AAV-Mediated CRISPR/Cas Gene Editing of Retinal Cells In Vivo

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PURPOSE. Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/CRISPR-associated protein (Cas) has recently been adapted to enable efficient editing of the mammalian genome, opening novel avenues for therapeutic intervention of inherited diseases. In seeking to disrupt yellow fluorescent protein (YFP) in a Thy1-YFP transgenic mouse, we assessed the feasibility of utilizing the adeno-associated virus 2 (AAV2) to deliver CRISPR/Cas for gene modification of retinal cells in vivo.

METHODS. Single guide RNA (sgRNA) plasmids were designed to target YFP, and after in vitro validation, selected guides were cloned into a dual AAV system. One AAV2 construct was used to deliver Streptococcus pyogenes Cas9 (SpCas9), and the other delivered sgRNA against YFP or LacZ (control) in the presence of mCherry. Five weeks after intravitreal injection, retinal function was determined using electroretinography, and CRISPR/Cas-mediated gene modifications were quantified in retinal flat mounts.

RESULTS. Adeno-associated virus 2-mediated in vivo delivery of SpCas9 with sgRNA targeting YFP significantly reduced the number of YFP fluorescent cells of the inner retina of our transgenic mouse model. Overall, we found an 84.0% (95% confidence interval [CI]: 81.8–86.9) reduction of YFP-positive cells in YFP-sgRNA–infected retinal cells compared to eyes treated with LacZ-sgRNA. Electroretinography profiling found no significant alteration in retinal function following AAV2-mediated delivery of CRISPR/Cas components compared to contralateral untreated eyes.

CONCLUSIONS. Thy1-YFP transgenic mice were used as a rapid quantifiable means to assess the efficacy of CRISPR/Cas-based retinal gene modification in vivo. We demonstrate that genomic modification of cells in the adult retina can be readily achieved by viral-mediated delivery of CRISPR/Cas.

Keywords: Cas9, guide RNA, CRISPR, in vivo, gene editing

Many ophthalmic diseases manifest due to well-defined genetic mutations, and inherited retinal diseases now compose the leading cause of blind registrations in working-aged individuals.1 Inherited retinal dystrophies are a very heterogeneous group of conditions, all of which are as yet currently untreatable.2,3 For example, over 100 disease-causing variants across 21 loci have been found to cause Leber congenital amaurosis (LCA).4 To date, much work with LCA has focused on viral-mediated gene replacement therapy, where gene expression is augmented by ectopic replacement of a normal gene product.5 However, emerging data for LCA2 suggest that the efficacy of such viral-mediated gene replacement therapy may decrease over time.6,7 Additionally, genetic heterogeneity and restrictions in viral payloads limit the broad application of such an approach for many inherited retinal diseases.8–10

The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated protein (Cas) system used by bacteria to counter viral intrusion has recently been adapted to allow efficient editing of the mammalian nuclear genome.11,12 CRISPR/Cas-based technology is particularly attractive for treating inherited diseases caused by genes with very specific spatial and stoichiometric expression.5
function. Nonetheless, despite these promising applications, it was found to prevent retinal degeneration and improve visual Rho dominant Streptococcus pyogenes mutation, the majority of subsequent reports have used directed repair pathway to correct the precise disease-causing vivo using electroporation. Wang and colleagues electro-CRISPR/Cas technology is used to disrupt the mutant allele. be readily amenable to preemptive intervention whereby joining, and as such, diseases caused by gain of function, are preferentially repaired through nonhomologous end breaks as those found in the adult retina, double-stranded DNA breaks are preferentially repaired through nonhomologous end joining, and as such, diseases caused by gain of function, dominant negative, or increased copy number variants could be readily amenable to preemptive intervention whereby CRISPR/Cas technology is used to disrupt the mutant allele.

CRISPR/Cas gene editing has been applied to the retina in vivo using electroporation. Wang and colleagues electro-Cas9 domain, http://crispr.mit.edu/) (Supplementary Table S1). Single guide RNAs targeting the 5\textprime; YFP gene in rats harboring the Rho S334ter mutation. Strikingly, this intervention is clear that such approaches for CRISPR/Cas delivery in vivo are not currently applicable as a human therapy. The aim of our work was to assess the feasibility and efficiency of CRISPR/Cas-mediated gene editing in the retina using a viral delivery system that could be adapted for use in a clinic setting in the future. To objectively quantify a phenotypic outcome for in vivo gene editing, we designed sgRNA constructs to disrupt a yellow fluorescent protein (YFP) in a transgenic mouse. Accordingly, we report the use of a viral delivery system for retinal modification and demonstrate clear robust, quantifiable means to explore the efficacy of a CRISPR/Cas technology for gene knockout. In postmitotic cells, such as those found in the adult retina, double-stranded DNA breaks

There have been a small number of studies, which have demonstrated the potential of in vivo gene editing for therapeutic applications. Although the first reported in vivo application of CRISPR/Cas used the endogenous homology-directed repair pathway to correct the precise disease-causing mutation, the majority of subsequent reports have used CRISPR/Cas for gene knockout. In postmitotic cells, such as those found in the adult retina, double-stranded DNA breaks are preferentially repaired through nonhomologous end joining, and as such, diseases caused by gain of function, dominant negative, or increased copy number variants could be readily amenable to preemptive intervention whereby CRISPR/Cas technology is used to disrupt the mutant allele.

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![Image](image-url)

**FIGURE 1.** sgRNA design, plasmid construction, and validation for knockout (KO) of yellow fluorescent protein (YFP). (A) YFP target sequence used for sgRNA design. Selected sgRNA ideograms display the PAM sequence (red) and putative cut site (green triangle). Indel analysis using a SURVEYOR assay identified YFP KO sgRNA2 as having the best KO efficiency in our 3T3-L1-YFP line (B), and this was confirmed in vitro using the HEK293A-YFP line (C). Scale bar: 100 μm. Spectrum and frequency of indels induced by YFP-sgRNA for knockout of yellow fluorescent protein (YFP) in our 3T3-L1-YFP cell line were determined using TOPO TA cloning (D). One clone was found to have a single nucleotide substitution (SNP) at the predicted cut site, but no associated indel. n = 45 clones.

**METHODS**

**Ethics Approval and Colony Maintenance**

Ethics approval for this work was obtained from the Animal Ethics Committee of the University of Tasmania (A14827) and St. Vincent’s Hospital (AEC 014/15), in accordance with the requirements of the National Health and Medical Research Council of Australia (Australian Code of Practice for the Care and Use of Animals for Scientific Purposes). We adhered to the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research.

Thy1-YFP transgenic mice [B6.Cg-Tg(Thy1-YFP)16Jrs/J], which express YFP in all retinal ganglion cells (RGCs) as well as amacrine cells and bipolar cells in the retina, were obtained from the Jackson Laboratory (mouse stock no: 003709; Bar Harbor, ME, USA) and bred at the mouse facility of the Menzies Institute for Medical Research (Hobart, Australia). Mice were housed in standard conditions (20°C, 12/12 hour light/dark cycle) with access to food and water ad libitum.

**sgRNA Design and Construct Generation**

Single guide RNAs targeting the 5\textprime; region of the YFP gene were designed using the CRISPR design tool (provided in the public domain, http://crispr.mit.edu/) (Supplementary Table S1). The MM9 mouse assembly was used as the reference genome, and three sgRNAs were selected for subsequent profile testing. Yellow fluorescent protein–overexpressing 3T3-L1 (ATCC CL-173; American Type Culture Collection, Manassas, VA, USA) and HEK293A (catalogue no. R70507; Life Technologies, Mulgrave, VIC, Australia) cell lines were used for indel analysis and in vitro validation, respectively (Fig. 1). Control sgRNA sequence targeting LacZ was based on the work by Swiech and colleagues. Single guide RNAs were initially cloned into the pSpCas9(BB)purov2.0 vector (a gift from Feng Zhang; Addgene plasmid no. 62988), and the best performing sgRNAs were subsequently cloned into pX552-mCherry (a gift from Feng Zhang; Addgene plasmid nos. 60957 and 60958). pX552-mCherry was generated by replacing the GFP with mCherry using Sall and BspEI restriction sites.

**Cell Culture and Transfection**

Stable cell lines of HEK293A and mouse 3T3-L1 expressing YFP were generated using pA52.EYFP.puro lentivirus (RNAiCore; Academia Sinica, Taipei, Taiwan) and selected using puromycin or fluorescence-activated cell sorting (FACS). All media components were purchased from Life Technologies. Cell lines were maintained in Dulbecco’s modified Eagle’s medium (DMEM) (catalogue no. 11995040) supplemented with 10%
fetal bovine serum (FBS; catalogue no. 26140079), 2 mM L-glutamine (catalogue no. 25030081), and 50 U/ml penicillin-streptomycin (catalogue no. 15070065) and cultured at 37°C with 5% CO₂ incubation. Transfection of CRISPR/Cas constructs was performed using lipofectamine 2000 (catalogue no. 11668027; Life Technologies), with 2.5 µg plasmid per well of six-well plates, according to the manufacturer’s instructions. Fluorescence images were visualized and captured with a Nikon Eclipse TE2000 inverted microscope (Nikon, Melville, NY, USA).

**Indel Analysis**

Genomic DNA was extracted using QIAamp DNA mini kit (catalogue no. 51304; Qiagen, Chadstone, VIC, Australia). Indel analysis was performed with the SURVEYOR assay kit (catalogue no. 706020; Integrated DNA Technologies, Inc., Coralville, IA, USA) using 200 to 400 ng PCR products generated from genomic DNA of transfected cells. SURVEYOR primers flanking the cleavage sites are listed in Supplementary Table S1. Polymerase chain reaction cleaved products were resolved on 1.8% Tris/Borate/EDTA (TBE) agarose gel and visualized using GelRed nucleic acid gel stain (catalogue no. 41003; Biotium, Hayward, CA, USA). To determine the spectrum and frequency of indels induced by the sgRNA selected for in vivo work, 3T3L1-YFP cells were transfected with 1.5 µg of each adeno-associated virus 2 (AAV2) plasmid, pX551 and pX552-mCherry with YFP KO sgRNA2, using Fugene HD (catalogue no. E2311; Promega; Madison, WI, USA) following the manufacturer’s protocol. Cells were collected on day 6 and FACS sorted for mCherry-positive cells and genomic DNA extracted using QuickExtract DNA Extraction Solution (catalogue no. QE09050; Epicentre, Madison, WI, USA) following the heating cycle 62°C for 20 minutes, 68°C for 20 minutes, and 98°C for 20 minutes. Polymerase chain reaction product was synthesized using Taq DNA polymerase with Thermopol buffer (catalogue no. M0267S; New England Biolabs, Ipswich, MA, USA). TOPO TA cloning of the PCR fragment into pCR2.1-TOPO vector was conducted following the manufacturer’s protocol (catalogue no. 450641; Life Technologies). Sanger sequencing was used to identify mutations in the YFP fragment using the M13 forward primer (−20) included in the kit.

**Virus Production**

Recombinant AAV2 viruses were produced in HEK293 cells packaging either pX551, containing SpCas9, or pX552-mCherry with the respective sgRNAs, and pseudotyped with the AAV2 capsid (pX22) as previously outlined.23 Viral vectors were purified by AAV2pro Purification Kit (catalogue no. G232; Clontech Laboratories, Inc., Mountain View, CA, USA), and vector genomes were titered by real-time quantitative PCR using the following primer sets: (pX551-F: CCGAAGAGGTCTGTTAGAAAG, pX551-R: GCCTTATCCAGTTCGCTCAG, pX552-F: TGTGGAAAGACGACAAACC, pX552-R: TGTTCTCTAACCACGTTGCTG) with the SYBR Green Master Mix (catalogue no. 4509155; Life Technologies).

**Intraocular Injection of AAV Vectors**

A total of 22 adult mice, aged between 14 and 16 weeks, were randomly allocated to receive YFP-sgRNA or LacZ-sgRNA (n = 11 per group). Mice were anesthetized by intraperitoneal injection of ketamine (60 mg/kg) and xylazine (10 mg/kg). Intravitreal injections were performed using a surgical microscope similar to that previously described.24 In brief, after making a guide track through the conjunctiva and sclera at the superior temporal hemisphere using a 30-gauge needle, a hand-pulled glass micropipette was inserted into the midvitreal cavity. A total of 1 µl dual-viral suspension (AAV2/SpCas9 3×10⁹ vector genomes [vg]/µl with AAV2-LacZ-sgRNA 2.5×10⁹ vg/µl or AAV2-YFP-sgRNA 3×10⁹ vg/µl) or balanced salt solution was injected into each eye at a rate of 100 nL/s using a UMP-2 Ultra Micro Pump (World Precision Instruments, Inc., Sarasota, FL, USA). Patency was confirmed following needle removal.

**Electrophysiological Assessment and Retinal Morphology**

Mice were euthanized 5 weeks after intraocular injection. Immediately prior to terminal anesthesia, electroretinography was used to assess retinal function in six mice treated with SpCas9/YFP-sgRNA and six mice treated with SpCas9/LacZ-sgRNA.

Our methods for electroretinogram recordings have been well described previously.25–27 In brief, overnight dark adaptation (minimum 12 hours) was performed and all animals were prepared for recording under dim red illumination. Following general anesthesia (ketamine 80 mg/kg, xylazine 10 mg/kg), pupil dilation and corneal anesthesia were obtained with 0.5% tropicamide and 0.5% proxymetacaine, respectively. A Ganzfeld sphere (Photometric Solutions International, Oakleigh, VIC, Australia) was used to deliver luminous energy ranging from −6.26 to 2.07 log cd m⁻² s⁻¹ calibrated with an IL1700 integrating photometer (International Light Technologies, Peabody, MA, USA). Electrical signals were recorded with a chlorided silver electrode on the corneal apex and referenced to a ring electrode placed on the conjunctiva posterior to the limbs. A ground needle electrode was placed in the tail. Full-field flash electroretinograms were recorded using standard settings. Response amplitudes of the scotopic a-wave, scotopic b-wave, scotopic threshold response (STR), photopic negative response, and photopic b-wave were measured. Signals were amplified (>1000) over a band pass of 0.3 to 1000 Hz (−3 dB) and digitized using an acquisition rate of 4 kHz. Ganglion cell response was measured as the peak-to-trough amplitude of the STR recorded at −5.25 log cd m⁻² s⁻¹.25–27

Retinal morphology was assessed in vivo using spectral-domain optical coherence tomography (OCT; Biotigien, Morrisville, NC, USA). Immediately following ERG recordings, a 1.4-mm-wide horizontal B-scan (consisting of 1000 A-scans) of the retina centered at the optic nerve head was obtained. Total retinal thickness (inner retinal surface to retinal pigment epithelium), retinal nerve fiber layer (RNFL; inner retinal surface to nerve fiber layer), and ganglion cell complex (GCC) thickness (inner retinal surface to inner plexiform layer) were returned after manually segmenting key retinal layers (in a masked fashion) followed by averaging thicknesses across a region of interest of 200 to 400 µm from center of the optic nerve. Values from both nasal and temporal retina were averaged.

**Retinal Tissue Processing**

Enucleated eyes were fixed in 4% paraformaldehyde (PFA; catalogue no. C004; ProSciTech, Townsville City, QLD, Australia) for 1 hour, and retinal flat mounts were prepared and stained with a 4’,6-diamidino-2-phenylindole (DAPI; 0.2 µg/mL; catalogue no. D9542; Sigma-Aldrich; Sydney, NSW, Australia) counterstain. For histologic assessment, enucleated eyes were fixed in 4% PFA for 1 hour and embedded in optimal cutting temperature compound prior to frozen sectioning on a microtome cryostat. Serial 10-µm-thick sections were cut, mounted on silanated glass slides, and then stained with DAPI.
Retinal Imaging, Cell Counting, and Statistical Analysis

A fluorescence microscope (Zeiss Axio Imager Microscope; Carl Zeiss, Oberkochen, Germany) equipped with a charge-coupled device digital camera (AxioCam MRm, Zeiss) and image acquisition software (ZEN2, Zeiss) was used. Following whole mounting, each retinal quadrant was Photographed using an appropriate filter for the fluorescence emission spectra of mCherry (605 nm, Zeiss Filter set 64HE) and YFP (495 nm, Zeiss Filter set 38HE). Confocal images were taken using a Nikon C1 confocal laser scanning microscope using a ×20 0.75 NA lens, and images were tile stitched using the NIS Elements AR program. Retinal cell quantification was performed using individual fluorescent images captured at ×400 magnification. A total of 18 images from four flat-mounted eyes treated with SpCas9/LacZ-sgRNA, as well as 26 images from five flat-mounted eyes treated with SpCas9/YFP-sgRNA, were quantified manually using ImageJ v1.49 by an experienced grader (FL), masked to treatment status. To investigate retinal cellular subpopulations targeted by our AAV2 vectors, five retinal cross sections from five SpCas9/LacZ-sgRNA-treated eyes and five retinal cross sections from SpCas9/YFP-sgRNA–treated eyes were also quantified (at ×200 magnification). Sample group decoding was performed only once data were quantified and analyzed.

The efficiency of YFP knockout was determined by the proportion of YFP-negative cells among mCherry-expressing cells. Specifically, the mean proportion of YFP knockout for all eyes treated with SpCas9/YFP-sgRNA was calculated by ∆YFP ve/(∆YFP ve + YFP ve), where ∆YFP ve was the number of mCherry transfected cells in SpCas9/YFP-sgRNA–treated eyes, which did not express YFP, minus the average number of mCherry-expressing cells in SpCas9/LacZ-sgRNA–treated eyes, which did not express YFP (YFP ve); YFP ve was the number of cells that expressed both YFP and mCherry.

To profile the putative in vivo activity of the promoters used to drive SpCas9 and mCherry expression in our plasmids, we interrogated the single-cell mouse retina expression data generated by Macosko et al.29 (GSE64472). In brief, transcriptomic data from 44,808 retinal cells collected from P14 C57BL/6 mice were analyzed. Hierarchical clustering was used to separate cells into distinct clusters (RGCs, amacrine cells, rods, and so on), and the percentage of cells in each cluster that expressed MeCP1 and Syn1 (i.e., a transcripts per million [TPM] value ≥ 1) was quantified. The mean value from clusters of the same cell type were merged.

Comparisons between continuous traits were made using the paired t-test, while categorical data were analyzed using the χ2 or Fisher exact test. Unless otherwise specified, data are presented as mean ± SD. A total of 14 images were processed twice to determine intragrader variability. The intraclass correlation coefficient for YFP ve cell counts was 0.945 (95% confidence interval [CI]: 0.842–0.982) and for YFP ve cell counts was 0.954 (95% CI: 0.867–0.985). Analyses were performed in the R statistical environment (version 3.2.2; in the public domain: https://cran.r-project.org/).

RESULTS

sgRNA Selection and In Vitro Validation

We assessed three sgRNAs targeting the YFP sequence, together with a LacZ-sgRNA control,22 for cleavage efficiency in 3T3-L1 YFP cells (Fig. 1A). Indel analysis for the quantification of sgRNA-induced nucleotide mismatches revealed that one of our sgRNAs (designated YFP KO sgRNA2) targeted YFP most effectively (Fig. 1B). Following TOPO TA cloning we found approximately 73% cleavage activity of this YFP-sgRNA, which was then used for all subsequent experiments (Fig. 1D). When transfected into HEK293A-YFP cells, our selected YFP-sgRNA resulted in almost complete reduction in yellow fluorescence compared with untransformed and LacZ-sgRNA controls (Fig. 1C).

In Vivo AAV Delivery and Gene Targeting of CRISPR/Cas9 in the Mouse Retina

To evaluate the YFP disruption in vivo by CRISPR/Cas-mediated gene editing, Thy1-YFP mice received a single intravitreal injection of our dual-viral suspension of AAV2-SpCas9 and AAV2-sgRNA-mCherry (Fig. 2A). In the murine retina, the promoters used for each plasmid (MeCP2 and Syn1 for SpCas9 and mCherry, respectively) have the greatest expression in RGCs and amacrine cells (Supplementary Fig. S1). Five weeks following treatment, inspection of retinal whole-mount images, captured under a stereomicroscope, revealed a lower number of YFP-positive cells from SpCas9/YFP-sgRNA-treated eyes compared to SpCas9/LacZ-sgRNA–treated eyes (Fig. 2) or contralateral control eyes. To quantify the efficiency of YFP disruption following AAV2 delivery of SpCas9 and sgRNA, high-magnification flat-mount images were obtained, and the proportion of YFP-positive and -negative mCherry-expressing cells was calculated. A marked decrease in the number of YFP-positive cells in the inner retina was found in SpCas9/YFP-sgRNA–treated eyes compared to SpCas9/LacZ-sgRNA–treated eyes. The proportion of YFP/mCherry-expressing cells in eyes treated with SpCas9/YFP-sgRNA was 0.106 ± 0.022 compared to SpCas9/LacZ-sgRNA–treated eyes, where the proportion of YFP/mCherry-expressing cells was 0.664 ± 0.050 (Fig. 2D).

Electrophoretic Assessment of Retinal Function

Electrophysiological assessment of mice 5 weeks after treatment with SpCas9/YFP-sgRNA or SpCas9/LacZ-sgRNA confirmed no adverse effects on photoreceptor (a-wave: YFP P = 0.64; LacZ P = 0.35) or bipolar cell (b-wave: YFP P = 0.38; LacZ P = 0.40) function (Fig. 3; Supplementary Figs. S2–S4). Importantly, given the AAV2 transfection profile following intravitreal injection, inner retinal function as indicated by the oscillatory potentials (YFP P = 0.42; LacZ P = 0.68) was also not disrupted (Fig. 3; Supplementary Fig. S2). The amplitude, indicative of ganglion cell activity, did not significantly differ between YFP-sgRNA–treated and contralateral control eyes (P = 0.48), or between LacZ-sgRNA–treated and their contralateral eyes (P = 0.87) (Supplementary Fig. S4).

There was no statistically significant difference in retinal morphologic profiles in situ between treated and contralateral control eyes (Supplementary Fig. S5). In particular, the RNFL and GCC thickness as measured by OCT did not significantly differ between eyes treated with YFP-sgRNA and contralateral control eyes (RNFL P = 0.30, GCC P = 0.80) or between LacZ-sgRNA and their control eyes (RNFL P = 0.70, GCC P = 0.39).
DISCUSSION

We have successfully demonstrated viral-mediated delivery of essential CRISPR/Cas components to retinal cells in vivo. Using a transgenic fluorescent mouse model, we have definitive evidence for CRISPR/Cas-mediated gene editing of Thy1-expressing retinal cells. With our dual-viral SpCas9/sgRNA suspension, we observed a reduction of YFP-positive cells of approximately 84.0% (95% CI: 81.8–86.9). This level of gene modulation in vivo is similar to that reported for other tissues, such as brain (~68% using AAV) and liver (80–90% using adenovirus).22,30

Our study builds on recent work in which the CRISPR/Cas system was introduced into rodent retinas using an electroporation delivery method.18,19 By demonstrating that CRISPR/Cas can also cause substantial gene modification activity when introduced by a viral delivery method in the retina, we are closer to translating gene editing technology for therapeutic purposes. Importantly, we found that AAV2-delivered SpCas9 was not retinotoxic over a 5-week treatment period. Nonetheless, it is clearly possible that adverse effects from ongoing or prolonged CRISPR/Cas expression could arise. As such it will be important to continue to develop CRISPR/Cas systems that could be tightly regulated and thereby be able to create an optimal window for gene modification while reducing the chance for potential off-target activity.31–34

Adeno-associated viral vectors have been widely exploited as a promising tool for gene delivery in vivo, and it is clear that combining alternate AAVs and sgRNA promoters will extend the CRISPR/Cas therapeutic repertoire. Specifically, different AAV serotypes have the ability to transfect distinct cell populations within the retina,35 and while the AAV2 capsid used in our study is known to primarily transduce RGCs when injected intravitreally,36 a different AAV2 variant, 7m8, can infect photoreceptors following intravitreal delivery.37 Additionally, to overcome the packaging size limitation of AAV vectors,38 we used a dual-vector system to package SpCas9 and sgRNA expression cassettes in two separate viral vectors. Although a single vector that packages a smaller Cas9 orthologue, such as Staphylococcus aureus Cas9 (SaCas9), together with a sgRNA, could achieve greater knockout efficiencies in vivo,17,39,40 dual-vector systems may still be required for mutation correction by enabling the cellular delivery of additional donor templates and appropriate promoter elements. For example, a recent study from Yang and colleagues41 demonstrated that a two-vector approach with SaCas9 resulted in mutation correction in approximately 10% of hepatocytes in ornithine transcarbamylase-deficient newborn mice. With ongoing advances in viral
engineering and the development of new serotypes, future research investigating the efficacy of different viral-CRISPR/Cas systems in the retina is warranted.

An important limitation of our work is the fact that off-target effects were not directly quantified. Nonetheless, to some extent this is a minor consideration for our initial proof-of-concept work, which sought to primarily assess “on-target” efficacy of virally delivered CRISPR/Cas in the adult retina. Additionally, it is well appreciated that CRISPR/Cas technology is advancing rapidly, and although a major limitation of gene editing has been the prospect of off-target effects, this issue is being addressed. For example, with careful design of the guide RNA (using a double nick; truncated sgRNA), it is already possible to avoid most off-target cuts; and recently, two independent studies reported modifications to SpCas9, which can dramatically reduce off-target activity. In any case, it is clear that safety will be paramount prior to the use of CRISPR/Cas in mainstream medical care, and off-target profiling will need to be considered before current research is translated into clinical trials.

In summary, this work suggests that a relatively high efficiency of gene editing in the retina can be achieved by a dual AAV2-mediated CRISPR/Cas system. While ex vivo transcription activator-like effector nucleases (TALEN)-based approaches are now in clinical trials, given the versatility and relative ease of design, CRISPR/Cas techniques appear to be more clinically applicable. Inherited eye diseases share several features that make them appealing for the application of in vivo gene editing. For example, nonsyndromic retinal diseases generally have a specific and well-defined pathogenesis, such that only a specific subpopulation of cells would need to be targeted. Additionally, following any intervention, the eye can be directly examined for the development of any adverse effects. Nonetheless, any in vivo gene editing therapies will require a number of functionally active cells, and it is possible that the threshold for viable cells will vary across genes and diseases.

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