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Efficient transduction and optogenetic stimulation of retinal bipolar cells by a synthetic adeno-associated virus capsid and promoter

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Abstract

In this report, we describe the development of a modified adeno-associated virus (AAV) capsid and promoter for transduction of retinal ON-bipolar cells. The bipolar cells, which are post-synaptic to the photoreceptors, are important retinal targets for both basic and preclinical research. In particular, a therapeutic strategy under investigation for advanced forms of blindness involves using optogenetic molecules to render ON-bipolar cells light-sensitive. Currently, delivery of adequate levels of gene expression is a limiting step for this approach. The synthetic AAV capsid and promoter described here achieves high level of optogenetic transgene expression in ON-bipolar cells. This evokes high-frequency (~100 Hz) spiking responses in ganglion cells of previously blind, rd1, mice. Our vector is a promising vehicle for further development toward potential clinical use.

Keywords adeno-associated virus; capsid library; multi-electrode array; optogenetics; promoter optimization

Subject Categories Genetics, Gene Therapy & Genetic Disease; Neuroscience

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Introduction

Much of the early-stage processing of visual inputs occurs within the retinal bipolar cells, and the failure of available vectors to effectively transduce these cells has impacted both basic research and blindness therapies. In this article, we describe a synthetic adeno-associated virus (AAV) capsid and promoter for transduction of ON-center bipolar cells.

The bipolar cells carry the light-induced vertical flow of information from photoreceptors in the outer part of the retina to ganglion cells in the inner part of the retina. Thereby, they serve not only as a conduit from outer to inner retina: The bipolar cells are also “integrating centers” for the retina’s response to light (Masland, 2012). To facilitate downstream processing by ganglion cells, the bipolar cells need to combine information from two sources: information coming from photoreceptors on the light hitting the center of the receptor field, and indirect information pertaining to the surround, as shaped by inhibitory inputs from neighboring cells. A second level of processing is achieved by having the two classes of bipolar cells, ON-center (ON-bipolars) and OFF-center (OFF-bipolars), provide parallel information channels responding to increases versus decreases in light intensity. Extensive molecular and physiological studies have revealed how bipolar cells transform information arriving from photoreceptors, and transmit it to retinal ganglion cells (Masland, 2012). In vitro systems, transgenic models, and mutation analysis have been used to great effect to characterize the bipolar cells’ differing glutamate receptors, signaling proteins, and ion channels (Hanna & Calkins, 2007; Dhingra et al., 2009; Audo et al., 2009; Peachey et al., 2012; Ray et al., 2014). However, the molecular effort has been hampered by the lack of a suitable vector to further probe bipolar cell function through conditional labeling and gene knockdown studies.

The need for such a vector is especially pressing in translational research. Recent efforts have pursued a therapeutic strategy using optogenetic molecules to render inner retinal cells light-sensitive (Bi et al., 2006; Lagali et al., 2008). These efforts have revealed how light-activated channels, such as the various channelrhodopsins...
Rationale for targeted mutagenesis of AAV8 capsid

Of the many cell types in the retina, the bipolar cells have thus far been the least amenable to transduction by AAV. This may be due to a lack of appropriate receptor expression on the cell surface to mediate uptake, or the presence of an extracellular inhibitory factor on or near the cell surface, or intrinsic factors governing viral trafficking and processing in the cell, or a lack of an appropriate promoter. We argued that the lack of AAV-mediated expression in the bipolar cells is partly due to failure of the capsid to bind and transduce this cell type. When injected subretinally, AAV2/8 was shown to penetrate deeper into the retinal layers than other serotypes (Vandenbergh et al., 2011). Due to this capacity to “reach” the bipolar cell layer, the AAV8 capsid was chosen as the template for modification.

A 9-amino acid stretch of a conformationally variable region of the AAV8 capsid protein between positions 585 and 593 was specifically selected for its potential to alter receptor attachment and cellular transduction properties of the virus. This was based on information from 3-D models and targeted mutagenesis studies of the capsid (Xie et al., 2002; Padron et al., 2005; Nam et al., 2007; Gurd et al., 2012). The AAV shell is assembled from 60 copies of viral proteins (VP), VP1 (87 kDa), VP2 (73 kDa), and VP3 (61 kDa). The conserved core of each VP subunit consists of an eight-stranded β-barrel motif and an α-helix (Xie et al., 2002). The outer surface of the capsid is formed of large loops that connect the strands of the β-barrel. For example, the residues from amino acids 585–594 of the AAV8 capsid protein encompass finger-like loops for one VP subunit. The amino acid sequences and structural topology of these large outer loops have been reported to facilitate tissue tropism and transduction efficiency (Agbandje-McKenna & Kleinschmidt, 2011). The loop formed by the residues from 585 to 594 contributes to the top of the protrusions that surround the icosahedral threefold axes that are formed through symmetric interactions between the VPs. Thus, this 9-amino acid region holds a prominent position on the capsid and includes sites shown in some serotypes (notably AAV2) to be critical for heparan sulfate binding and cellular uptake (Kern et al., 2003; Opie et al., 2003). The nine residues, which are conserved in many serotypes, are altered in the AAV8 capsid, suggesting that AAV8 does not show any affinity for heparan sulfate (Wobus et al., 2000; Wu et al., 2006). Furthermore, an analogous domain within the heparan sulfate binding region was previously interchanged between AAV serotypes and shown to alter tropism profiles dramatically (Asokan et al., 2010). It is possible that this surface-exposed epitope region of residues 585–594 in AAV8 is amenable to changes that may influence tissue tropism and transduction characteristics and still yield viable capsids.

Strategy used to modify AAV tropism

From crystallography studies carried out at 2.6-Å resolution, Nam et al have attributed the lack of heparan sulfate binding by AAV8 to be in part due to the structural differences in the region utilized for receptor recognition by AAV2 [highlighted in red in Fig 1A, from PDB 2QA0, (Nam et al., 2007)]. Two critical residues, R585 and R588, are particularly necessary in order for AAV2 to bind heparan sulfate (Kern et al., 2003; Opie et al., 2003). These positions align with Q588 and T591, respectively, in AAV8 (Lochrie et al., 2006). To produce an AAV capsid library, the residues from amino acids 585 to 593 of the AAV8 capsid were replaced with a mixture of sequences to produce randomized codons (Fig 1B). To maximize diversity while reducing the chances of introducing a premature stop, the NNK saturation mutagenesis strategy was applied which should eliminate all stops with the exception of TAG (Muranaka et al., 2006).
This mutated capsid region was cloned into the pAAV8Caps-Lib vector designed for AAV library production and encoding a red fluorescent protein (Supplementary Fig S1B). This plasmid, which has the AAV2 ITRs flanking the minimal rep/cap gene of AAV8 positioned in reverse orientation to the cDNA for dsRed, was used to produce the AAV viral library. An estimated plasmid library degeneracy of $2.6 \times 10^5$ was derived from colony-counting of plated test ligation following initial transformation.

The plasmid was cotransfected with a helper plasmid into HEK293 cells for library production and preparation. An infectious titer of $1 \times 10^5$ IU/µl was estimated for the resulting viral library by limiting dilution analysis on HEK293 cells. Up to 2 µl of the viral library was subretinally injected into Grm6-GFP transgenic mice, in which the ON-bipolar cells are labeled with EGFP expressed under the control of the Grm6 promoter. After 3 weeks, cell dissociation and cell sorting (FACS) were used to isolate the ON-bipolar cells. For most of the tested serotypes, AAV-mediated retinal expression has been shown to require 2–3 weeks to reach optimal levels (Stieger et al., 2011). These cells included a subset of cells double-labeled with EGFP and dsRED, that is, library-transfected ON-bipolar cells. The sorted EGFP-labeled cells were lysed, and the mutant region of the capsid was amplified by PCR and recloned back into the pAAV8Caps-Lib plasmid for a second round of viral library production (library R1) and injection. The library R1 thus carried a population of virus particles that, through passive selection, were capable of ON-bipolar cell transduction.

However, it was desirable to select for viruses that could effectively compete with the wild-type virus. Therefore, in the second round, the viral library was spiked with the unmutated virus AAV2/8-dsRed, which in effect served as a competing selective force (Fig IC). From this round, unmutated and mutant sequences were found in double-positive EGFP/dsRED-labeled cells (transduced ON-bipolar cells) with only unmutated AAV8 capsid sequences isolated from the dsRed-positive, EGFP-negative cells (transduced non-bipolar cells) (Fig ID). The R1 library carries a heterogeneous mix of capsids; each one producing a unique virus at greatly reduced titer compared to the wild-type co-injected AAV2/8-dsRed. Therefore, it is expected that mutant viruses cannot compete with the wild-type virus in the non-bipolar cells of the retina. However, as the wild-type virus is inefficient at transducing bipolar cells, the R1 library-derived viruses can compete for bipolar cell transduction, and the mutant sequences emerge. From the double-positive red/green cells, the AAVs were isolated and sequenced. Six variants were identified in DNA samples from 44 colonies (Table 1). It is notable that the wild-type capsid sequence was considerably more abundant (30 wild-type sequences versus 14 mutant sequences, Table 1). This was expected, due to the very dilute titer for each individual variant. The WT viral titer is $1 \times 10^{12}$ gc/ml, hence the emergence of any mutant sequence against a saturating WT background is significant.

One variant (variant 5) carried a stop codon and was likely to have been carried through the screen when packaged in another viable capsid. During viral production in the packaging HEK293 cell, the stop-codon-containing sequence may have been taken up by a capsid encoded by another AAV genome within the cell. By using a low plasmid/(packaging-cell) ratio, we hope to minimize the number of alternative AAV genomes within the cell. Nonetheless, due to the random nature of the transfection, it is not guaranteed that the genome encoding a capsid will be the same as the genome packaged within the encoded capsid and this most likely accounts for the presence of AAV8/BP5. We have confirmed that this serotype is non-viable in luminescence assay (Fig IE). Its persistence in the screen may be accounted for when you consider that the TAG residue may arise 1.56% of the time (1/64) such that across 9 residues its frequency will be 14%. It served as a negative control for titration.

The variant sequences were processed for further analysis, and four variants were further selected based on the titration data from small-scale (Fig IE and Supplementary Fig S3) and large-scale preps (Fig IF) as well as structural predictions of the targeted region anticipated to potentially affect receptor/ligand interactions (Supplementary Fig S2).

**Analysis of AAV2/8BP2 in the retina using a non-cell-specific promoter**

AAV vectors were created using each of the selected mutant sequences in place of the wild-type AAV8 capsid gene, and this modified rep/cap plasmid was used to produce AAV(EF1α-EGFP) viruses. Variant 6 yielded low titer and therefore was not used in any further analysis. For this initial analysis, the normal recombinant AAV2/8 virus was injected at a titer of $1 \times 10^{13}$ gc/ml and the variant viruses injected at a titer of $1 \times 10^{12}$ gc/ml. Mouse retinal sections were examined 3 weeks after subretinal or intravitreal injection with the selected AAV variants (Fig 2A and B, Supplementary Fig S4). These qualitative tests using a generic promoter led to the selection of AAV2/8BP2 for further investigation. The cell-type transduction pattern was assessed based on cell soma position in the retina, with the strata of the IPL delineated using a marker for choline acetyl transferase (anti-ChAT). The normal recombinant AAV2/8 shows fluorescence in a diverse range of cell types, with the sparsest fluorescence between the outer (OPL) and inner (IPL) plexiform layers, where the bipolar cell subtypes are found (upper panel of Fig 2A and B). For variant 2, the strongest fluorescent staining was found between the OPL and IPL (lower panel Fig 2A and B), with bipolar and amacrine cells stained. In addition, the photoreceptor cell bodies in the outer nuclear layer (ONL) and their outer segments, as well as cells in the ganglion cell layer (GCL), are stained.

Based on these data, a purified large-scale preparation of AAV2/8BP2 was prepared and *in vitro* and *in vivo* transduction was assayed. This virus was confirmed to transduce HEK293 cells *in vitro* in a similar way to the parental AAV2/8, suggesting that the modified epitope was not having a significant negative impact on the natural tropism (Fig 2C). Adult C57Bl6 mice were subretinally injected with genomic-titer-matched AAVs expressing EGFP under the control of the EF1α promoter and made using either the unmutated AAV8 capsid or the mutant AAV8BP2. After 3 weeks, the retinas were dissociated and processed for FACS analysis. Cell counts (Fig 2D) show 20% transduction of retinas injected with AAV2/8 versus 32% transduction of retinas injected with AAV2/8BP2. However, this difference in transduction of total retinal cells is nonsignificant. In order to determine what proportion of the transduced cells are ON-bipolar cells, a pool of 80,000 cells was taken from each sorted fraction, and the relative expression of retinal genes in the
**Figure 1.**

- **A.** Diagram showing the transduction process of AAV library R1.
- **B.** Sequence alignment showing differences between wild-type and mutant capsid sequences.
- **C.** Schematic of the experimental setup for Round 1 transduction using GRM6-GFP mouse.
- **D.** Scatter plots illustrating expression levels of dsRED-A and GFP-A.
- **E.** Luminescence (p/s) graph comparing AAV library R1 and R2.
- **F.** Graph showing GC/ml concentrations for different treatments.

**a.** Capsid sequence amplified from red-positive, green-negative cells (AAV-transfected, non-bipolar).

**b.** Capsid sequence amplified from red-positive, green-positive cells (AAV-transfected, bipolar).

**EMBO Molecular Medicine**

Bipolar cell transduction to restore vision

Therese Cronin et al
green and non-green cell populations was tested using RT-qPCR. The expression of bipolar cell-specific genes, Grm6 and the long form of a transient receptor potential cation channel, TrpM1L (Zeitz et al, 2005; Morgans et al, 2009), were examined to determine the number of ON-bipolar cells in the transduced cell populations. A 120% increase in Grm6 expression, and a 67% increase in TrpM1L expression, was detected for AAV2/8BP2BP2 compared to AAV2/8-injected retinas (Fig 2F). The gene expression from the cells suggests that improved targeting to the bipolar cells is being achieved with the variant AAV, even when coupled with a strong constitutive promoter such as EF1x. This validated further development of the AAV2/8BP2 virus for bipolar cell-enriched transduction.

**Development of a strong and specific ON-bipolar cell promoter**

A specific metabotropic glutamate receptor (mGluR6) is responsible for synaptic transmission from photoreceptors to ON-type bipolar cells (Shiells & Falk, 1994; Masu et al, 1995; Ueda et al, 1997). This receptor is expressed exclusively in the bipolar cell layer, where it is confined to the postsynaptic site of ON-bipolar cells (Nomura et al, 1994; Vardi & Morigiwa, 1997) and is encoded by the Grm6 gene. The approximate range of the Grm6 promoter relative to the GRM6 transcriptional start site has been known for some time. Ueda et al (1997) generated transgenic mice using the 5' flanking mouse Grm6 sequence fused to a reporter gene. This 10-kb region was capable of directing the cell-type-specific and developmentally regulated expression of the Grm6 gene. Kim et al refined the sequence to a 200-bp critical enhancer region (−8126 to −7927 relative to the first

**Table 1. Altered sequence of the AAV8 capsid in amino acid region 585–594 in variants selected from library screen.**

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B, basic; A, acidic; P, polar; N, non-polar.
*Hydrophobic.
Stop signal.

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Figure 2.
nucleotide of GenBank accession number BC021919, NIH) that could be used to drive reporter gene expression specifically on ON-bipolar cells (Kim et al., 2008; Lagali et al., 2008). We tested expression constructs in which the minimal SV40 promoter was preceded by multiple 200-bp enhancer elements. The constructs tested carried 2, 4, 8, or 16 copies of the 200-bp enhancer cassettes in tandem. The strength of reporter gene expression increased with multiple enhancer cassettes, plateauing with the use of four enhancer elements (4 × Grm6). This arrangement facilitated a high level of expression restricted to the ON-bipolar cells in electroporated mouse retinal explants (Supplementary Fig S5). However, it did not achieve this level of expression when packaged in wild-type AAV vectors and subretinally injected into mice. To test how the variant AAV works in concert with the 4 × Grm6 promoter, we injected C57Bl/6 mice with AAV2/8 or AAV2/8BP2 viruses carrying 4 × Grm6-ChR2-EGFP constructs. Both subretinal and intravitreal injection routes were examined (Fig 2G and H). Both injection routes yield stronger fluorescence using the AAV2/8BP2 virus compared to the AAV2/8 virus. This was evident for stained as well as unfixed and unstained retinas (right-hand panel of Fig 2G and H). Subretinal injection of AAV2/8BP2 gave stronger fluorescence than intravitreal injection, though the latter gave a wider spread of transduction. There was non-specific staining of the ONL and outer segments with the AAV2/8BP2 vector following subretinal injection. At lower titers (7 × 10^{12} gc/ml), these off-target effects were not observed (Supplementary Fig S6). To facilitate comparison with the wild-type vector, it was necessary to use high titers as no signal was obtained from AAV2/8-4 × Grm6-injected retinas at titers below 1 × 10^{12} gc/ml.

**Quantification of AAV2/8BP2 transduction in the retina using a bipolar-cell-specific promoter**

Images of the retinas at low magnification (10×) show the difference in fluorescence intensity in the INL of retinas injected with the wild-type virus AAV2/8 (4 × Grm6-EGFP) virus compared to the variant AAV2/8BP2 (4 × Grm6-EGFP) virus (Fig 3A). The laser power of the confocal microscope was unchanged in comparisons between retinas, and as a result a saturating fluorescence signal was unavoidable in the AAV2/8BP2-4 × Grm6 retinas. To quantify the improvement in transduction observed, wholemounts of fresh, unfixed retinas from injected mice were used. Local z-projections encompassing the ON-bipolar cell body were imaged, and the compressed stack used for fluorescent spot detection (Fig 3B). These cell counts across three randomly chosen regions of each of five retinas show that an average of 2.3 fluorescent cells were found in a 60 μm² area in the AAV2/8 group compared to 89 fluorescent cells for the AAV2/8BP2-injected group (Fig 3C).

In order to test the efficiency of the combined AAV2/8BP2 capsid and 4 × Grm6 promoter in optogenetic stimulations, we created AAVs with AAV2/8BP2-4 × Grm6 or AAV2/8-4 × Grm6–promoter combination, which expressed the channelrhodopsin-2 variant “CatCh”. This channelrhodopsin shows reduced desensitization due to a L132C mutation, and as a consequence yields increased photocurrent at a given light intensity (Kleinlogel et al., 2011). Before embarking on studies to test light stimulation in the retina, the specificity and efficiency of transduction by these vectors had to be tested. Therefore, immunolabeling for the ON-bipolar-cell-specific protein TrpM1 was carried out on retinas from mice injected with virus expressing 4 × Grm6-CatCh-EGFP (Fig 3F). Counting cells in slices from confocal images of the retinas determined the level of colocalization between the virally expressed GFP and the TrpM1-immunolabel in cells. The number of colabeled cells was normalized either to the total trpM1-labeled cells to determine the efficiency of transduction, or to the total number of GFP-labeled cells to determine the specificity of transduction. Compared to wild-type virus, the AAV2/8BP2 retinas showed a threefold increase in ON-bipolar-cell transduction efficiency (Fig 3D). The wild-type and the AAV2/8BP2 retinas showed similar specificity in transduction of bipolar cells, with 80–83% of the green virus-transduced cells also labeling as ON-bipolar cells (Fig 3E).

A FACS analysis was also carried out to more precisely determine the difference in transduced cell number between the variant and wild-type viruses 3 weeks post-injection. We aimed to quantify the range of fluorescence intensity for both viruses and therefore took counts from each of seven subdivisions of the GFP scatter-plot (Fig 3G). Both subretinal (upper panel of Fig 3H) and intravitreal (lower panel of Fig 3H) injection routes were examined. The cells that were brightest, encompassing the subdivisions from Fr12 to Fr14, have a combined percentage of 0.5% of the total retinal cells for mice injected with AAV2/8 versus 4.96% transduction for mice injected with AAV2/8BP2. The RNA from the Fr12-14 pool of cells from AAV2/8BP2 mice was isolated for expression analysis. However, as there were too few corresponding cells in the Fr12-14 cells from AAV2/8 mice this was not included in the analysis. Instead, a comparative study was carried out between this RNA and the RNA from total unsorted retinal cells. We compared the expression of three genes that were shown by Siegert et al (2009) to be differentially expressed among the ON-bipolar cell subtypes. Kcng4

**Figure 2. Analysis of transduction properties of AAV2/8BP2 virus.**

A, B Representative 20x confocal images of immunostained vibratome sections from retinas of mice subretinally injected (A) or intravitreally injected (B) with viruses. The upper panels show AAV28BP2(EF1α-EGFP) injected retinas, and the lower panels show AAV28BP2(EF1α-EGFP) injected retinas. The retinas are stained for EGFP (green), cell nuclei (gray), and for the inner plexiform layer strata using choline acetyltransferase (ChAT) (magenta). POS, photoreceptor outer segments; ONL, outer nuclear layer; OPL, outer plexiform layer; IPL, inner plexiform layer; CGL, ganglion cell layer.

C The number of genome copies per cell was estimated for purified AAV2/8BP2 compared to AAV2/8 following transduction of HEK293 cells.

D Cell counts from FACS analysis of retinas from mice (n = 4) subretinally injected with AAV28(EF1α-EGFP) or AAV28BP2(EF1α-EGFP) vector.

E RT-qPCR on RNA from the sorted cells used to determine bipolar cell gene expression levels with 120% increase in Grm6 expression (P = 0.05) and 67% increase in TrpM1 expression (P = 0.04) in the AAV2/8BP2(EF1α-EGFP) cell pool.

F Equivalent expression levels measured between cell pools for the cone photoreceptor genes Opnum1 and Opnum2.

G Representative 40x confocal images of sections from the retinas of mice subretinally injected with AAV28(4 × Grm6-EGFP) (upper panel) and AAV28BP2(4 × Grm6-EGFP) (lower panel). The panel on the left shows sections stained for EGFP (green) and cell nuclei (blue), while the panel on the right shows live fluorescence images.

H Retinas from mice that were intravitreally injected were similarly analyzed.
Figure 3.
drives expression mostly in type 5, 6, and 7 bipolar cells and showed a fourfold increase in the level of expression in the AAV2/8BP2-4 × GRM6-CatCh-EGFP pool of cells; 4×4 drives expression in a subset of bipolar cells terminating between chat strata and showed a 13.6-fold increase in expression; the rod-bipolar-cell-specific prkca showed a 10.4-fold increase, and the pan-ON-bipolar cell marker Grm6 showed a 8.6-fold increase in expression. The high expression of the rod-bipolar-cell-specific protein PKCα in the GFP-pool reflects the high proportion of rod-bipolar cells in the ON-bipolar cell population. Immunostaining for the PKCα protein is shown in retinas of mice subretinally injected with the 4 × GRM6-CatCh-EGFP construct in wild-type AAV2/8 compared to AAV2/8BP2 virus (Fig 3I).

It is also worth noting that no rhodopsin expression was detected from rod photoreceptors, which comprise 70% of the retinal cells, in the RNA from the AAV2/8BP2-4 × GRM6-transduced cell population (Supplementary Fig S7). These results offer us a reasonable estimate of the percentage of ON-bipolar cells we can transduce in the mouse retina. The ON-bipolar cells comprise approximately 7% of the total retinal cells in mice (Jeon et al, 1998), and from FACS data, we find 5% transduction of retinal cells following subretinal injection of the AAV2/8BP2-4 × GRM6-CatCh-EGFP virus. TrpML immunolabeling suggests that 83% of these cells are the target ON-bipolar cells (Fig 3E). Therefore, this novel vector is transducing an estimated 59% of ON-bipolar cells. This figure is supported by the TrpML-colocalization counts (Fig 3D). However, it is arguably a conservative estimate, and total cell counts on flat-mounted retinas transduced with viruses carrying 4 × GRM6-EGFP suggest the upper limit of transduction (Fig 3B).

**Optogenetic stimulation of AAV2/8BP2-transduced ON-bipolar cells in rd1 retina**

In order to test the efficiency of the combined AAV2/8BP2 capsid and 4 × GRM6 promoter in optogenetic stimulations, we injected rd1 mice (which lack photoreceptors after 1 month of age) subretinally with AAV2/8BP2-4 × GRM6-CatCh-EGFP or AAV2/8-4 × GRM6-CatCh-EGFP and recorded from ganglion cells of mice between 12 and 14 weeks of age using multi-electrode arrays. We were unable to detect any ganglion cell photoreceptors in mice injected with AAV2/8-4 × GRM6-CatCh-EGFP except in intrinsically photosensitive retinal ganglion cells (results not shown). However, in mice injected with AAV2/8BP2-4 × GRM6-CatCh-EGFP, ganglion cells responded to light stimulation with short latency, high-frequency spiking (Fig 4). Unlike in previous reports (Lagali et al, 2008; Doroudchi et al, 2011), we found responses from ON, OFF, and ON-OFF cells (Fig 4A), suggesting that both rod-bipolar and cone ON-bipolar cells were driving ganglion cells. Notably, the average peak firing rate of the recorded ganglion cells reached approximately 100 Hz (Fig 4B and D), and we found several ganglion cells with peak firing in the range of 120–180 Hz (Fig 4B). This contrasts with a previous report using AAV-delivered channelrhodopsin-2 stimulation of ON-bipolar cells where the firing frequency reached 20–25 Hz. As shown before (Lagali et al, 2008), we found that stimulation with larger light spots evoked less efficient stimulation than with smaller spots, suggesting the presence of lateral inhibition.

**AAV2/8BP2-mediated transduction of ON-bipolar cells in human retina**

In order to determine whether AAV2/8BP2 is capable of transducing human bipolar (and other) retinal cells, the AAV2/8BP2 capsid carrying a cytomegalovirus (CMV) promoted EGFP cDNA was used to infect human retinal explants. The CMV promoter was used as the explant system shows downregulation of expression of mGluR6 (data not shown), and CMV has previously been shown to function in this tissue system (Fradot et al, 2011). As shown in Supplementary Fig S8, human ON-bipolar cells were GFP-positive and also labeled by immunofluorescence with an antibody against Goz.

**Discussion**

It is most likely that early human trials of optogenetics in the coming years will focus on bipolar cells and persisting cones, which have lost light sensitivity. While headway has been made in achieving viral-mediated transduction and restoring function in the cones of blind mouse retinas in vivo (Busskamp et al, 2010), efficient viral-mediated transduction of optogenetic channels has not been possible in bipolar cells. Nonetheless, Lagali et al (2008) demonstrated that some functional properties of image processing could be restored in rd1 retinas even where only 7% of the bipolar cells express ChR2 delivered by electroporation. Moreover, the ChR2-mediated signals were relayed to the visual cortex and resulted in improvements in visual behavioral tasks. These results hold significant promise for therapeutic outcomes when both the number of bipolar cells expressing the channel and the level of channel expression are increased. Achieving these enhanced levels of expression is the primary goal of this paper. The library screen used to select a virus was designed to...
encompass as much diversity as possible taking into consideration the loss of degeneracy that occurs during library transformation, expansion, and packaging. Many variations on AAV libraries have been done to date, and the success of these libraries relies heavily on the screening process used. We consider the \textit{in vivo} screen using the mglur6-gfp mouse key to the isolation of this virus. Furthermore, the preferential uptake of WT AAV2/8 by non-bipolar cells validated a selection strategy whereby we could isolate variants against a satu- rating background of WT virus.

The synthetic AAV and promoter combination described here will allow us to further probe the molecular basis of bipolar cell function. However, its immediate promise is a strong candidate for the delivery of light-sensing molecules to the bipolar cell. Bipolar cell-based strategies, which use inner retinal processing, might be used after the loss of cone vision, but before the massive reorganization of the inner retina that probably occurs at later stages of retinal degeneration (Jones \textit{et al}, 2003). Preliminary data from experiments in human retinal explants show GFP-positive ON-bipolar cells after infection with AAV2/8BP2 (Supplementary Fig S8), thereby providing evidence that the viral tropism and transgene expression characteristics in mice and humans are similar. Such transduction of human explants could not be achieved using the unmodified AAV2/8 (Busskamp \textit{et al}, 2010). This argues that the strategy developed in mice can ultimately be extrapolated to humans. Further studies, in progress, aim to evaluate variables that may affect the translational potential. In summary, the work described here is an essential first step in the development of optogenetic agents for the reversal of advanced forms of blindness.

**Figure 4.** Light responses in \textit{rd1} mice after transducing with AAV2/8BP2 expressing CatCh.

A Light responses to full field stimulation from six example cells. Both ON, OFF and ON-OFF cells are recorded.
B Histogram of peak firing frequencies.
C Response to increasing spots.
D Firing rate as a function of light intensity.
Materials and Methods

Terminology

Expression construct for capsid genes isolated from the AAV genome is referred to as pAAV. The plasmid expressing the unmutated AAV8 capsid gene is referred to as pAAV8, and the plasmid expressing the mutated AAV8 capsid gene is referred to as pAAV8BP. The virus carrying the AAV2 Inverted Terminal Repeats (ITRs) and with the unmutated AAV8 capsid is referred to as AAV2/8, while the virus carrying the AAV2 ITRs and with the mutated AAV8 capsid is referred to as AAV2/8BP. For simplicity, the recombinant AAV2/8 virus with unmutated capsid is referred to as the “wild-type” virus.

AAV library production

The plasmid pRed-Caps-Lib was created incorporating the AAV8 rep/cap gene expressed from a PGK promoter in reverse orientation to the dsRed gene expressed from a CMV promoter. This double cassette was cloned between the AAV2 ITRs. A fragment of the AAV8 rep/cap gene between the sbf1 and mlu1 sites was synthesized by the company DNA2.0 (https://www.dna20.com/). This region includes the amino acids 587–595 (counting from the first amino acid of AAV8 vp1), and mutations were incorporated at each of these nine positions. The plasmid pRed-Caps-Lib was linearized with sbf1 and mlu1. A second sbf1 site further upstream was initially mutated using a site-directed mutagenesis kit (Agilent Technologies, Wilmington, DE), prior to cloning. It was crucial that no single-cut, partially digested backbone from the wild-type plasmid escaped during the cloning as it would contaminate and saturate the library. Initially therefore a stuffer element was cloned into the region of the wild-type capsid between the sbf1 and mlu1 sites to ensure adequate separation of double-cut and partially digested single-cut fragments on a gel. This 3.2-kb stuffer element also carried a kanamycin resistance containing region. Upon restriction enzyme digest of this “pre-library” plasmid (Supplementary Fig S1A) with sbf1 and mlu1, the larger 3.2-kb kanamycin-containing element was excised and replaced with the 370-bp library fragment carrying the 9 NNK residues. As further control, the transformation was screened for no-growth on agar-kanamycin plates. Hence, the final library plasmid contains 4.27 kb between the ITRs as shown in Supplementary Fig S1B. The synthesized mutated region was ligated with the sbf1/mlu1 digested backbone using T4 DNA ligase (New England Biolabs). Three ligation reactions were pooled, ethanol precipitated, and electroporated into DH10b electrocompetent bacteria (Invitrogen).

To titrate the plasmid library, a series of tenfold dilutions from 100 μl of the 1-ml starter culture of transformation broth were plated on agar-ampicillin plates. This sample was taken from the starter culture after 30 min of incubation of the newly transformed bacteria. We make the assumption that each colony is derived from a single random member of the library and that minimal divisions have taken place prior to plating. Therefore, colony-counting can give an estimate of library diversity and a plasmid library diversity of $2.6 \times 10^5$ cfu/ml was counted. The remainder of the starter culture was used to inoculate 2 l of broth to prepare rep/cap plasmid library DNA for AAV production. (Note: To maximize diversity of the plasmid library, the NNK mutagenesis saturation strategy was applied which theoretically covers all 20 amino acids at each of the 9 sites yielding a potential degeneracy at the amino acid level of 5.12E9. It is clear that only a fraction of the combinations theoretically generated was represented in the recovered library and the efficiency could be improved with further optimization of the cloning process). The AAV library was prepared by cotransfection using the plasmid library DNA and a helper plasmid. This was carried out according to standard procedure with some alterations: To minimize the transfection of multiple different rep/cap genes into each cell (which would lead to encapsidation of a non-“self-coding” genome), a low plasmid concentration was used for the triple transfection (Maheshri et al., 2006)—150 ng of rep/cap library plasmid was used per 150-mm confluent HEK293 cell culture plate. Ultimately, the transfected cell lysates, and broths from 70 confluent 150-mm transfected plates were used to prepare the library. The broth and benzonase-treated lysates were concentrated 20-fold using a tangential flow filtration system before virus purification using a discontinuous iodixanol gradient (Sigma, Optiprep). To estimate the infectious titer of the AAV library, HEK293 cells were seeded at 50% confluency on poly-L-lysine-coated glass coverslips across 10 wells of a 24-well plate. Serial dilutions of the AAV library were added directly onto each well. After 72 h, the cells were fixed with 4% paraformaldehyde (PFA) and washed with PBS and dH2O. The number of fluorescent cells from the well with highest dilution factor that still showed infection was recorded and multiplied by the dilution factor to give the number of infectious units per microliter (IU/μl).

AAV preparation

Standard AAV production of individual viruses was performed as previously described (Grieger et al., 2006) by triple transfection of HEK293 cells with branched polyethyleneimine (PEI) (Polysciences, no. 23966) with a plasmid containing the transgene between the ITRs of AAV2, the AAV-helper plasmid encoding Rep2 and Cap for serotype variants, and the pHGTI-Adeno1 plasmid harboring helper adenoviral genes (both kindly provided by C. Cepko, Harvard Medical School, Boston, MA, USA). The HEK293 cells express the helper E1A/E1b gene (American Type Culture Collection, catalogue number CRL-157). Vectors were purified using a discontinuous iodixanol gradient (Sigma, Optiprep). Encapsidated DNA was quantified by TaqMan RT–PCR (using primers “AAV titer”, Supplementary Table S1), following denaturation of the AAV particles by proteinase-K, and titers were calculated as genome copies (gc) per ml.

In vitro titer assay for individual AAV capsid variants

Capsid genes were cloned in an AAV packaging plasmid for vector production, and used for small-scale vector preparations encoding firefly luciferase to obtain the titer shown (Fig 1E). Physical particle titers were established by TaqMan qPCR (Supplementary Fig S3). Subsequently, AA2/8BP variants were assayed for transduction at equal multiplicity of infection on HEK293 cells. For large-scale viral titer, the encapsidated DNA was quantified by TaqMan RT–PCR (using primers “AAV titer”, Supplementary Table S1),
following denaturation of the AAV particles by proteinase-K, and titers were calculated as genome copies (gc) per ml (Fig 1F).

**Mice**

The GRM6-EGFP mice were kindly provided by Dr. Noga Vardi (University of Pennsylvania). C57Bl/6J were obtained from breeding stock at the Jackson Laboratory (Bar Harbor, ME), and C57Bl/6NCrl and C3HeN mice from breeding stock at the Charles River Laboratories (L’Arbresle Cedex, France). All animal experiments and procedures performed in the US were reviewed and approved according to the guidelines set out in the National Institutes of Health’s Guide for Care and Use of Laboratory Animals with approval by the University of Pennsylvania Institute for Animal Care and Use Committee (IACUC), protocols 804546,804543. All animal experiments and procedures performed in Switzerland were approved by the Swiss Veterinary Office. For these experiments, both eyes of the animals and procedures performed in Switzerland were approved by the Committee (IACUC), protocols 804546,804543. All animal experiments and procedures performed in Switzerland were approved by the Swiss Veterinary Office.

**Construction of the 4 × Grm6 promoter**

The 4 × Grm6 promoter construct was created by iterative cloning of the single Grm6 enhancer element contained within the pGrm6-CY expression plasmid (Lagali et al., 2008). First, the Grm6 enhancer element was amplified by PCR using the primers “Grm6 enhancer” (Supplementary Table S1) to generate XbaI and SspI restriction sites upstream of the Grm6 sequence, and a SalI site at the 3′ terminus of the enhancer element. The PCR product was blunt-ended with the Klenow fragment of DNA polymerase I and then digested with SalI. This DNA fragment was subsequently inserted into the SspI/SalI end and Klenow-blunted 3′ end of the promoter construct to yield the 4 × Grm6 promoter construct.

**Immunohistochemistry and imaging**

Retinas were dissected from the eyecup, fixed in 4% (wt/vol) paraformaldehyde in PBS for 20–30 min, and washed overnight in PBS. They were incubated in 30% sucrose for 30 min at 22–23°C before being submitted to three freeze–thaw cycles. Wholemounts or 150-μm vertical sections cut with a Leica VT1000S vibratome were used. The retinas were then incubated in blocking solution (10% normal donkey serum (vol/vol, Chemicon), 1% bovine serum albumin (wt/vol), and 0.5% Triton X-100 (vol/vol) in PBS, pH 7.4) for 1 h. Primary and secondary antibody applications were done in 3% normal donkey serum, 1% bovine serum albumin, 0.02% sodium acid (wt/vol), and 0.5% Triton X-100 in PBS. Primary antibodies [rabbit antibody to GFP (1:200; Molecular Probes) and goat antibody to ChAT (1:300; Chemicon)] were applied for 3–7 days. In addition, an antibody against the long isoform of TrpM1 (NP_001034193.2) was raised and purified by Eurogentec. We designed this antibody to target a TrpM1L-isoform-specific epitope (C+PQISRSAALTVDPE) and used it for ON-bipolar cell labeling. Secondary antibodies were purchased from Invitrogen (Alexa Fluor 488, Alexa Fluor 555, Alexa Fluor 633) or from Jackson Laboratory (Cy3, Cy5) and used at a concentration of 1:200. The wholemounts and retinal sections were mounted on slides with ProLong Gold antifade reagent (Molecular Probes). Confocal three-dimensional scans of 1024 × 1024 pixel images in a z-stack were taken with a Zeiss LSM 700 confocal microscope using three excitation laser lines (405 nm for DAPI, 488 nm for GFP, and 633 nm for ChAT) and imaged using Zen imaging software (Carl Zeiss MicroImaging GmbH). Images were processed using Fiji (http://fiji.sc/wiki/index.php/ImageJ). Equivalent processing was carried out for both test and control 32-bit images. A z-projection was made on fixed stack size, and the gamma changed to visualize low-value pixels. The images were saved as RGB color and imported into Adobe Illustrator. For wholemount retinas, a local stack was made spanning the bipolar cell body in 40× images of the retinas, and the spot detection performed using fixed threshold in Fiji. For the colocalization study, slices from a stack of 40× images acquired for the red and green color channels were processed as composite in Fiji. The “cell counter” plug-in was used to record cells in different color channels using fixed brightness and contrast settings.

<table>
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<th>Procedure</th>
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FACS analysis and RT-qPCR

Retinas were dissociated as previously described (Siegert et al., 2012). The retinas from left and right eyes were processed separately and counted as separate experiments. Cells were sorted immediately following dissociation on a BD FACSARia cell sorter (Becton Dickinson), and 80,000 cells were collected directly in 600 μl of Trizol LS (Life Technologies) for RNA purification according to the manufacturer’s protocol. The RNA was quantified using a NanoDrop, and all samples normalized to 35 ng/μl concentration before reverse transcription using random hexamer primers (Roche) and transcriptor reverse transcriptase (Roche). The cDNA was diluted 1/5 and a 3 μl volume used in the qPCR. For the TaqMan assay, the probes outlined in Supplementary Table S2 were used (Actb, Rho, Gnr6, TrpM1L, Opm Sul, and Opm wal) with universal master mix (Applied Biosystems). For SYBR Green assays, the desalted primers outlined in Supplementary Table S1 were used (Prkcz, Kcng4, Lhx4, Actb) with SYBR Green reagent (Invitrogen). The mouse β-actin gene was used to normalize the expression levels in the TaqMan reaction, and 18srrRNA used in the SYBR Green reaction. Samples were loaded in triplicate where possible. Relative quantification was performed as previously described (Pfaffl, 2001).

Human retinal explants

Use of human tissue was in compliance with local and federal regulations. De-identified tissue was provided by Miracles in Sight, North Caroline Eye Bank, Winston-Salem, NC, USA, an organization which provides ocular tissue to assist researchers to ultimately find cures for eye conditions/diseases. Experiments conformed to the principles set out in the WMA Declaration of Helsinki and the NIH Belmont Report. A postmortem human retina was obtained and treated with AAV2/8BP2-CMV-GFP at a titer of 4.38 × 1012 gc/ml (and delivering 5.5E10 gc) using methods described (Fradot et al., 2011). Immunofluorescence was carried out 12 days after infection using a mouse primary antibody against Goz to label ON-bipolar cells (Chemicon; mAB3073; 1:500), an Alexa fluorophore-conjugated secondary antibody (Invitrogen, Grand Island, NY, USA), DAPI, and a FV1000 confocal microscope (Olympus, Center Valley, PA, USA).

Electrophysiology

The retina was isolated under dim red light in Ringer’s medium (in mM: 110 NaCl, 2.5 KCl, 1 CaCl2, 1.6 MgCl2, 10 D-glucose, 22 NaHCO3) bubbled with 5% CO2/95% O2. The retina, ganglion side down, was then immobilized on the multi-electrode array by gentle pressing with a cell culture membrane (Transwell 3450-Clear) having hexagonally arranged holes with 200 μm diameter and a center-to-center distance of 400 μm. For the duration of the experiment, the retina was perfused with Ringer’s medium bubbled with 5% CO2/95% O2 at a flow rate of 1.5 ml/min at 35°C. Extracellular voltage was measured with a multi-electrode array (MEA1060 Up-BC amplifier, Multichannel Systems) at 20 kHz. The array was fixed on a motorized table (Scientifica). Light stimulus was generated using a DLP projector (PLUS U1375F) and projected onto the retina by the condenser lens of an inverted microscope (Nikon TE300).

The paper explained

Problem

Excellent safety and efficacy data relating to AAV-mediated retinal gene augmentation therapy have been collected in early- and late-phase clinical trials in children and adults with a rare, early onset blindness called Leber’s Congenital Amaurosis. While this approach could theoretically be used to reverse blindness in other inherited diseases, there are practical limits to its utility, including requirements for intervention before the target cells (photoreceptors/retinal pigment epithelium) have died and identity of the disease-causing gene. There is a large unmet need for a therapy that could be used in any inherited or acquired form of blindness. One possibility for such a broad-based therapy lies in the burgeoning field of optogenetics. In advanced stages of disease where photoreceptors are no longer viable, the inner retinal and CNS visual pathway circuitry can be harnessed by rendering the second-order retinal neurons light-sensitive through delivery of an appropriate optogenetic channel. Until now, this was not possible due to a lack of vectors, which can efficiently and stably transduce such neurons, bipolar cells.

Results

The AAV2/8 recombinant virus was used as a template for library screening of viral capsid mutants that would efficiently transduce bipolar cells. In parallel, a bipolar-cell-specific promoter was optimized for strong, cell-specific expression. One capsid variant, together with a transgene cassette carrying the enhanced promoter, showed high and stable levels of transduction of bipolar cells. This vehicle was used to deliver a channelrhodopsin optogenetic molecule to the retinas of the rd1 mouse. The retina of this mouse typically shows no response to visual stimuli; however, when transduced with the novel channelrhodopsin-expressing virus, robust spiking responses were recorded.

Impact

The engineering of this vector represents an essential step in the development of optogenetic agents for the reversal of advanced forms of blindness.

The spectrum of the stimulus light was determined using a spectrophotometer (Ocean Optics USB2000), and the light intensity was measured using a power meter (Thorlabs S130VC). The stimulation intensity was calculated by integrating the product of the projector spectrum and the normalized absorption spectrum of CatCh. The recorded voltage was bandpass-filtered (400-4000 Hz), and spikes were sorted using the UltraMegaSort software (Kleinfeld Lab, University of California, San Diego). Spike frequency was calculated using 50 ms moving bins. Intrinsically photosensitive retinal ganglion cells were discriminated by their delayed spiking. For quantification, we only used spike frequency values in the first 200 ms after light onset or offset.

Statistics and software

CLC Main Workbench was used for sequence annotation and in silico cloning (CLC-bi, Denmark). PyMOL was used for 3-D visualization of the mutated capsid structures (The PyMOL Molecular Graphics System, Version 1.5.0.4, Schrödinger, LLC.). Zen imaging software (Carl Zeiss MicroImaging GmbH) was used to load images taken by confocal microscopy, and these images were processed using Fiji (http://fiji.sc/wiki/index.php/ImageJ). StepOne software v2 (Applied Biosystems, Life Technologies, Switzerland) was...
used to process qPCR data. Excel (Microsoft Office) and GraphPad Prism 6 (GraphPad Software, Inc., CA, USA) were used for all other statistical calculations. The Mann–Whitney U-test was used to determine significance in differences between pairs. Data were expressed as the mean ± standard error of mean (SEM) where $n \geq 7$, and mean ± standard deviation (SD) where $n < 7$. In the figures, different levels of significance are indicated by * for $P \leq 0.05$, **$P < 0.01$.

**Acknowledgements**

The GRM6-GFP mice used for library screening were kindly provided by Noga Vardi (Perelman School of Medicine, University of Pennsylvania). TC was funded by grants from Hope for Vision and the Marie Heim-Vögtlin Foundation. Additional support was provided by NEI/NIH 8DP1 EY023177, 1R24EY019861-01A1, Foundation Fighting Blindness, Research to prevent blindness, FM Kirby Foundation.

**Author contributions**

AAV viral libraries were prepared by TC and LV. The original pAAV-Lib was designed by LV. AAVs for comparative viral testing were prepared by JF. Mouse injections for comparative viral testing were carried out by JF, and electroporation was carried out by VB. Cell sorting was performed by HK. The $4 \times$ Crm6 promoter was conceived and designed by PL. It was constructed and tested by AR. Histology, RT-qPCR, and data analysis were done by TC. PH and VB performed the physiology experiments, and PH and AK analyzed the MEA experiments. RH carried out and analyzed the human retinal explant experiments. Experiment planning involved TC, LV, BR, and JB, and manuscript preparation was carried out by TC, BR, and JB.

**Conflict of interest**

TC, LH, and JB are co-authors on a US patent application for “Enhanced AAV-mediated gene transfer for retinal therapies”. The other authors declare that they have no conflict of interest.

**References**


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