity of serum from DMSO- or perhexiline-treated mice is expressed as the percentage of cholesterol efflux of total cell cholesterol (n = 10 per group). *P < 0.05, Student’s t test. Pooled serum samples from DMSO- or perhexiline-treated mice were assayed by HPLC, and cholesterol (F) and TG (G) levels (fractions 1 to 32) were determined. (H–K) KLF14-LKO and littermate control mice were treated with DMSO or perhexiline maleate salt (10 mg/Kg/d) for 5 consecutive days by gavage administration, and plasma samples were collected at day 7 (n = 5–8 for each genotype). HDL-C levels were determined (H) and ApoA-I levels were quantified by Western blot analysis (I) (n = 5–8 for each genotype). (J and K) qRT-PCR analysis showing the expression levels of Klf14 and Apoa1 in indicated groups. Data are expressed relative to 18S RNA (n = 5–8 for each genotype). Values represent mean ± SEM. *P < 0.05; **P < 0.01, 2-way ANOVA and multiple comparisons.
associated with increased expression of KLF14 in adipose tissue (50). In addition, the T allele carriers have higher ApoA-I levels in the Mulao population in China (21). We observed that KLF14 is downregulated in dyslipidemia mouse models and found that overexpression of KLF14 increases HDL-C levels by upregulating hepatic ApoA-I levels. To determine the contribution of hepatic KLF14 to both ApoA-I and HDL-C production, we generated LKO mice and found that they displayed a decrease in HDL-C levels. Thus, the combined results of experiments using a wide variety of complementary genetic approaches firmly establish a regulatory role for KLF14 in HDL functionality and atherosclerosis.

In aggregate, our present study has uncovered the central role of KLF14 in lipid metabolism and atherosclerosis. This conclusion is based on several findings, including the following: (a) KLF14 binds to the human APOA1 promoter to regulate the transcription of this gene, (b) KLF14 and its activator, perhexiline, increase ApoA-I and HDL-C levels in vivo and improve hepatic ApoA-I levels. To determine the contribution of hepatic KLF14 to both ApoA-I and HDL-C production, we generated LKO mice and found that they displayed a decrease in HDL-C levels. Thus, the combined results of experiments using a wide variety of complementary genetic approaches firmly establish a regulatory role for KLF14 in HDL functionality and atherosclerosis.

Unbiased human genetic studies can identify new pathways relevant to complex diseases, and the newly confirmed pathways could become novel therapeutic targets for CVDs. GWAS play a major role in the identification of lipid-associated loci with substantial effect on CHD risk. Although HDL-C levels inversely correlate with CHD, both genetic and pharmacological studies have not definitively confirmed a causative role of HDL-C in CHD. Notably, genetic studies performed during the past decade have tested the causal relationship between HDL-C and CHD using gene variants associated with elevated HDL levels, such as CETP, lecithin-cholesterol acyltransferase (LCAT), ABCA1, and hepatic TG lipase (LIPC) (47–49). These investigations, however, have largely failed to support a strong causal association between genetically raised plasma HDL-C levels and CHD risk. One important limitation of these studies, for instance, is that the functional characteristics of the HDL particles were not determined. On the other hand, recently, population-based cohort studies have demonstrated that a high HDL-C efflux capacity is associated with a decreased risk of coronary disease (8). Nevertheless, the causal relationship of the functional role of HDL, such as cholesterol efflux capacity and antiinflammatory effects, with the risk of CHD remains to be further investigated. Among those genes identified by GWAS, the T allele of rs4731702, located near the KLF14 gene, is significantly associated with HDL-C levels and a decreased risk of CHD and type 2 diabetes (17, 18, 50). Functional studies demonstrate that the T allele of rs4731702 is associated with increased expression of KLF14 in adipose tissue (50). In addition, the T allele carriers have higher ApoA-I levels in the Mulao population in China (21). We observed that KLF14 is downregulated in dyslipidemia mouse models and found that overexpression of KLF14 increases HDL-C levels by upregulating hepatic ApoA-I levels. To determine the contribution of hepatic KLF14 to both ApoA-I and HDL-C production, we generated LKO mice and found that they displayed a decrease in HDL-C levels. Thus, the combined results of experiments using a wide variety of complementary genetic approaches firmly establish a regulatory role for KLF14 in HDL functionality and atherosclerosis.

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Currently, perhexiline is clinically used to treat angina and heart failure primarily in Australia, New Zealand, and the United Kingdom (51–55), with beneficial effects attributed to
inhibition of mitochondrial CPT1. In the present study, we did not observe an obvious change of ApoA-I production in the medium from hepatocytes treated with etomoxir, another member of the CPT1 inhibitor group (56), suggesting the effect of perhexiline on ApoA-I expression is not likely the result of CPT1 inhibition. To examine whether upregulation of ApoA-I by perhexiline required hepatic KLF14, we treated KLF14-LKO mice with this drug and looked at the levels of this lipoprotein. We found that perhexiline administration increased HDL-C levels in WT mice, but this effect was attenuated in KLF14-LKO mice. The only exon of the KLF14 gene was flanked by loxP sites. Germline transmission of the loxP-flanked allele and Flp recombinase–mediated removal of the frt-flanked selection marker in vivo yielded mice (C57BL/C) harboring a Klf14 allele with 1 frt and 2 loxP sites (Klf14fl/fl). Klf14fl/fl mice were crossed with Alb-Cre transgenic mice (stock number: 003574) purchased from the Jackson Laboratory. Two-month-old male mice were used for experiments. Genomic DNA was extracted from mouse tails and was used for genotyping. Genotyping of KLF14-LKO mice was performed using 2 sets of primers. The first primer set was designed to amplify the Alb-Cre construct (forward, 5′-GAAGCAGAAGCT-TAGGAAGATGG-3′; reverse, 5′-TGGGCCCTTACCATAACTG-3′). Genotyping of Klf14fl/fl mice was performed by PCR amplification (forward, 5′-TAGTGAGAAGAGACGGACGTAGGA-3′; reverse, 5′-TCACATGAGAAAGACGGACGTAGGA-3′).

Animals and diets. C57BL/6, ob/ob (leptin-deficient mice), ApoE−/−, and Alb-Cre transgenic mice were purchased from the Jackson Laboratory and were housed at 22 ± 1°C on a 12-hour light/12-hour dark cycle. C57BL/6 mice had free access to water and rodent chow before switching to adjusted kcal HFD (44% from fat, Harlan, T.D. 06415). For hepatic overexpression of LacZ or KLF14, mice were administered AdKLF14 or AdLacZ at a dose of 5 × 10⁹ plaque-forming units via tail vein injection after 12 weeks of HFD feeding. For knockdown of Klf14 in liver, mice were administered AdshKlf14 or AdshLacZ at a dose of 1 × 10⁸ plaque-forming units via tail vein injection after 12 weeks of HFD feeding. Six days after the adenoviral infection, the animals were fasted for 12 hours and then sacrificed. Collected serum and liver tissues were stored at −80°C until processed. A mouse atherosclerosis model was generated by feeding 8-week-old male ApoE−/− mice an atherogenic diet (HCD, 21% fat, 34% sucrose, and 0.2% cholesterol, Harlan, T.D. 88137) for 10 weeks. Then the mice were treated 3 times a week (Monday, Wednesday, and Friday) with perhexiline (10 mg/kg) or DMSO for 6 weeks via gavage administration with continuous HCD.

Blood biochemical tests. Direct LDL-C, direct HDL-C, and enzymatic-colorimetric assays used to determine serum TC and TG were carried out at the Chemistry Laboratory of the Michigan Diabetes Research and Training Center (University of Michigan). Blood glucose was measured using an ACCU-CHEK glucometer and glucose strips.

Lipoprotein separation by FPLC or HPLC. Plasma lipoprotein profiles were determined by fast-performance liquid chromatography (FPLC) or by HPLC. For FPLC assay, 180 μl of serum pooled from mice was loaded and eluted at a constant flow rate of 0.50 ml/minute. The 40 fractions per sample were collected after running 36 minutes. For HPLC assay, 50 μl of serum pooled from mice was loaded and eluted at a constant flow rate of 1.0 ml/minute. The 32 fractions per sample were collected after running 5 minutes. Sample...
elution was monitored spectrophotometrically at an optical density of 280 nm. The cholesterol and TG contents in each fraction were measured with a fluorometric enzymatic assay (Cayman) and TG colorimetric assay in a GloMax-Multi+ plate reader (Promega).

Cells. The cell lines 293AD, HepG2, J774.1, and Caco2 were obtained from ATCC and cultured according to ATCC protocols. Adenovirus-mediated gene transfer was performed by exposing 70% confluent HepG2 cells to the adenoviruses at a multiplicity of infection of 20 for 2 hours. Primary hepatocytes were isolated from 6- to 10-week-old mice as described previously (58). In brief, mice were anesthetized and the liver was exposed. The liver was perfused with liver perfusion medium and liver digestion medium (Invitrogen), and hepatocytes were washed and separated from other types of cells with Percoll (Sigma-Aldrich). Hepatocytes were seeded on rat tail type I collagen-coated plates or dishes in Williams’ E medium supplemented with 10% FBS for 3 hours, followed by a change to fresh DMEM containing 10% FBS.

Preparation of adenoviral vectors. The full-length human KLF14 cDNA encoding KLF14 was subcloned into the pCR8/GW/TOPO entry vector (Invitrogen). After sequencing, the LR recombination reaction was carried out between the entry clone pCR8/GW/TOPO/KLF14 and the destination vector pAd/CMV/V5-DEST according to the manufacturer’s protocol (Invitrogen). For knockdown experiments, a siRNA oligo, which targets a region 100% conserved between human and mouse, was purchased from Invitrogen. To prepare adenovirus-containing shRNA for KLF14, synthesized oligos were annealed and inserted into BLOCK-IT U6 entry vector. The U6 promoter and shRNA were cloned into the adenoviral plasmid pAd/BLOCK-IT-V5-DEST according to the manufacturer’s instructions. The sequences for shRNA were as follows: shKlf14, 5′-CAGCAGGCATCCGACACATCACAGCTGATTTGTGTAGC-3′, 5′-AAAAAGATCAGGCATCGAACATCTGACTGACGTATGTCGTTGTGGATGC-3′; shLacZ, 5′-CACCGCTACAAATACGAGATTTCCGGTTGCTGATCCC-3′; shLacZ, 5′-CACCGCTACAAATACGAGATTTCCGGTTGCTGATCCC-3′; 5′-AAAAATACAAATCAGGATTGTTCTGGAATATGTTGTAGC-3′; 5′-AAAAATACAAATCAGGATTGTTCTGGAATATGTTGTAGC-3′.

The 293AD cells were transfected with Pael linearized recombinant adenoviruses. After propagation, the recombinant adenoviruses were purified by CsCl density gradient ultracentrifugation. Adenovirus titration was performed using the Adeno-X qPCR Titration Kit (Clontech).

RNA isolation and RT-PCR. Total RNA from tissues and cells was purified using QIAGEN’s RNeasy kits (QIAGEN). cDNA was synthesized using SuperScript III (Invitrogen), and qPCR was performed using SYBR green reagents (Bio-Rad). Primer pairs for reverse-transcriptase PCR (RT-PCR) are shown in Supplemental Table 2. Gene expression was measured with 18S RNA as the reference gene.

Cholesterol efflux capacity assays. The sera from AdKLF14- or AdLacZ-treated mice and DMSO- or perhexiline-treated mice were used for cholesterol efflux studies (6). J774.1 murine macrophages were labeled with 2 μCi/ml 3H-cholesterol for 24 hours in the presence of ACAT inhibitor (Sando 58-035) and equilibrated overnight with 0.5 mM 8-(4-chlorophenylthio)-cyclic AMP in the present of ACAT inhibitor. apOB-depleted serum was obtained by PEG precipitation. 2.8% v/v apOB-depleted serum from mice was used as an efflux acceptor for 4 hours. Efflux was quantified by liquid scintillation and expressed as a percentage of total cell 3H-cholesterol content. All assays were performed in duplicate.

Immunoblotting. Protein was extracted from the cells or liver tissues with lysis buffer (Thermo Scientific) supplemented with protease inhibitor cocktail (Roche Applied Science). The lysates were resolved by 4% to 12% SDS-PAGE, transferred to nitrocellulose membranes, and immunoblotted with the indicated antibodies. Antibodies used in this study were obtained from the following sources: ApoA-I (Sigma-Aldrich, SAB3500270, 1:2000 working dilution; Santa Cruz Biotechnology Inc., sc-30089, 1:1000 working dilution), KLF14 antibody (Santa Cruz Biotechnology Inc., sc-104345, 1:1000 working dilution was used to detect the overexpression samples; Thermo Scientific, PA5-23784, 1:1000 working dilution was used to detect mouse samples), SREBP1 antibody (Santa Cruz Biotechnology Inc., sc-366, 1:10000 working dilution), and actin and GAPDH antibody (Santa Cruz Biotechnology Inc., sc-1616 and sc-25778, 1:2000 working dilution). IRDye 680RD and 800CW secondary antibodies (LI-COR Biotechnology, 926-32212, 926-32213, 926-32214, 926-68074, 1:10000 working dilution) were used as secondary antibodies. Western blots were visualized and quantified using an Odyssey Infrared Imaging System (LI-COR Biosciences, version 2.1). Full uncult gels are shown in the supplemental material. The ApoA-I concentrations and ApoC-III in the serum were quantitated by ELISA according to the manufacturer’s protocol. Apo-A1 ELISA kits were from Abcam (ab108804) and MyBioSource (MBS702111); the Apo-C-III ELISA kit was from Abnova (KA1030).

Plasmin and transient transfection assays. The genomic fragments harboring the putative KLF-binding sites in human APOAI promoter were cloned by PCR from the human genomic DNA. The amplified products of 2.1 and 0.7 kb upstream of the translation start site of human APOAI gene were ligated into the pGL4-luciferase reporter vector (Promega) to generate pGL4-1979/+163-luc, pGL4-710/+163-luc, and pGL4-94/+163-luc plasmids. Promoter activity was further validated by mutation of the 2 putative KLF14-binding sites on the promoter at −943/−1938 or −491/−486 by replacing CACCC with CATAc using the QuikChange Site-Directed Mutagenesis Kit (Stratagen). The numbers indicate the distance in nucleotides from the transcription start site (+1) of the human APOAI gene. To prepare human KLF14 promoter-driven luciferase reporter, the amplified product of 1.6 kb upstream of the translation start site of the human KLF14 gene (−1567 to +65) was ligated into the pGL4-luciferase reporter vector to generate KLF14-luc plasmid. All PCR-generated constructs were verified by sequencing the DNA. Luciferase activity was measured as described before (58). In brief, HepG2 cells were transfected with pGL4-luciferase reporter plasmids and pRenilla-null as internal control (Promega) using Lipofectamine 2000 (Life Technologies). Cells were cultured for 24 hours after transfection, and cell lysates were measured using the Dual Luciferase Reporter System Kit (Promega). For the screen to identify compounds activating KLF14, HepG2 cells were cultured for 24 hours after transfection with KLF14-luc and stimulated with compounds for another 24 hours. Luciferase activity was measured.

ChIP. ChIP assays were performed according to the manufacturer’s protocol, with minor modifications using the EZ ChIP kit (Millipore) (58). In brief, HepG2 cells or mouse primary hepatocytes were infected with AdKLF14 or AdLacZ for 24 hours and then crosslinked with 1% formaldehyde and quenched prior to harvest and sonication. The sheared chromatin was immunoprecipitated with anti-KLF14 antibody
(or control immunoglobulin G) conjugated to protein A/G sepharose beads. The eluted immunoprecipitates were digested with proteinase K, and DNA was extracted and underwent PCR with primers (Supplementary Table 2) flanking the putative KLF14-binding site within APOA1. The supernatant of the control group was used as an input control.

Analysis of atherosclerotic lesions (59). Two quantitative methods were used in this study. First, en face analysis of atheromatous plaques was used: after staining with oil red O (Sigma-Aldrich) and removal of the adventitia of the whole aorta, aortas were opened longitudinally and pinned flat onto a black-wax plate. The percentage of the plaque area stained by oil red O with respect to the total luminal surface area was quantified with ImageJ analysis software (http://imagej.nih.gov/ij/). Second, the extent of the atherosclerotic lesions in the aortic root was determined: the atherosclerotic lesions in the aortic sinus region were examined at 5 locations, each separated by 80 μm, with the most proximal site starting after the appearance of at least 2 aortic valve leaflets. The largest plaques of the 3 valve leaflets were adopted for morphological analysis. All morphometric analyses were performed in a double-blinded manner.

Statistics. Statistical analyses were performed using GraphPad Prism 6 software (GraphPad Software, Inc). Statistical comparisons and analyses between 2 groups were performed by 2-tailed, unpaired Student’s t test. Comparisons among 3 groups or more were analyzed with 1-way ANOVA followed by a Newman-Keuls test or 2-way ANOVA and multiple comparisons. P < 0.05 was considered statistically significant. Data are presented as mean ± SEM.

Study approval. All animal studies were performed according to protocols approved by the University Committee on Use and Care of Animals (UCUCA) of the University of Michigan.

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