Permanent Alteration of PCSK9 With In Vivo CRISPR-Cas9 Genome Editing

Qiurong Ding, Alanna Strong, Kevin M. Patel, Sze-Ling Ng, Bridget S. Gosis, Stephanie N. Regan, Chad A. Cowan, Daniel J. Rader, Kiran Musunuru

Rationale: Individuals with naturally occurring loss-of-function proprotein convertase subtilisin/kexin type 9 (PCSK9) mutations experience reduced low-density lipoprotein cholesterol levels and protection against cardiovascular disease.

Objective: The goal of this study was to assess whether genome editing using a clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated system can efficiently introduce loss-of-function mutations into the endogenous PCSK9 gene in vivo.

Methods and Results: We used adenovirus to express CRISPR-associated 9 and a CRISPR guide RNA targeting Pcsk9 in mouse liver, where the gene is specifically expressed. We found that <3 to 4 days of administration of the virus, the mutagenesis rate of Pcsk9 in the liver was as high as >50%. This resulted in decreased plasma PCSK9 levels, increased hepatic low-density lipoprotein receptor levels, and decreased plasma cholesterol levels (by 35–40%). No off-target mutagenesis was detected in 10 selected sites.

Conclusions: Genome editing with the CRISPR–CRISPR-associated 9 system disrupts the Pcsk9 gene in vivo with high efficiency and reduces blood cholesterol levels in mice. This approach may have therapeutic potential for the prevention of cardiovascular disease in humans. (Circ Res. 2014;115:488-492.)

Key Words: coronary disease ■ genetic therapy ■ lipoproteins ■ molecular biology ■ prevention and control

Among the best established causal risk factors for cardiovascular disease, the leading cause of death worldwide is the blood concentration of low-density lipoprotein cholesterol (LDL-C), and pharmacological therapy that reduces LDL-C levels, namely statin drugs, has proven to be the most effective means of reducing the risk of coronary heart disease (CHD). Yet even with the use of statin therapy, there remains a large residual risk of CHD, and a substantial proportion of patients are intolerant of statin therapy. Thus, there is a critical need to develop new strategies for the reduction of LDL-C.

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Proprotein convertase subtilisin/kexin type 9 (PCSK9) has emerged as a promising therapeutic target for the prevention of CHD. A gene specifically expressed in and secreted from the liver and believed to function primarily as an antagonist to the LDL receptor (LDLR), PCSK9 was originally identified as the cause of autosomal dominant hypercholesterolemia in some families, with gain-of-function mutations in the gene driving highly elevated LDL-C levels and premature CHD.1 In subsequent studies, individuals with single loss-of-function mutations in PCSK9 were found to experience a significant reduction of both LDL-C levels (≈30–40%) as well as CHD risk (88%).2,3 Notably, even individuals with 2 loss-of-function mutations in PCSK9—resulting in ≈80% reduction in LDL-C levels—seem to suffer no adverse clinical consequences.4 This observation suggests that therapies directed against PCSK9 would offer cardiovascular benefit without any accompanying undesirable effects. Just 10 years after the discovery of PCSK9, PCSK9-targeting monoclonal antibodies are being evaluated in clinical trials.6 Yet even if these antibody-based drugs prove effective, their effects on LDL-C are short-lived, and patients will have to receive injections of drugs every few weeks, which will limit their use as preventative therapy.

The ability to permanently alter the human genome has been made possible by the technology now commonly known as genome editing. Recently published clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated...
We initially screened candidate CRISPR guide RNAs targeting sequences in exon 1 and exon 2 of the mouse *Pcsk9* gene in 3T3-L1 cells. We found that the guide RNA targeting exon 1 displayed ≈50% mutagenesis at the on-target site in *Pcsk9*, as judged by the Surveyor assay (Figure 1A; Online Figure 1). We made an adenovirus coexpressing Cas9 and this guide RNA (CRISPR-**Pcsk9**), using an adenovirus expressing GFP as a control.

In a pilot experiment, the CRISPR-**Pcsk9** virus and the GFP virus were administered to two 11-week-old male mice each.

![Figure 1](http://circres.ahajournals.org/)

**Figure 1.** On-target and off-target effects in mouse cells and livers receiving clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated 9 (Cas9).

**A.** Surveyor assays performed with genomic DNA from 3T3-L1 cells transfected with **Pcsk9** exon 1 (gRNA-1) or a guide RNA targeting **Pcsk9** exon 2 (gRNA-2). **B.** Surveyor assays performed with genomic DNA from liver samples taken from mice 3 d after receiving a control adenovirus expressing green fluorescent protein (GFP; A and B) or an adenovirus expressing Cas9 and gRNA-1 (CRISPR-**Pcsk9**; C and D). **C.** Surveyor assays performed with genomic DNA from liver samples taken from mice 4 d after receiving no virus (1–5), the GFP virus (6–10), or the CRISPR-**Pcsk9** virus (11–15). **D.** Surveyor assays performed with liver genomic DNA from the A and C mice. The **Pcsk9** exon 1 on-target site and 10 genomic sites deemed to be the most likely off-target sites for CRISPR-Cas9 were assayed. Arrows show the cleavage products resulting from the Surveyor assays; the intensity of the cleavage product bands relative to the uncleaved product band corresponds to the mutagenesis rate.

(Cas) systems use *Streptococcus pyogenes* Cas9 nuclease that is targeted to a genomic site by complexing with a synthetic guide RNA that hybridizes a 20-nucleotide DNA sequence (protospacer) immediately preceding an NGG motif (protospacer-adjacent motif) recognized by Cas9.7,8 CRISPR-Cas9 generates a double-strand break that is usually repaired by nonhomologous end-joining, which is error-prone and conducive to frameshift mutations resulting in knock-out alleles of genes.

In light of the observed high efficiencies of CRISPR-Cas9 in mammalian cells in vitro,7,8 we assessed whether CRISPR-Cas9 can be used to disrupt the mouse *Pcsk9* gene in vivo with high efficiency. A proof of principle that the gene can be targeted in mammalian hepatocytes in vivo would suggest that the approach might be viable in humans.

### Methods

We hypothesized that CRISPR-Cas9 would disrupt the mouse *Pcsk9* gene in hepatocytes in vivo to a sufficient degree that plasma PCSK9 levels and cholesterol levels would be reduced. We further hypothesized that these would be specific effects, such that the use of CRISPR-Cas9 would affect neither plasma triglyceride levels nor alanine transaminase (ALT) levels.

Candidate guide RNAs were designed to target exon 1 or exon 2 of the *Pcsk9* gene, transfected into 3T3-L1 cells, and assessed for efficacy with Surveyor assays. Adenoviruses either expressing green fluorescent protein (GFP) or coexpressing Cas9 plus a guide RNA were generated. In a pilot experiment, a total of four 11-week-old male C57BL/6 mice were used, 2 each for the GFP and CRISPR-**Pcsk9** adenoviruses. In a second, more comprehensive experiment, a total of fifteen 5-week-old female C57BL/6 mice were used, 5 each for the GFP and CRISPR-**Pcsk9** adenoviruses and 5 with no virus. After 3 days (in the first experiment) or 4 days (in the second experiment) after virus administration, the mice were euthanized after overnight fasting, and the livers were harvested and terminal blood samples collected.

For the second experiment, we tested the null hypotheses that on CRISPR-Cas9 genome editing, each of 4 plasma analytes—PCSK9, triglyceride, cholesterol, and ALT—did not differ among the groups of mice. The levels of the analytes were each compared among 3 groups—mice that received no virus (n=5), mice that received GFP virus (n=5), and mice that received CRISPR-**Pcsk9** virus (n=5). Initially, the Kruskal–Wallis test was performed for each of the 4 analytes, with a statistical significance threshold of P<0.0125 to account for multiple testing (Bonferroni correction for 4 tests). Two analytes (PCSK9 and total cholesterol) were found to reach statistical significance. For each of these 2 analytes, the Mann–Whitney *U* test was performed for each possible pairwise comparison among the 3 groups of mice, with a statistical significance threshold of P<0.00833 to account for multiple testing (Bonferroni correction for 2 sets of 3 pairwise comparisons performed). All statistical analyses were performed using GraphPad Prism 6 for Mac OS X.

An expanded Methods section is available in Online Data Supplement.
After 3 days, we euthanized the mice to harvest liver tissue. Whereas there was no evidence of mutagenesis in the control mice, the CRISPR-Pcsk9 mice displayed substantial levels of mutagenesis, with 1 of the mice showing ≈50% mutagenesis in the Surveyor assay, consistent with alteration of at least half of the Pcsk9 alleles in the liver (Figure 1B; Online Figure I). Analyzing liver DNA from that mouse, we found that a wide variety of indels were produced in Pcsk9, ranging from 1 to 228 bp, with the possibility of larger indels that were not detected by polymerase chain reaction analysis (Online Figure I). The most frequent indels were a 1-bp insertion and a 2-bp deletion. We assessed for off-target mutagenesis at the 10 sites deemed most closely matched to the on-target site and most likely to harbor off-target effects (6 sites with 3 mismatches to the on-target site and the 4 highest-scoring sites with 4 mismatches to the on-target site; see the Online Data Supplement for site sequences). We found no evidence of significant off-target mutagenesis, within the limit of detection by the Surveyor assay (Figure 1D).

To test the hypotheses that genome editing would result in reduced plasma PCSK9 and cholesterol and no differences in triglycerides and ALT, we next performed a more comprehensive experiment in which the CRISPR-Pcsk9 virus and the GFP virus were administered to five 5-week-old female mice each, with an additional group of 5 mice receiving no virus. After 4 days, the CRISPR-Pcsk9 mice all displayed substantial levels of mutagenesis, in some cases >50%, with no mutagenesis observed in any of the mice in the 2 control groups (Figure 1C). We compared plasma PCSK9 levels at 4 days by ELISA; the CRISPR-Pcsk9 mice displayed substantially lower PCSK9 levels compared with each of the control groups of mice (2597 pg/mL with CRISPR-Pcsk9 virus versus 26461 pg/mL with GFP virus [P=0.0079] versus 21 734 pg/mL with no virus [P=0.0079]; n=5 per group; Figure 2A).

Whereas there was no significant difference in plasma triglyceride levels among the 3 groups at 4 days, CRISPR-Pcsk9 mice had significantly lower levels of total plasma cholesterol, with 35% to 40% reduction compared with the control groups (101 mg/dL with CRISPR-Pcsk9 virus versus 157 mg/dL with GFP virus [P=0.0079] versus 161 mg/dL with no virus [P=0.0079]; n=5 per group; Figure 2A). We performed complete lipoprotein profiling of pooled plasma samples from each group, observing reduced high-density lipoprotein and LDL fractions in CRISPR-Pcsk9 mice (Figure 2B), consistent with prior observations in Pcsk9-knockout mice.3 (Of note, reduction of PCSK9 in humans is not expected to reduce plasma high-density lipoprotein cholesterol levels, as observed in these experiments in mice, because of differences between human and mouse high-density lipoprotein metabolism.) No significant difference in blood ALT levels at 4 days among the 3 groups was observed, and hematoxylin/eosin staining of liver sections from representative mice that received either the GFP virus or the CRISPR-Pcsk9 virus showed no inflammation (Figure 2C). Finally, we assessed LDLR levels in liver by Western blot analysis. PCSK9 functions to downregulate LDLR; consistent with this relationship, the CRISPR-Pcsk9 mice had higher levels of LDLR protein than the control groups of mice (Figure 2D).

Discussion

In this proof-of-principle study, we found that CRISPR-Cas9 could disrupt the mouse Pcsk9 gene in vivo with high efficiency and result in decreased circulating PCSK9 levels, increased hepatic LDLR levels, and decreased plasma cholesterol levels. The 35% to 40% lower cholesterol levels in the CRISPR-Pcsk9 mice compared with control mice is consistent with the 36% to 52% lower levels previously observed in Pcsk9-knockout mice compared with wild-type mice.9 Thus, this approach may have therapeutic potential for the prevention of cardiovascular disease in humans.

Although the use of adenovirus allows for efficient delivery to the liver and sustained expression of the CRISPR-Cas9 system, it is not the optimal therapeutic vehicle because of the immune response to the virus. Indeed, inflammation and acute phase responses could potentially have affected the plasma cholesterol levels in the mice receiving adenovirus. However, we included a control group that did not receive any adenovirus, and the plasma PCSK9, triglyceride, cholesterol, and ALT levels were similar to the levels observed in the control group that received the GFP virus. There was no apparent inflammation in the liver within the timeframe of the experiments. Thus, we did not see any evidence of confounding because of the use of adenovirus.

Although the use of adeno-associated virus would be preferable, the gene encoding Streptococcus pyogenes Cas9 (≈4.2 kb) in combination with a CRISPR guide RNA-expressing cassette (≈500 bp) is too large to fit into standard liver-targeting adeno-associated virus vectors (eg, AAV2/8). Furthermore, the rapidity with which robust alteration of the Pcsk9 gene occurred in our experiments—up to >50% mutagenesis in just 3 to 4 days—suggests that a single brief pulse of CRISPR-Cas9 expression would be sufficient to achieve a therapeutic effect. Thus, a virus-free delivery method that transiently expresses CRISPR-Cas9 (eg, RNAs in lipid nanoparticles) might be optimal. A recent study showed that hydrodynamic tail vein injection of DNA vectors encoding CRISPR-Cas9 successfully targeted a liver gene (Fah) with no apparent long-term adverse effects.10

A possible barrier to therapeutic CRISPR-Cas9 applications is the issue of off-target mutagenesis. In our study, we did not observe significant off-target mutagenesis at several potential off-target sites, but we cannot rule out low-frequency events in vivo. Strategies to greatly reduce off-target mutagenesis without impairing on-target mutagenesis are being developed and can be adapted for use in therapeutic applications.

With cardiovascular disease being the number one killer worldwide, a safe and effective PCSK9 genome editing therapy could have a significant impact on human health. A single administration could confer the benefits of naturally occurring PCSK9 loss-of-function mutations—a permanent reduction in LDL-C levels and CHD risk, equivalent to taking statins every day for the rest of one’s life but without the need for long-term therapy. It could represent a paradigm shift in thinking about cardiovascular therapeutics: a one-shot, long-term solution—not unlike a vaccination—rather than a pill to be taken every day or an injection to be received every few weeks. It could also open the door to a whole new class of therapies, where
one might be able to target not just PCSK9 but several other potential therapeutic genes; indeed, given the multiplexing capacity of CRISPR-Cas9,7,8 it might be feasible to efficiently target multiple genes simultaneously with a single therapy.

Acknowledgments

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Sources of Funding

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Disclosures

None.

References


What Is Known?

• Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated systems allow for high-efficiency genome editing, particularly gene knockout, in vitro.
• Proprotein convertase subtilisin/kexin type 9 (PCSK9) loss-of-function mutations confer reduced blood cholesterol levels and protection against coronary heart disease in humans.

What New Information Does This Article Contribute?

• When delivered by adenovirus, CRISPR–CRISPR-associated 9 produces efficient knockout of Pcsk9 in mouse hepatocytes in vivo.
• Knockout of Pcsk9 by CRISPR–CRISPR-associated 9 in mouse liver results in reduced plasma PCSK9 protein and cholesterol levels.

Novelty and Significance

Individuals with naturally occurring loss-of-function PCSK9 mutations experience reduced blood cholesterol levels and protection against coronary heart disease without any known adverse consequences. Genome editing allows for permanent alteration of genes in mammalian cells. We report that a single administration of the CRISPR–CRISPR-associated 9 genome editing system to mice produced a high proportion of loss-of-function alleles of the Pcsk9 gene in the liver in vivo, resulting in substantially reduced cholesterol levels (35–40%). This approach may be therapeutically useful in humans, potentially taking the form of a 1-time vaccination that would permanently reduce cholesterol levels and protect against coronary heart disease.
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SUPPLEMENTAL MATERIAL

DETAILED METHODS

Screening of guide RNAs

Candidate guide RNAs were designed by visual inspection of the sequences of exons 1 and 2 of the \( Pcsk9 \) gene. Protospacers corresponding to the guide RNAs were inserted into gRNA_Cloning Vector (Dr. George Church, http://www.addgene.org/41824/) as previously described. Each guide RNA plasmid was co-transfected with pCas9_GFP (http://www.addgene.org/44719/) into mouse 3T3-L1 cells with TransIT-2020 Reagent (Mirus Bio) according to the manufacturer’s instructions. After two days, the cells were subjected to fluorescent activated cell sorting (FACSAria II; BD Biosciences) to isolate green fluorescent protein (GFP)-positive cells. Genomic DNA was extracted from the isolated cells using the DNeasy Blood & Tissue Kit (QIAGEN), and \( Pcsk9 \) exon 1 and exon 2 were PCR amplified. The PCR products were purified, analyzed using the Surveyor Mutation Detection Kit (Transgenomic) according to the manufacturer’s instructions, and run on ethidium bromide-stained 1.5% agarose gels. The guide RNA showing the higher mutagenesis rate (exon 1) was chosen for further studies.

Generation of adenoviruses

The protospacer corresponding to the selected guide RNA was inserted into the pX330 plasmid (Dr. Feng Zhang, http://www.addgene.org/42230/) that coexpresses the guide RNA and Cas9, as previously described. The coexpression cassette was cut out of the pX330 plasmid with AflIII and NotI and subcloned into the pShuttle vector (Clontech) cut with NcoI and NotI. A corresponding pShuttle vector with GFP was used as a control. In either case, the expression cassettes were then cut out of pShuttle with I-CeuI and PI-SceI and subcloned into the Adeno-X vector (Clontech) cut with the same enzymes. The Penn Vector Core at the University of Pennsylvania used these vectors to generate recombinant adenoviral particles (designated GFP and CRISPR-\( Pcsk9 \)).

Animal studies

All procedures used in animal studies were approved by the pertinent Institutional Animal Care and Use Committees at the University of Pennsylvania and Harvard University and were consistent with local, state, and federal regulations as applicable. A total of four 11-week-old male C57BL/6 mice were simultaneously used for the first experiment, two each for the GFP and CRISPR-\( Pcsk9 \) adenoviruses. A total of 15 5-week-old female C57BL/6 mice were simultaneously used for the second experiment, five each for the GFP and CRISPR-\( Pcsk9 \) adenoviruses and five with no virus. Mice were administered 2.5 \( \times \) 10\(^{10} \) particles each via retro-orbital injection. After three or four days, the mice were sacrificed by carbon dioxide asphyxiation after overnight fasting. Whole liver samples were harvested and split for DNA analysis, hematoxylin/eosin staining, and/or Western blot analysis, and terminal blood samples were collected.

Enzyme-linked immunosorbent assays (ELISAs), measurement of plasma analytes, and Western blot analysis

ELISAs were performed on mouse plasma samples using the Mouse Proprotein Convertase 9/PCSK9 Quantikine ELISA Kit (R&D Systems) according to the manufacturer’s instructions. Triglyceride and total cholesterol levels were measured using Infinity Triglycerides Reagent and Infinity Cholesterol Reagent (Thermo Fisher) independently according to the manufacturer’s instructions. Pooled plasma from each experimental group (150 \( \mu \)L for each group) was separated by FPLC gel filtration. Cholesterol plate assays were performed on FPLC fractions using the Infinity Cholesterol Reagent. ALT levels were
measured using the Alanine Transaminase Activity Assay Kit (Cayman Chemical) according to the manufacturer’s instructions. Western blot analysis was performed with liver lysates using antibodies against LDLR and against β-actin (Sigma).

**On-target and off-target mutagenesis analyses**

Liver genomic DNA samples were isolated and subjected to Surveyor assays as described above. To further analyze the Pcsk9 exon 1 on-target site, PCR amplicons for the on-target site were subcloned using the TOPO TA Cloning Kit with the pCRII-TOPO vector (Thermo Fisher) according to the manufacturer’s instructions. Plasmid DNAs obtained from individual bacterial clones were subjected to Sanger sequencing; usable sequence data was obtained from ~135 clones.

Off-target sites were predicted using the CRISPR Design server (http://crispr.mit.edu/). Ten sites were chosen based on either sequence similarity (three-base mismatches) or high scoring (the top-scoring four-base mismatches), as shown below. There were no sites that were zero-base, one-base, or two-base mismatches.

Guide RNA sequence:

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*duplicated region in the annotated mouse genome

**Primer sequences**

Genomic amplification of on-target sites. Pcsk9 exon 1: 5’, GGAGGACACGTTTTTCTGCAT; 3’, CTGCTGCTGTTGCTGCTAC. Pcsk9 exon 2: 5’, TGGAAGAATTCTGCTGATACGC; 3’, TGATGCCTCTGGGTCTCCTC.

Genomic amplification of off-target sites. OT1: 5’, TGTAAGCTCTGTTGCTCCTC; 3’, GAATTCCTTCCTGTGAGCTG. OT2: 5’, CAGTGTCAGGGAGAGGAGGAC; 3’,
GGAACTGACCCTACGATCCA. OT3: 5’, GGATTCAATGGCCAGAGCTA; 3’
CTCACCTCTAGGGCCGAAC. OT4: 5’, ACCATAGCGCTTCTGGTGT; 3’
TCCTGAAGGAGCTGGAGAAA. OT5: 5’, CGTGACACACATTCATTCA; 3’
CGTCTCATGGTGCATAGTG. OT6: 5’, TGTTCCTTCTGCCTCTGCTT; 3’
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CAAACTCGTTCATGTGGTG. OT10: 5’, CTTCCAAGGCAGCATGTGTA; 3’
TGTGCTTCCACTGGAGCAG.
Online Figure I. Mutagenesis of Pcsk9 in vivo with CRISPR-Cas9. The CRISPR-Cas9 target site in Pcsk9 exon 1 is shown. The boxes indicate the 20-bp sequence matching the protospacer and the 3-bp PAM. The predicted site of Cas9-induced double-strand breaks is indicated with an arrow. Deletions and insertions detected by PCR amplification and Sanger sequencing of the on-target site in liver genomic DNA from a representative mouse (“C” in Figure 1) that received an adenovirus expressing Cas9 and the guide RNA for the target site (CRISPR-Pcsk9) are shown. At the bottom are deletions that spanned the entire site.