

Rationale and strategies for the development of safe and effective optimized AAV vectors for human gene therapy

Arun Srivastava¹

¹Division of Cellular and Molecular Therapy, Departments of Pediatrics, Molecular Genetics and Microbiology, Powell Gene Therapy Center, University of Florida College of Medicine, Gainesville, FL, USA

Recombinant adeno-associated virus (AAV) vectors have been, or are currently in use, in 332 phase I/II/III clinical trials in a number of human diseases, and in some cases, remarkable clinical efficacy has also been achieved. There are now three US Food and Drug Administration (FDA)-approved AAV "drugs," but it has become increasingly clear that the first generation of AAV vectors are not optimal. In addition, relatively large vector doses are needed to achieve clinical efficacy, which has been shown to provoke host immune responses culminating in serious adverse events and, more recently, in the deaths of 10 patients to date. Thus, there is an urgent need for the development of the next generation of AAV vectors that are (1) safe, (2) effective, and (3) human tropic. This review describes the strategies to potentially overcome each of the limitations of the first generation of AAV vectors and the rationale and approaches for the development of the next generation of AAV serotype vectors. These vectors promise to be efficacious at significant reduced doses, likely to achieve clinical efficacy, thereby increasing the safety as well as reducing vector production costs, ensuring translation to the clinic with higher probability of success, without the need for the use of immune suppression, for gene therapy of a wide variety of diseases in humans.

INTRODUCTION

Adeno-associated virus (AAV), first discovered in 1965¹ and considered a "biological oddity,"² continued to fascinate only a handful of investigators. Following determination of the complete nucleotide sequence,³ molecular cloning^{4,5} of the wild-type (WT) AAV genome, and the demonstration that the WT AAV possessed the remarkable ability of site-specific integration of the AAV DNA into the long arm of human chromosome 19 (19q13.3),^{6,7} although it must be noted that site-specific integration was observed in cell cultures *in vitro*, the first recombinant AAV vectors were subsequently developed by two independent groups.^{8,9} Further refinements followed,^{10,11} and interest in this vector system has continued to grow exponentially in the past two decades.^{12–14}

The first generation of AAV vectors have been or are currently in use in 331 phase I/II/III clinical trials for a wide variety of human diseases, and in some cases, such as Leber's congenital amaurosis,^{15–17} lipopro-

tein lipase deficiency,¹⁸ hemophilia B,^{19–26} aromatic L-amino acid decarboxylase deficiency,²⁷ choroideremia,²⁸ Leber hereditary optic neuropathy,^{29,30} hemophilia A,^{31–34} and spinal muscular atrophy,³⁵ unexpected, remarkable clinical efficacy has also been achieved. Several AAV serotype vectors are now available, which have shown clinical efficacy in a number of human diseases in animal models.^{36,37} Thus far, three AAV "drugs"—Luxturna, Zolgensma, and Hemgenix—have been approved by the US Food and Drug Administration (FDA).^{38,39}

Despite these remarkable achievements, it has become increasingly clear that the first generation of AAV vectors currently in use are not optimal. For example, despite their efficacy in animal models, these vectors have failed to show clinical efficacy in some cases. In addition, relatively large vector doses are needed to achieve clinical efficacy. The use of high doses has been shown to provoke host immune responses culminating in serious adverse events and, more recently, in the deaths of 10 patients to date. Thus, it has become increasingly clear that there is an urgent need for the development of the next generation of AAV vectors that are (1) safe, (2) effective, and (3) human tropic. Since AAV evolved as a virus, and not as a vector for the purposes of delivery of therapeutic genes, the host immune system cannot distinguish between AAV as a virus versus AAV as a vector. Thus, the use of AAV vectors composed of naturally occurring capsids is likely to induce immune responses, especially at high doses, since the host immune response is directly correlated with the AAV vector dose. Similarly, AAV as a virus does not express its own genes effectively since its single-stranded DNA genome is transcriptionally inactive. Most of the single-stranded AAV (ssAAV) vectors currently in use are also sub-optimal in expressing therapeutic genes. And finally, the tropisms of AAV vectors in animal models do not necessarily translate well in humans, and hence there is a need to identify and further develop human-tropic AAV vectors. This review describes the strategies to overcome each of the limitations of the first

https://doi.org/10.1016/j.omtn.2023.05.014.

E-mail: aruns@peds.ufl.edu



Correspondence: Arun Srivastava, Cancer and Genetics Research Complex, University of Florida College of Medicine, Room 492-A, 2033 Mowry Road, Gainesville, FL 32611-3633, USA.

Table 1. Reported cases of deaths associated with the use of the first generation of AAV vectors

Sponsor	Disease	Serotype	Vector dose (vg/kg)	Number of patients
Audentes Therapeutics	XLMTM	AAV8	$\begin{array}{c} 3\times10^{14} \\ 1\times10^{14} \end{array}$	3 1
Lysogene	MPS-IIIA	AAVrh10	$7 imes 10^{12}$	1
Pfizer	DMD	AAV9	$2 imes 10^{14}$	1
Novartis	SMA	AAV9	$1.1 imes 10^{14}$	3
Cure Rare Disease	DMD	AAV9	1x10 ¹⁴	1

XLMTM, X-linked myotubular myopathy; MPSIIIA, mucopolysaccharidosis type IIIA; DMD, Duchenne muscular dystrophy; SMA, spinal muscular atrophy.

generation of AAV vectors and the rationale and approaches for the development of the next generation of AAV serotype vectors. These vectors promise to be efficacious at significant reduced doses, likely to achieve clinical efficacy, thereby increasing the safety as well as reducing vector production costs, ensuring translation to the clinic with higher probability of success, without the need for the use of immune suppression, for gene therapy of a wide variety of human diseases.

Problems associated with the first generation of AAV vectors

Despite their remarkable achievements, it has become increasingly clear that the first generation of AAV vectors that are currently in use in clinical trials in humans are not optimal. For example, in some cases, relatively large vector doses are needed to achieve clinical efficacy.^{22,26,31,32,34} It has also become increasingly clear that the currently available first generation of AAV vectors being used at high doses have been shown to provoke host immune responses culminating in serious adverse events and, more recently, in the deaths of 10 patients,^{40–46} as shown in Table 1.

Furthermore, the use of the first generation of AAV serotype vectors has also been reported to lead to serious adverse events or has failed to reach the primary clinical endpoints.^{47–49} These details are provided in Table 2. Similarly, the use of shuffled AAV vectors derived from directed evolution has also led to serious adverse events that have been reported in gene therapy trials with AAV vectors derived from directed evolution^{50–53} (Table S1).

Taken together, the following conclusions can be drawn: (1) the use of the first generation of AAV vectors composed of naturally occurring capsids is likely to induce immune responses, especially at high doses, because the host immune system cannot distinguish between AAV as a virus versus AAV as a vector; (2) the host immune response is directly correlated with the AAV vector dose; and (3) because the WT AAV did not evolve for the purposes of delivery of therapeutic genes, recombinant AAV (rAAV) vectors composed of naturally occurring capsid are unlikely to be optimal in human clinical trials.^{54,55}

Sponsor	Disease	Serotype	Vector dose (vg/kg)	Symptoms/outcome			
Solid Biosciences	DMD	AAV9	$3 imes 10^{14}$	thrombocytopenia, renal failure, cardio-pulmonary insufficiency			
Pfizer	DMD	AAV9	2×10^{14}	acute kidney injury, atypical hemolytic uremic syndrome-like complement activation, thrombocytopenia			
Sarepta Therapeutics	DMD	AAVrh74	$2 imes 10^{14}$	failed to reach primary clinical endpoint			
Amicus Therapeutics	BD	AAV9	$5 imes 10^{13}$	failed to reach primary clinical endpoint			
DMD, Duchenne muscular dystrophy; BD, Batten disease.							

Thus, it is clear that there is an urgent need for the development of the next generation of AAV vectors that are

- Capable of high-efficiency transduction at lower doses,
- Capable of mediating efficient transgene expression,
- Less immunogenic,
- Capable of obviating the need for immune suppression,
- O Capable of transducing primary human cells and tissues, and
- More cost-effective.

Several elegant approaches have been employed by a number of investigators to overcome the limitations of the first generation of AAV vectors. These include the use of directed evolution,^{56–60} peptide insertions,^{61–66} DNA shuffling,^{67–71} rational design,^{72–74} ancestral vectors,^{75,76} chimeric vectors,^{77,78} dual vectors,^{79–82} protease activation,^{83,84} chemical modifications,⁸⁵ and machine learning.^{86,87} A brief account of our strategies to achieve most, if not all, of the objectives outlined above follows.

Development of capsid-modified AAV vectors

Since AAV evolved as a virus, and not as a vector, the naturally occurring AAV and the first generation of rAAV vectors appear identical externally. Thus, the host immune system cannot distinguish between the two and targets both equally well. It could be argued that the two are not identical because the naturally occurring AAV contains the WT AAV DNA, whereas the rAAV vector contains a therapeutic gene. However, the immune system cannot "see" what is inside of the virus or the vector and, again, targets them both just the same. In other words, we want our immune system to work perfectly when it comes to viruses but not when we use them as vectors, which is unrealistic. It should be pointed out, however, that the vector genome has been shown to increase the Toll-like receptor 9-dependent immune response, at least in a murine models,^{88,89} and that immune response to transgene products can and does occur.⁹⁰



We nonetheless reasoned that the vector has to be different from the virus. The strategy that led to the development of the next generation ("NextGen") of AAV vectors was reported in 2008⁹¹ and is described briefly as follows.

As depicted schematically in Figure 1A, the first generation of AAV2 vectors have 7 tyrosine (Y) residues that are surface exposed. These Y residues are targeted by cellular epidermal growth factor receptor protein tyrosine kinase (EGFR-PTK)⁹² such that a large fraction of incoming AAV vectors become phosphorylated, which serves as a signal for ubiquitination, followed by proteasome-mediated degradation,^{93–95} which negatively impacts not only on the transduction efficiency, but the broken down peptides also trigger a cytotoxic T cell response.⁹⁶

Each of the seven Y residues in AAV2 capsids were replaced them with phenylalanine (F) residues to generate 7 different Y-F AAV vec-

Figure 1. Intracellular fate of the first generation of AAV vectors

(A) Schematic representation of the first generation of AAV2 vectors that contain 7 surface-exposed tyrosine (Y) residues, undergo (1) phosphorylation, ubiquitination, and proteasome-mediated degradation in the cytoplasm, and the broken down peptides trigger the MHC class I-mediated CD8⁺ cytotoxic T cell response. Site-directed mutagenesis ② of each of the Y residues to phenylalanine (F) residues leads to the next generation ("NextGen") of AAV vectors, and the transduction efficiency of each Y-F mutant vector is increased, ranging between ${\sim}2\text{-}$ and 11-fold. The combination of the three most efficient mutations 3 into one capsid results in the triple-mutant vector, the transduction efficiency of which is up to \sim 30-fold higher than the first generation of AAV2 vectors. (B) Schematic representation of the life cycle of the first generation of AAV2 vectors that in addition to 7 Y residues, also contain 15 serine (S), 17 threonine (T), and 10 lysine (K) residues that are surface exposed and undergo phosphorylation and ubiquitination, followed by proteasome-mediated degradation in the cytoplasm. Site-directed mutagenesis each of these residues was also performed, and the transduction efficiencies of the resulting NextGen AAV vectors were documented to be significantly increased.

tors. By changing just one amino acid on the capsid, it was observed that the transduction efficiency of these vectors could be improved ranging from between \sim 2- and 11-fold in the mouse liver following tail vein injections.⁹⁴ When the three most efficient mutations were combined into one capsid, the resulting triple-mutant vector was up to \sim 30-fold more efficient than the conventional AAV2 vector in the mouse liver.⁹⁷ More specifically, the triple-mutant AAV2 vectors were shown to mediate phenotypic correction in a mouse model of hemophilia B.⁹⁷ Thus, it was concluded that the NextGen

AAV2 vectors are more efficient than the conventional first generation of AAV2 vectors. Furthermore, the triple-mutant AAV2 vectors were documented to be less immunogenic since they minimize the cytotoxic T cell response by avoiding phosphorylation, ubiquitination, and proteasome-mediated degradation.^{91,96,98} The NextGen AAV2 vectors have also been used in a phase I/II clinical trial and have shown clinical efficacy in patients with Leber hereditary optic neuropathy (LHON), with no adverse events.^{29,30} More specifically, 14 legally blind patients were enrolled in this trial and were followed for up to 24 months. Thirteen of 14 patients showed improved visual acuity, and 1 patient lost vision because of the course of bilateral visual loss, which is characteristic of LHON.

Since 6 of the 7 tyrosine residues are also conserved in all AAV serotypes, mutagenesis of these residues also increases the transduction efficiencies of all AAV serotype vectors evaluated thus far.⁹⁹ In addition to the 7 surface-exposed Y residues, AAV vectors also



Figure 2. Rate-limiting step of viral second-strand DNAsynthesis of the first generation of ssAAV vectors

(A) Schematic model of inhibition of AAV second-strand DNA synthesis by a cellular chaperone protein, FKBP52, phosphorylated forms of which bind to the single-stranded D-sequence at the 3' end of the AAV-ITR, which is also the "packaging signal" of the AAV genome and is indispensable. (B) The D-sequence at the 5' end of the AAV-ITR, on the other hand, is dispensable, deletion of which leads to generation X ("GenX") AAV vectors, transgene expression from which is significantly higher than that from conventional ssAAV vectors.

contain 15 serine (S), 17 threonine (T), and 10 lysine (K) residues that are surface exposed and can be phosphorylated (Y, S, T) or ubiquitinated (K), which leads to proteasome-mediated degradation, as illustrated in Figure 1B. Each of the 15 S residues,¹⁰⁰ 17 of the T residues,¹⁰¹ and 10 of the K residues¹⁰² were mutagenized. Combination of various permutations and combinations of Y-, S-, T-, and K-mutants led to the identification of the most efficient quadruple mutant (QM) that was observed to be ~80-fold more efficient in the mouse liver.¹⁰¹

Thus, the NextGen AAV2 vectors overcome the first major limitation of first-generation AAV2 vectors. Since most, if not all, surface-exposed Y, S, T, and K residues are also highly conserved in all AAV serotypes, the transduction of these vectors can also be significantly increased.⁹⁹

Development of genome-modified AAV vectors

The second major limitation of the first generation of AAV vectors is illustrated in Figure 2. The WT AAV and most of the rAAV vectors contain a ssDNA, which is a problem because there is no host cell RNA polymerase that can transcribe a ssDNA genome.

AAV as a virus does not express its own genes efficiently since viral second-strand DNA synthesis is needed before gene expression can occur. The expectation that AAV as vectors express therapeutic genes to high levels is also unrealistic. Thus, it was reasoned that in the ssAAV vector, the ssDNA genome also needed to be modified to allow viral second-strand DNA synthesis to occur.

This problem has been known since 1997, when it was discovered that a tyrosine-phosphorylated cellular chaperone protein, FKBP52, binds to the single-stranded D-sequence (ssD-sequence) at the 3' inverted rerminal repeat (ITR) and strongly inhibits AAV second-strand DNA synthesis.¹⁰³ Deletion of the D-sequence at the 3' ITR to prevent FKBP52 binding, thus leading to robust second-strand DNA synthesis, resulted in the failure for the AAV genome to undergo packaging, leading to the conclusion that the D-sequence at the 3' end is the "packaging signal" for AAV^{104,105} and thus could not be deleted.^{106,107} However, it was subsequently observed that the deletion of the D-sequence at the 5' end allowed AAV DNA to undergo successful packaging, which led to the development of the generation X ("GenX") vectors, shown schematically in Figure 3B, the extent of the transgene expression from which was up to 8-fold higher than that from the conventional ssAAV vectors.¹⁰⁸ Thus, GenX vectors overcome the second major limitation of the first generation of ssAAV vectors.

A few additional strategies involving the AAV-ITRs deployed by other investigators include the use of ITRs from different AAV serotypes. For example, Engelhardt and colleagues engineered more efficient vectors using AAV2 and AAV5 ITRs at opposite ends of the vector genome.¹⁰⁹ Interestingly, the hybrid ITR-containing vectors were also more efficient in intermolecular and intramolecular homologous recombination and *trans*-splicing compared with those containing the homologous ITRs. In addition, the use of the hybrid-ITR vectors also improved the delivery of transgenes that exceed the AAV packaging capacity.¹¹⁰ Samulski and colleagues described the transcriptional activity of AAV ITRs from several



different serotypes and identified three distinct levels of transcriptional activity independent of the promoter function.¹¹¹ Recently, Duan and colleagues reported the development of CpG-free ITRs and documented that although the vector genome encapsidation was not affected, the vector yield was decreased by ~3-fold.¹¹²

More recently, our own efforts have focused on the development of additional genome-modified AAV vectors, with which it has become feasible to achieve significantly enhanced transgene expression from ssAAV genomes. For example, we observed that the distal 10 nt in the AAV2 D-sequence share partial homology with the glucocorticoid response element (GRE) $\frac{1}{2}$ binding site and that the AAV2 genomes in which the distal 10 nt were replaced with the 15-nt consensus fulllength GRE site resulted in generation Y (GenY) AAV vectors that mediate up to ~6-fold increased transgene expression.¹¹³ Similarly, we previously reported that AAV second-strand DNA synthesis is strongly inhibited by phosphorylated forms of a host cell chaperone protein, FKBP52, which binds to the D-sequence at the 3' end,¹⁰³ but it has not been possible to delete the D-sequence at the 3' ITR as it serves as the "packaging signal" for the AAV genome. $^{\rm 104-107}$ We recently also developed generation Z (GenZ) AAV vectors in which the proximal 10 nt in the D-sequence were replaced with random 10 nt, and one sequence was identified that allowed successful rescue, replication, and packaging of the AAV genome. This sequence was inserted in a rAAV2 genome, replacing the proximal

Figure 3. Strategies for the development of capsid-, genome-, and capsid+genome-modified AAV serotype vectors

(A) Schematic structures of first generation, NextGen, ssAAV, GenX, and optimized (Opt) AAV2 vectors. (B) Schematic structures of Opt AAV2, Opt AAV3, and Opt AAV6 serotype vectors.

10 nt in the D-sequence at both ITRs. The extent of the transgene expression from the resulting GenZ ssAAV vectors is up to \sim 20-fold higher than that from the WT ssAAV vectors.¹¹⁴ Thus, the GenZ ssAAV vectors not only overcome the problem of viral second-strand DNA synthesis, but they behave more like scAAV vectors but without the size limitation.

Development of optimized AAV vectors

The next obvious question was whether GenX genomes could be packaged into NextGen capsids to achieve even higher efficiency of transduction. As shown schematically in Figure 3A, the packaging of the D-sequence-deleted GenX genomes into NextGen capsids would be expected to lead to optimized (Opt) AAV vectors. Indeed, the development of not only Opt AAV2 vectors but also Opt AAV3 vectors, depicted schematically in Figure 5, was reported, and Opt AAV2 and

Opt AAV3 serotype vectors were observed to be \sim 20- to 30-fold more efficient than the corresponding NextGen AAV2 and AAV3 vectors, respectively.¹¹⁵ This strategy can and does work with several additional AAV serotype vectors that have been evaluated. Thus, it can be concluded that Opt AAV serotype vectors overcome both major limitations of the first generation of AAV serotype vectors.

Development of strategies to evade the humoral response to AAV vectors

Beyond the cell-mediated immune response, the humoral response to AAV vectors also remains a major challenge since B cells generate anti-AAV antibodies, making repeat vector dosing difficult, and pre-existing neutralizing anti-AAV antibodies preclude patients from being enrolled in clinical trials. This problem has been addressed by the following three distinct strategies: first, by using anti-CD20 antibodies, transient B cell ablation has been used.^{116,117} Second, the partial sequence homology between the AAV D-sequence and the major histocompatibility complex (MHC) class II promoter has been exploited to generate AAV vectors that can downregulate the host cell MHC class II promoter function leading to suppression of B cell-helper T cell interaction, resulting in inhibition of differentiation and production of plasma cells that generate antibodies.¹¹⁸ And third, two independent groups have reported a promising approach to address this problem by using immunoglobulin G (IgG) antibody-degrading enzymes, IdeS¹¹⁹ and IdeZ.¹²⁰ These



Figure 4. Strategies for dampening the host humoral immune response to AAV vectors ① Transient depletion of B lymphocytes using CD20 antibody, ② AAV D-sequence-mediated suppression of MHC class II gene expression, and ③ transient degradation of pre-existing IgG antibodies using IgG-cleaving IdeS and IdeZ bacterial endopeptidases. Modified image from.¹²¹

strategies are depicted and summarized in Figure 4.¹²¹ More recently, an additional strategy has been described that utilizes neonatal Fc receptor inhibition to enable AAV gene therapy even in the presence of pre-existing humoral immunity.¹²²

Development of human-tropic AAV serotype vectors

Since the tropisms of AAV vectors in animal models do not necessarily translate well in humans, we next wished to identify AAV vectors that specifically and efficiency transduce primary human cell types. In this quest, two human-tropic AAV vectors have been identified that selectively and efficiently transduce primary human cell types. First, of the 10 most commonly used serotypes, AAV3 was observed to be by far the most efficient in transducing primary human hepatocytes,^{123,124} and second, AAV6 was identified to be the most efficient in transducing primary human hematopoietic stem cells.^{125,126} This is depicted schematically in Figure 5. Several other independent investigators have corroborated these observations for both AAV3 and AAV6 serotype vectors for primary human hepatocytes¹²⁷⁻¹³¹ and primary human hematopoietic stem cells,¹³²⁻¹⁴¹ respectively. NextGen AAV3 vectors have also been shown to be significantly more efficient in primary hepatocytes in "humanized" mice¹⁴²⁻¹⁴⁴ and NextGen AAV6 vectors more efficient in primary human hematopoietic stem cells.145,146

However, another important consideration is to develop NextGen AAV vectors that are less liver tropic and instead transduce other organs better for non-liver-specific diseases. This would reduce the risk of severe adverse events (SAEs) associated with liver transduction of most AAV serotype vectors upon systemic administration for non-liver-based diseases.^{40–43}

Concerns regarding the use of high doses of AAV vectors

It has been known for more than four decades that infection by the WT AAV2 in infants and young children leads to no significant clinical sequalae.¹⁴⁷ It has also become increasingly clear that the host immune response to AAV vectors directly correlates with the vector dose and that at a dose of 2×10^{11} vg/kg, AAV vectors are only mildly immunogenic.¹⁴⁸ Thus, it was of interest to reexamine the total doses of AAV vectors that were, or are currently, being used in a number of clinical trials in humans. These details are provided in Table 3.

As can been seen, the estimated total number of cells in a human body is ~30 trillion.¹⁴⁹ Thus, it is quite a testament to the remarkable safety of even the first generation of AAV vectors that humans are easily able to tolerate roughly ~140× (4.2 quadrillions) of AAV vectors as there are number of cells in the body. However, serious adverse events and



deaths have occurred when the vector doses exceed \sim 467× (or higher) the number of cells in the body. Thus, again, the use of Opt AAV serotype vectors is likely to be less immunogenic and more effective at significantly lower doses.⁵⁵

Conclusions

Based on the account presented above, the following conclusions can be drawn.

- The use of the first generation of AAV serotype vectors composed of naturally occurring capsids is not optimal, given the induction of the host cell-mediated immune response, especially at high doses.
- The use of the ssAAV genomes with WT ITRs is also not optimal, given the sub-optimal levels of transgene expression.
- The use of NextGen, GenX, and, preferably, Opt AAV serotype vectors in all future clinical trials should be considered.

Epilogue

AAV, as a virus, did not evolve to be used as a vector for the purposes of delivery of therapeutic genes. Thus, the full potential of AAV as a vector will only be realized after its capsid is modified to evade the host im-

Table 3. Total number of AAV particles/cell in the human body								
Sponsor	Disease	Vector	Dose (vg/kg)	Total dose (quadrillioin)	AAV particles/cell			
uniQure	HB	AAV5	2×10^{13}	1.4	~47			
LogicBio Therapeutics	ММА	LB-001	5×10^{13}	3.5	~117			
BioMarin	HA	AAV5	$6 imes 10^{13}$	4.2	~ 140			
Pfizer	DMD	AAV9	$2 imes 10^{14}$	14.0	~467			
Audentes	XLMTM	AAV8	3×10^{14}	21.0	\sim 700			

Based on the estimated $\sim 3 \times 10^{13}$ (30 trillion) total number of cells in the human body.¹⁴⁹ HB, hemophilia B; MMA, methylmalonic acidemia; HA, hemophilia A; DMD, Duchenne muscular dystrophy; XLMTM, X-linked myotubular myopathy.

Figure 5. Schematic structures of the 10 most commonly used recombinant AAV serotype vectors

AAV3 and AAV6 vectors have been documented to be selectively tropic for high-efficiency transduction of primary human hepatocytes and primary human hematopoietic stem cells, respectively.

mune response and its genome is modified to express optimal levels of the therapeutic transgene. More, the potential use of Opt AAV vectors at significantly reduced doses promises to achieve clinical efficacy, thereby increasing the safety as well as reducing vector production costs, ensuring translation to the clinic with higher probability of success, without the need for the use of immune-suppression, for gene therapy of human diseases. Specifically, Opt AAV serotype vectors are likely

to be less immunogenic and more effective at lower doses, thus further increasing the safety as well as reducing vector production costs, ensuring translation to the clinic with a higher probability of success.¹⁵⁰

SUPPLEMENTAL INFORMATION

Supplemental information can be found online at https://doi.org/10. 1016/j.omtn.2023.05.014.

ACKNOWLEDGMENTS

I wish to thank my colleagues for their helpful comments and suggestions. This research was funded in part by Public Health Service grants R01 GM-119186 and R21 AR-081018 from the National Institutes of Health; a 2021 Global Hemophilia ASPIRE grant from Pfizer; and support from the Kitzman Endowment.

I would like to dedicate this article to the memory of Dr. Nicholas Muzyczka (1947-2023), the Father of AAV vectors.

AUTHOR CONTRIBUTIONS

The author conceptualized and wrote this review article.

DECLARATION OF INTERESTS

The author is a cofounder of, and holds equity in, Lacerta Therapeutics. He is an inventor on several issued/filed patents on rAAV vectors that have been licensed to various gene therapy companies. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

REFERENCES

- Atchison, R.W., Casto, B.C., and Hammon, W.M. (1965). Adenovirus-associated defective virus particles. Science 149, 754–756.
- Berns, K.I. (2013). My life with adeno-associated virus: a long time spent studying a short genome. DNA Cell Biol. 32, 342–347.
- Srivastava, A., Lusby, E.W., and Berns, K.I. (1983). Nucleotide sequence and organization of the adeno-associated virus 2 genome. J. Virol. 45, 555–564.

www.moleculartherapy.org

Review

- Samulski, R.J., Berns, K.I., Tan, M., and Muzyczka, N. (1982). Cloning of adenoassociated virus into pBR322: rescue of intact virus from the recombinant plasmid in human cells. Proc. Natl. Acad. Sci. USA 79, 2077–2081.
- Laughlin, C.A., Tratschin, J.D., Coon, H., and Carter, B.J. (1983). Cloning of infectious adeno-associated virus genomes in bacterial plasmids. Gene 23, 65–73.
- Kotin, R.M., Siniscalco, M., Samulski, R.J., Zhu, X.D., Hunter, L., Laughlin, C.A., McLaughlin, S., Muzyczka, N., Rocchi, M., and Berns, K.I. (1990). Site-specific integration by adeno-associated virus. Proc. Natl. Acad. Sci. USA 87, 2211–2215.
- Samulski, R.J., Zhu, X., Xiao, X., Brook, J.D., Housman, D.E., Epstein, N., and Hunter, L.A. (1991). Targeted integration of adeno-associated virus (AAV) into human chromosome 19. EMBO J. 10, 3941–3950.
- Hermonat, P.L., and Muzyczka, N. (1984). Use of adeno-associated virus as a mammalian DNA cloning vector: transduction of neomycin resistance into mammalian tissue culture cells. Proc. Natl. Acad. Sci. USA 81, 6466–6470.
- Tratschin, J.D., West, M.H., Sandbank, T., and Carter, B.J. (1984). A human parvovirus, adeno-associated virus, as a eucaryotic vector: transient expression and encapsidation of the procaryotic gene for chloramphenicol acetyltransferase. Mol. Cell Biol. 4, 2072–2081.
- 10. Samulski, R.J., Chang, L.S., and Shenk, T. (1987). A recombinant plasmid from which an infectious adeno-associated virus genome can be excised in vitro and its use to study viral replication. J. Virol. 61, 3096–3101.
- Nahreini, P., Woody, M.J., Zhou, S.Z., and Srivastava, A. (1993). Versatile adeno-associated virus 2-based vectors for constructing recombinant virions. Gene 124, 257–262.
- Wang, D., Tai, P.W.L., and Gao, G. (2019). Adeno-associated virus vector as a platform for gene therapy delivery. Nat. Rev. Drug Discov. 18, 358–378.
- Li, C., and Samulski, R.J. (2020). Engineering adeno-associated virus vectors for gene therapy. Nat. Rev. Genet. 21, 255–272.
- Pupo, A., Fernández, A., Low, S.H., François, A., Suárez-Amarán, L., and Samulski, R.J. (2022). AAV vectors: the Rubik's cube of human gene therapy. Mol. Ther. 30, 3515–3541.
- 15. Hauswirth, W.W., Aleman, T.S., Kaushal, S., Cideciyan, A.V., Schwartz, S.B., Wang, L., Conlon, T.J., Boye, S.L., Flotte, T.R., Byrne, B.J., et al. (2008). Treatment of Leber congenital amaurosis due to RPE65 mutations by ocular subretinal injection of adeno-associated virus gene vector: short-term results of a phase I trial. Hum. Gene Ther. 19, 979–990.
- 16. Bainbridge, J.W.B., Smith, A.J., Barker, S.S., Robbie, S., Henderson, R., Balaggan, K., Viswanathan, A., Holder, G.E., Stockman, A., Tyler, N., et al. (2008). Effect of gene therapy on visual function in Leber's congenital amaurosis. N. Engl. J. Med. 358, 2231–2239.
- Maguire, A.M., Simonelli, F., Pierce, E.A., Pugh, E.N., Jr., Mingozzi, F., Bennicelli, J., Banfi, S., Marshall, K.A., Testa, F., et al. (2008). Safety and efficacy of gene transfer for Leber's congenital amaurosis. N. Engl. J. Med. 358, 2240–2248.
- 18. Stroes, E.S., Nierman, M.C., Meulenberg, J.J., Franssen, R., Twisk, J., Henny, C.P., Maas, M.M., Zwinderman, A.H., Ross, C., Aronica, E., et al. (2008). Intramuscular administration of AAV1-lipoprotein lipase S447X lowers triglycerides in lipoprotein lipase-deficient patients. Arterioscler. Thromb. Vasc. Biol. 28, 2303–2304.
- Nathwani, A.C., Tuddenham, E.G.D., Rangarajan, S., Rosales, C., McIntosh, J., Linch, D.C., Chowdary, P., Riddell, A., Pie, A.J., Harrington, C., et al. (2011). Adenovirus-associated virus vector-mediated gene transfer in hemophilia B. N. Engl. J. Med. 365, 2357–2365.
- 20. Nathwani, A.C., Reiss, U.M., Tuddenham, E.G.D., Rosales, C., Chowdary, P., McIntosh, J., Della Peruta, M., Lheriteau, E., Patel, N., Raj, D., et al. (2014). Longterm safety and efficacy of factor IX gene therapy in hemophilia B. N. Engl. J. Med. 371, 1994–2004.
- 21. George, L.A., Sullivan, S.K., Giermasz, A., Rasko, J.E.J., Samelson-Jones, B.J., Ducore, J., Cuker, A., Sullivan, L.M., Majumdar, S., Teitel, J., et al. (2017). Hemophilia B gene therapy with a high-specific-activity factor IX variant. N. Engl. J. Med. 377, 2215–2227.
- 22. Miesbach, W., Meijer, K., Coppens, M., Kampmann, P., Klamroth, R., Schutgens, R., Tangelder, M., Castaman, G., Schwäble, J., Bonig, H., et al. (2018). Gene therapy with adeno-associated virus vector 5-human factor IX in adults with hemophilia B. Blood 131, 1022–1031.

- 23. Konkle, B.A., Walsh, C.E., Escobar, M.A., Josephson, N.C., Young, G., von Drygalski, A., McPhee, S.W.J., Samulski, R.J., Bilic, I., de la Rosa, M., et al. (2021). BAX 335 hemophilia B gene therapy clinical trial results: potential impact of CpG sequences on gene expression. Blood 137, 763–774.
- 24. Chowdary, P., Shapiro, S., Makris, M., Evans, G., Boyce, S., Talks, K., Dolan, G., Reiss, U., Phillips, M., Riddell, A., et al. (2022). Phase 1-2 trial of AAVS3 gene therapy in patients with Hemophilia B. N. Engl. J. Med. 387, 237–247.
- 25. Xue, F., Li, H., Wu, X., Liu, W., Zhang, F., Tang, D., Chen, Y., Wang, W., Chi, Y., Zheng, J., et al. (2022). Safety and activity of an engineered, liver-tropic adeno-associated virus vector expressing a hyperactive Padua factor IX administered with prophylactic glucocorticoids in patients with haemophilia B: a single-centre, single-arm, phase 1, pilot trial. Lancet. Haematol. 9, e504–e513.
- 26. Pipe, S.W., Leebeek, F.W.G., Recht, M., Key, N.S., Castaman, G., Miesbach, W., Lattimore, S., Peerlinck, K., Van der Valk, P., et al. (2023). Gene therapy with etranacogene dezaparvovec for Hemophilia B. N. Engl. J. Med. 388, 706–718.
- Hwu, W.L., Muramatsu, S., Tseng, S.H., Tzen, K.Y., Lee, N.C., Chien, Y.H., Snyder, R.O., Byrne, B.J., Tai, C.H., and Wu, R.M. (2012). Gene therapy for aromatic L-amino acid decarboxylase deficiency. Sci. Transl. Med. 4, 134ra161.
- 28. MacLaren, R.E., Groppe, M., Barnard, A.R., Cottriall, C.L., Tolmachova, T., Seymour, L., Clark, K.R., During, M.J., Cremers, F.P.M., Black, G.C.M., et al. (2014). Retinal gene therapy in patients with choroideremia: initial findings from a phase 1/2 clinical trial. Lancet 383, 1129–1137.
- 29. Feuer, W.J., Schiffman, J.C., Davis, J.L., Porciatti, V., Gonzalez, P., Koilkonda, R.D., Yuan, H., Lalwani, A., Lam, B.L., and Guy, J. (2016). Gene therapy for leber hereditary optic neuropathy: initial results. Ophthalmology *123*, 558–570.
- 30. Guy, J., Feuer, W.J., Davis, J.L., Porciatti, V., Gonzalez, P.J., Koilkonda, R.D., Yuan, H., Hauswirth, W.W., and Lam, B.L. (2017). Gene therapy for leber hereditary optic neuropathy: low- and medium-dose visual results. Ophthalmology 124, 1621–1634.
- 31. Rangarajan, S., Walsh, L., Lester, W., Perry, D., Madan, B., Laffan, M., Yu, H., Vettermann, C., Pierce, G.F., Wong, W.Y., et al. (2017). AAV5-Factor VIII gene transfer in severe Hemophilia A. N. Engl. J. Med. 377, 2519–2530.
- 32. Pasi, K.J., Rangarajan, S., Mitchell, N., Lester, W., Symington, E., Madan, B., Laffan, M., Russell, C.B., Li, M., Pierce, G.F., et al. (2020). Multiyear follow-up of AAV5hFVIII-SQ gene therapy for Hemophilia A. N. Engl. J. Med. 382, 29–40.
- 33. George, L.A., Monahan, P.E., Eyster, M.E., Sullivan, S.K., Ragni, M.V., Croteau, S.E., Rasko, J.E.J., Recht, M., Samelson-Jones, B.J., MacDougall, A., et al. (2021). Multiyear factor VIII expression after AAV gene transfer for Hemophilia A. N. Engl. J. Med. 385, 1961–1973.
- 34. Mahlangu, J., Kaczmarek, R., von Drygalski, A., Shapiro, S., Chou, S.-C., Ozelo, M.C., Kenet, G., Peyvandi, F., Wang, M., Madan, B., et al. (2023). Two-year outcomes of valoctocogene roxaparvovec therapy for Hemophilia A. N. Engl. J. Med. 388, 694–705.
- 35. Mendell, J.R., Al-Zaidy, S., Shell, R., Arnold, W.D., Rodino-Klapac, L.R., Prior, T.W., Lowes, L., Alfano, L., Berry, K., Church, K., et al. (2017). Single-dose gene-replacement therapy for spinal muscular atrophy. N. Engl. J. Med. 377, 1713–1722.
- 36. Gao, G.P., Alvira, M.R., Wang, L., Calcedo, R., Johnston, J., and Wilson, J.M. (2002). Novel adeno-associated viruses from rhesus monkeys as vectors for human gene therapy. Proc. Natl. Acad. Sci. USA 99, 11854–11859.
- 37. Gao, G., Vandenberghe, L.H., Alvira, M.R., Lu, Y., Calcedo, R., Zhou, X., and Wilson, J.M. (2004). Clades of Adeno-associated viruses are widely disseminated in human tissues. J. Virol. 78, 6381–6388.
- 38. Keeler, A.M., and Flotte, T.R. (2019). Recombinant adeno-associated virus gene therapy in light of Luxturna (and Zolgensma and glybera): where are we, and how did we get here? Ann Rev Virol 6, 601–621.
- https://www.fda.gov/news-events/press-announcements/fda-approves-first-genetherapy-treat-adults-hemophilia-b.
- 40. Wilson, J.M., and Flotte, T.R. (2020). Moving forward after two deaths in a gene therapy trial of myotubular myopathy. Hum. Gene Ther. 31, 695–696.
- Shieh, P.B., Bönnemann, C.G., Müller-Felber, W., Blaschek, A., Dowling, J.J., Kuntz, N.L., and Seferian, A.M. (2020). Letter to the editor. Hum. Gene Ther. 31, 787.
- .https://lysogene.com/lysogene-provides-update-on-the-aavance-clinical-trialevaluating-lys-saf302-in-patients-with-mps-iiia/.

www.moleculartherapy.org

Review

- 43. Philippidis, A. (2022). After patient death, FDA places hold on pfizer Duchenne muscular dystrophy gene therapy trial. Hum. Gene Ther. 33, 111–115.
- 44. Guillou, J., de Pellegars, A., Porcheret, F., Frémeaux-Bacchi, V., Allain-Launay, E., Debord, C., Denis, M., Péréon, Y., Barnérias, C., Desguerre, I., et al. (2022). Fatal thrombotic microangiopathy case following adeno-associated viral SMN gene therapy. Blood Adv. 6, 4266–4270.
- .https://www.fiercepharma.com/pharma/two-deaths-after-novartis-zolgensmabring-gene-therapys-liver-safety-spotlight-again.
- https://www.genengnews.com/topics/genome-editing/gene-therapy/gene-therapybriefs-cure-rare-disease-ceos-brother-died-in-clinical-trial/.
- 47. Mendell, J.R., Al-Zaidy, S.A., Rodino-Klapac, L.R., Goodspeed, K., Gray, S.J., Kay, C.N., Boye, S.L., Boye, S.E., George, L.A., Salabarria, S., et al. (2021). Current clinical applications of in vivo gene therapy with AAVs. Mol. Ther. 29, 464–488.
- Mullard, A. (2021). Sarepta's DMD gene therapy falls flat. Nat. Rev. Drug Discov. 20, 91.
- .https://www.fiercebiotech.com/biotech/jpm-2022-amicus-axes-gene-therapyprogram-for-type-batten-disease-advances-another.
- .https://www.globenewswire.com/news-release/2021/07/22/2267699/32452/en/ Adverum-Provides-Update-on-ADVM-022-and-the-INFINITY-Trial-in-Patientswith-Diabetic-Macular-Edema.html.
- https://sparktx.com/press_releases/spark-therapeutics-spk-8011-suggests-stableand-durable-factor-viii-expression-in-largest-phase-1-2-gene-therapy-study-inhemophilia-a-to-date/.
- Philippidis, A. (2023). Gene therapy briefs FDA places clinical hold on 4D Molecular Therapeutics Fabry Program. Hum. Gene Ther. 34, 177–179.
- https://globalgenes.org/2022/02/02/fda-places-hold-on-logicbios-trial-of-lb-001for-the-treatment-of-pediatric-patients-with-mma/.
- Srivastava, A. (2016). Adeno-associated virus: the naturally occurring virus versus the recombinant vector. Hum. Gene Ther. 27, 1–6.
- 55. Srivastava, A. (2020). AAV vectors: are they safe? Hum. Gene Ther. 31, 697-699.
- 56. Maheshri, N., Koerber, J.T., Kaspar, B.K., and Schaffer, D.V. (2006). Directed evolution of adeno-associated virus yields enhanced gene delivery vectors. Nat. Biotechnol. 24, 198–204.
- Perabo, L., Endell, J., King, S., Lux, K., Hallek, M., and Büning, H. (2006). Combinatorial engineering of a gene therapy vector: directed evolution of adenoassociated virus. J. Gene Med. 8, 155–162.
- 58. Grimm, D., Lee, J.S., Wang, L., Desai, T., Akache, B., Storm, T.A., and Kay, M.A. (2008). In vitro and in vivo gene therapy vector evolution via multispecies interbreeding and retargeting of adeno-associated viruses. J. Virol. 82, 5887–5911.
- 59. Li, W., Zhang, L., Johnson, J.S., Zhijian, W., Grieger, J.C., Ping-Jie, X., Drouin, L.M., Agbandje-McKenna, M., Pickles, R.J., and Samulski, R.J. (2009). Generation of novel AAV variants by directed evolution for improved CFTR delivery to human ciliated airway epithelium. Mol. Ther. 17, 2067–2077.
- 60. Maguire, C.A., Gianni, D., Meijer, D.H., Shaket, L.A., Wakimoto, H., Rabkin, S.D., Gao, G., and Sena-Esteves, M. (2010). Directed evolution of adeno-associated virus for glioma cell transduction. J. Neurooncol. *96*, 337–347.
- 61. Perabo, L., Büning, H., Kofler, D.M., Ried, M.U., Girod, A., Wendtner, C.M., Enssle, J., and Hallek, M. (2003). In vitro selection of viral vectors with modified tropism: the adeno-associated virus display. Mol. Ther. 8, 151–157.
- 62. Müller, O.J., Kaul, F., Weitzman, M.D., Pasqualini, R., Arap, W., Kleinschmidt, J.A., and Trepel, M. (2003). Random peptide libraries displayed on adeno-associated virus to select for targeted gene therapy vectors. Nat. Biotechnol. 21, 1040–1046.
- 63. Varadi, K., Michelfelder, S., Korff, T., Hecker, M., Trepel, M., Katus, H.A., Kleinschmidt, J.A., and Müller, O.J. (2012). Novel random peptide libraries displayed on AAV serotype 9 for selection of endothelial cell-directed gene transfer vectors. Gene Ther. 19, 800–809.
- 64. Yu, C.Y., Yuan, Z., Cao, Z., Wang, B., Qiao, C., Li, J., and Xiao, X. (2009). A muscletargeting peptide displayed on AAV2 improves muscle tropism on systemic delivery. Gene Ther. 16, 953–962.
- 65. Weinmann, J., Weis, S., Sippel, J., Tulalamba, W., Remes, A., El Andari, J., Herrmann, A.K., Pham, Q.H., Borowski, C., Hille, S., et al. (2020). Identification

of a myotropic AAV by massively parallel in vivo evaluation of barcoded capsid variants. Nat. Commun. 11, 5432.

- 66. Tabebordbar, M., Lagerborg, K.A., Stanton, A., King, E.M., Ye, S., Tellez, L., Krunnfusz, A., Tavakoli, S., Widrick, J.J., Messemer, K.A., et al. (2021). Directed evolution of a family of AAV capsid variants enabling potent muscle-directed gene delivery across species. Cell 184, 4919–4938.e22.
- 67. Li, W., Asokan, A., Wu, Z., Van Dyke, T., DiPrimio, N., Johnson, J.S., Govindaswamy, L., Agbandje-McKenna, M., Leichtle, S., Eugene Redmond, D., Jr., et al. (2008). Engineering and selection of shuffled AAV genomes: a new strategy for producing targeted biological nanoparticles. Mol. Ther. *16*, 1252–1260.
- Koerber, J.T., Jang, J.H., and Schaffer, D.V. (2008). DNA shuffling of adeno-associated virus yields functionally diverse viral progeny. Mol. Ther. 16, 1703–1709.
- 69. Yang, L., Jiang, J., Drouin, L.M., Agbandje-McKenna, M., Chen, C., Qiao, C., Pu, D., Hu, X., Wang, D.Z., et al. (2009). A myocardium tropic adeno-associated virus (AAV) evolved by DNA shuffling and in vivo selection. Proc. Natl. Acad. Sci. USA 106, 3946–3951.
- 70. Lisowski, L., Dane, A.P., Chu, K., Zhang, Y., Cunningham, S.C., Wilson, E.M., Nygaard, S., Grompe, M., Alexander, I.E., and Kay, M.A. (2014). Selection and evaluation of clinically relevant AAV variants in a xenograft liver model. Nature 506, 382–386.
- 71. Paulk, N.K., Pekrun, K., Zhu, E., Nygaard, S., Li, B., Xu, J., Chu, K., Leborgne, C., Dane, A.P., Haft, A., et al. (2018). Bioengineered AAV Capsids with combined high human liver transduction in vivo and unique humoral seroreactivity. Mol. Ther. 26, 289–303.
- 72. Lochrie, M.A., Tatsuno, G.P., Christie, B., McDonnell, J.W., Zhou, S., Surosky, R., Pierce, G.F., and Colosi, P. (2006). Mutations on the external surfaces of adeno-associated virus type 2 capsids that affect transduction and neutralization. J. Virol. 80, 821–834.
- 73. Gabriel, N., Hareendran, S., Sen, D., Gadkari, R.A., Sudha, G., Selot, R., Hussain, M., Dhaksnamoorthy, R., Samuel, R., Srinivasan, N., et al. (2013). Bioengineering of AAV2 capsid at specific serine, threonine, or lysine residues improves its transduction efficiency in vitro and in vivo. Hum. Gene Ther. Methods 24, 80–93.
- 74. Sen, D., Gadkari, R.A., Sudha, G., Gabriel, N., Kumar, Y.S., Selot, R., Samuel, R., Rajalingam, S., Ramya, V., Nair, S.C., et al. (2013). Targeted modifications in adeno-associated virus serotype 8 capsid improves its hepatic gene transfer efficiency in vivo. Hum. Gene Ther. Methods 24, 104–116.
- 75. Zinn, E., Pacouret, S., Khaychuk, V., Turunen, H.T., Carvalho, L.S., Andres-Mateos, E., Shah, S., Shelke, R., Maurer, A.C., Plovie, E., et al. (2015). In silico reconstruction of the viral evolutionary lineage yields a potent gene therapy vector. Cell Rep. 12, 1056–1068.
- 76. Santiago-Ortiz, J., Ojala, D.S., Westesson, O., Weinstein, J.R., Wong, S.Y., Steinsapir, A., Kumar, S., Holmes, I., and Schaffer, D.V. (2015). AAV ancestral reconstruction library enables selection of broadly infectious viral variants. Gene Ther. 22, 934–946.
- Hauck, B., Chen, L., and Xiao, W. (2003). Generation and characterization of chimeric recombinant AAV vectors. Mol. Ther. 7, 419–425.
- 78. Bowles, D.E., Rabinowitz, J.E., and Samulski, R.J. (2003). Marker rescue of adenoassociated virus (AAV) capsid mutants: a novel approach for chimeric AAV production. J. Virol. 77, 423–432.
- Duan, D., Yue, Y., Yan, Z., and Engelhardt, J.F. (2000). A new dual-vector approach to enhance recombinant adeno-associated virus-mediated gene expression through intermolecular cis activation. Nat. Med. 6, 595–598.
- Nakai, H., Storm, T.A., and Kay, M.A. (2000). Increasing the size of rAAV-mediated expression cassettes in vivo by intermolecular joining of two complementary vectors. Nat. Biotechnol. 18, 527–532.
- Sun, L., Li, J., and Xiao, X. (2000). Overcoming adeno-associated virus vector size limitation through viral DNA heterodimerization. Nat. Med. 6, 599–602.
- 82. Maina, N., Zhong, L., Li, X., Zhao, W., Han, Z., Bischof, D., Aslanidi, G., Zolotukhin, S., Weigel-Van Aken, K.A., Rivers, A.E., et al. (2008). Optimization of recombinant adeno-associated viral vectors for human beta-globin gene transfer and transgene expression. Hum. Gene Ther. 19, 365–375.
- Guenther, C.M., Brun, M.J., Bennett, A.D., Ho, M.L., Chen, W., Zhu, B., Lam, M., Yamagami, M., Kwon, S., Bhattacharya, N., et al. (2019). Protease-activatable

adeno-associated virus vector for gene delivery to damaged heart tissue. Mol. Ther. 27, 611–622.

- 84. Tong, J.G., Evans, A.C., Ho, M.L., Guenther, C.M., Brun, M.J., Judd, J., Wu, E., and Suh, J. (2019). Reducing off target viral delivery in ovarian cancer gene therapy using a protease-activated AAV2 vector platform. Mol. Ther. 307, 292–301.
- Kelemen, R.E., Mukherjee, R., Cao, X., Erickson, S.B., Zheng, Y., and Chatterjee, A. (2016). A precise chemical strategy to alter the receptor specificity of the adeno-associated virus. Angew. Chem. Int. Ed. Engl. 55, 10645–10649.
- 86. Ogden, P.J., Kelsic, E.D., Sinai, S., and Church, G.M. (2019). Comprehensive AAV capsid fitness landscape reveals a viral gene and enables machine-guided design. Science 366, 1139–1143.
- 87. Bryant, D.H., Bashir, A., Sinai, S., Jain, N.K., Ogden, P.J., Riley, P.F., Church, G.M., Colwell, L.J., and Kelsic, E.D. (2021). Deep diversification of an AAV capsid protein by machine learning. Nat. Biotechnol. 39, 691–696.
- 88. Martino, A.T., Suzuki, M., Markusic, D.M., Zolotukhin, I., Ryals, R.C., Moghimi, B., Ertl, H.C.J., Muruve, D.A., Lee, B., and Herzog, R.W. (2011). The genome of selfcomplementary adeno-associated viral vectors increases Toll-like receptor 9-dependent innate immune responses in the liver. Blood *117*, 6459–6468.
- 89. Herzog, R.W., Cooper, M., Perrin, G.Q., Biswas, M., Martino, A.T., Morel, L., Terhorst, C., and Hoffman, B.E. (2019). Regulatory T cells and TLR9 activation shape antibody formation to a secreted transgene product in AAV muscle gene transfer. Cell. Immunol. 342, 103682.
- Arjomandnejad, M., Dasgupta, I., Flotte, T.R., and Keeler, A.M. (2023). Immunogenicity of recombinant adeno-associated virus (AAV) vectors for gene transfer. BioDrugs 2, 1–19.
- 91. Zhong, L., Li, B., Mah, C.S., Govindasamy, L., Agbandje-McKenna, M., Cooper, M., Herzog, R.W., Zolotukhin, I., Warrington, K.H., Jr., Weigel-Van Aken, K.A., et al. (2008). Next generation of adeno-associated virus 2 vectors: point mutations in tyrosines lead to high-efficiency transduction at lower doses. Proc. Natl. Acad. Sci. USA 105, 7827–7832.
- 92. Mah, C., Qing, K., Khuntirat, B., Ponnazhagan, S., Wang, X.S., Kube, D.M., Yoder, M.C., and Srivastava, A. (1998). Adeno-associated virus type 2-mediated gene transfer: role of epidermal growth factor receptor protein tyrosine kinase in transgene expression. J. Virol. 72, 9835–9843.
- 93. Duan, D., Yue, Y., Yan, Z., Yang, J., and Engelhardt, J.F. (2000). Endosomal processing limits gene transfer to polarized airway epithelia by adeno-associated virus. J. Clin. Invest. 105, 1573–1587.
- 94. Zhong, L., Zhao, W., Wu, J., Li, B., Zolotukhin, S., Govindasamy, L., Agbandje-McKenna, M., and Srivastava, A. (2007). A dual role of EGFR protein tyrosine kinase signaling in ubiquitination of AAV2 capsids and viral second-strand DNA synthesis. Mol. Ther. 15, 1323–1330.
- 95. Zhong, L., Li, B., Jayandharan, G., Mah, C.S., Govindasamy, L., Agbandje-McKenna, M., Herzog, R.W., Weigel-Van Aken, K.A., Hobbs, J.A., et al. (2008). Tyrosine-phosphorylation of AAV2 vectors and its consequences on viral intracellular trafficking and transgene expression. Virology 381, 194–202.
- 96. Mingozzi, F., Maus, M.V., Hui, D.J., Sabatino, D.E., Murphy, S.L., Rasko, J.E.J., Ragni, M.V., Manno, C.S., Sommer, J., Jiang, H., et al. (2007). CD8(+) T-cell responses to adeno-associated virus capsid in humans. Nat. Med. 13, 419–422.
- 97. Markusic, D.M., Herzog, R.W., Aslanidi, G.V., Hoffman, B.E., Li, B., Li, M., Jayandharan, G.R., Ling, C., Zolotukhin, I., Ma, W., et al. (2010). High-efficiency transduction and correction of murine hemophilia B using AAV2 vectors devoid of multiple surface-exposed tyrosines. Mol. Ther. 18, 2048–2056.
- 98. Martino, A.T., Basner-Tschakarjan, E., Markusic, D.M., Finn, J.D., Hinderer, C., Zhou, S., Ostrov, D.A., Srivastava, A., Ertl, H.C.J., Terhorst, C., et al. (2013). Engineered AAV vector minimizes in vivo targeting of transduced hepatocytes by capsid-specific CD8+ T cells. Blood *121*, 2224–2233.
- 99. Berns, K.I., and Srivastava, A. (2019). Next generation of adeno-associated virus vectors for gene therapy for human liver diseases. Gastroenterol. Clin. North Am. 48, 319–330.
- 100. Aslanidi, G.V., Rivers, A.E., Ortiz, L., Govindasamy, L., Ling, C., Jayandharan, G.R., Zolotukhin, S., Agbandje-McKenna, M., and Srivastava, A. (2012). High-efficiency transduction of human monocyte-derived dendritic cells by capsid-modified recombinant AAV2 vectors. Vaccine 30, 3908–3917.

- 101. Aslanidi, G.V., Rivers, A.E., Ortiz, L., Song, L., Ling, C., Govindasamy, L., Van Vliet, K., Tan, M., Agbandje-McKenna, M., and Srivastava, A. (2013). Optimization of the capsid of recombinant adeno-associated virus 2 (AAV2) vectors: the final threshold? PLoS One 8, e59142.
- 102. Li, B., Ma, W., Ling, C., Van Vliet, K., Huang, L.Y., Agbandje-McKenna, M., Srivastava, A., and Aslanidi, G.V. (2015). Site-directed mutagenesis of surfaceexposed lysine residues leads to improved transduction by AAV2, but not AAV8, vectors in murine hepatocytes in vivo. Hum. Gene Ther. Methods 26, 211–220.
- 103. Qing, K., Wang, X.S., Kube, D.M., Ponnazhagan, S., Bajpai, A., and Srivastava, A. (1997). Role of tyrosine phosphorylation of a cellular protein in adeno-associated virus 2-mediated transgene expression. Proc. Natl. Acad. Sci. USA 94, 10879–10884.
- 104. Wang, X.S., Ponnazhagan, S., and Srivastava, A. (1995). Rescue and replication signals of the adeno-associated virus 2 genome. J. Mol. Biol. 250, 573–580.
- 105. Wang, X.S., Ponnazhagan, S., and Srivastava, A. (1996). Rescue and replication of adeno-associated virus type 2 as well as vector DNA sequences from recombinant plasmids containing deletions in the viral inverted terminal repeats: selective encapsidation of viral genomes in progeny virions. J. Virol. 70, 1668–1677.
- 106. Wang, X.S., Qing, K., Ponnazhagan, S., and Srivastava, A. (1997). Adeno-associated virus type 2 DNA replication in vivo: mutation analyses of the D sequence in viral inverted terminal repeats. J. Virol. 71, 3077–3082.
- 107. Ling, C., Wang, Y., Lu, Y., Wang, L., Jayandharan, G.R., Aslanidi, G.V., Li, B., Cheng, B., Ma, W., Lentz, T., et al. (2015). The adeno-associated virus genome packaging puzzle. J. Mol. Genet. Med. 9, 175.
- 108. Ling, C., Wang, Y., Lu, Y., Wang, L., Jayandharan, G.R., Aslanidi, G.V., Li, B., Cheng, B., Ma, W., Lentz, T., et al. (2015). Enhanced transgene expression from recombinant single-stranded D-sequence-substituted adeno-associated virus vectors in human cell lines in vitro and in murine hepatocytes in vivo. J. Virol. 89, 952–961.
- 109. Yan, Z., Zak, R., Zhang, Y., and Engelhardt, J.F. (2005). Inverted terminal repeat sequences are important for intermolecular recombination and circularization of adeno-associated virus genomes. J. Virol. 79, 364–379.
- 110. Yan, Z., Lei-Butters, D.C.M., Zhang, Y., Zak, R., and Engelhardt, J.F. (2007). Hybrid adeno-associated virus bearing nonhomologous inverted terminal repeats enhances dual-vector reconstruction of minigenes in vivo. Hum. Gene Ther. 18, 81–87.
- 111. Earley, L.F., Conatser, L.M., Lue, V.M., Dobbins, A.L., Li, C., Hirsch, M.L., and Samulski, R.J. (2020). Adeno-associated virus serotype-specific inverted terminal repeat sequence role in vector transgene expression. Hum. Gene Ther. 31, 151–162.
- 112. Pan, X., Yue, Y., Boftsi, M., Wasala, L.P., Tran, N.T., Zhang, K., Pintel, D.J., Tai, P.W.L., and Duan, D. (2022). Rational engineering of a functional CpG-free ITR for AAV gene therapy. Gene Ther. 29, 333–345.
- 113. Shoti, K., Qing, K., Keeler, G.D., Byrne, B.J., and Srivastava, A. (2022). Development of genome-modified generation Y (GenY) AAVrh74 vectors with improved transgene expression in a mouse skeletal muscle cell line and in primary human skeletal muscle cells. Mol. Ther. 30, 237.
- 114. Qing, K., Shoti, J., Nath, A., Keeler, G.D., and Srivastava, A. (2023). Development of genome-modified generation Z (GenZ) single-stranded AAV vectors with improved transgene expression in human cells in vitro and in mouse liver in vivo. Mol. Ther. 31, 234–235.
- 115. Ling, C., Li, B., Ma, W., and Srivastava, A. (2016). Development of optimized AAV serotype vectors for high-efficiency transduction at further reduced doses. Hum. Gene Ther. Methods 27, 143–149.
- 116. Corti, M., Elder, M., Falk, D., Lawson, L., Smith, B., Nayak, S., Conlon, T., Clément, N., Erger, K., Lavassani, E., et al. (2014). B-cell depletion is protective against anti-AAV capsid immune response: a human subject case study. Mol. Ther. Methods Clin. Dev. 1, 14033.
- 117. Corti, M., Cleaver, B., Clément, N., Conlon, T.J., Faris, K.J., Wang, G., Benson, J., Tarantal, A.F., Fuller, D., Herzog, R.W., et al. (2015). Evaluation of readministration of a recombinant adeno-associated virus vector expressing acid alpha-glucosidase in pompe disease: preclinical to clinical planning. Hum. Gene Ther. Clin. Dev. 26, 185–193.
- 118. Kwon, H.J., Qing, K., Ponnazhagan, S., Wang, X.S., Markusic, D.M., Gupte, S., Boye, S.E., and Srivastava, A. (2020). Adeno-associated virus D-sequence-mediated suppression of a human major histocompatibility class II gene:

implications in the development of adeno-associated virus vectors for modulating humoral immune response. Hum. Gene Ther. *31*, 565–574.

- 119. Leborgne, C., Barbon, E., Alexander, J.M., Hanby, H., Delignat, S., Cohen, D.M., Collaud, F., Muraleetharan, S., Lupo, D., Silverberg, J., et al. (2020). IgG-cleaving endopeptidase enables in vivo gene therapy in the presence of anti-AAV neutralizing antibodies. Nat. Med. 26, 1096–1101.
- 120. Elmore, Z.C., Oh, D.K., Simon, K.E., Fanous, M.M., and Asokan, A. (2020). Rescuing AAV gene transfer from neutralizing antibodies with an IgG-degrading enzyme. JCI Insight 5, e139881.
- 121. https://www.antibodiesinc.com/blogs/news/how-to-make-a-great-antibody.
- 122. Horiuchi, M., Hinderer, C.J., Shankle, H.N., Hayashi, P.M., Chichester, J.A., Kissel, C., Bell, P., Dyer, C., and Wilson, J.M. (2023). Neonatal Fc receptor inhibition enables adeno-associated virus gene therapy despite pre-existing humoral immunity. Hum. Gene Ther. 31. https://doi.org/10.1089/hum.2022.216.
- 123. Glushakova, L.G., Lisankie, M.J., Eruslanov, E.B., Ojano-Dirain, C., Zolotukhin, I., Liu, C., Srivastava, A., and Stacpoole, P.W. (2009). AAV3-mediated transfer and expression of the pyruvate dehydrogenase E1 alpha subunit gene causes metabolic remodeling and apoptosis of human liver cancer cells. Mol. Genet. Metab. 98, 289–299.
- 124. Ling, C., Lu, Y., Kalsi, J.K., Jayandharan, G.R., Li, B., Ma, W., Cheng, B., Gee, S.W.Y., McGoogan, K.E., Govindasamy, L., et al. (2010). Human hepatocyte growth factor receptor is a cellular coreceptor for adeno-associated virus serotype 3. Hum. Gene Ther. 21, 1741–1747.
- 125. Song, L., Kauss, M.A., Kopin, E., Chandra, M., Ul-Hasan, T., Miller, E., Jayandharan, G.R., Rivers, A.E., Aslanidi, G.V., Ling, C., et al. (2013). Optimizing the transduction efficiency of capsid-modified AAV6 serotype vectors in primary human hematopoietic stem cells in vitro and in a xenograft mouse model in vivo. Cytotherapy 15, 986–998.
- 126. Song, L., Li, X., Jayandharan, G.R., Wang, Y., Aslanidi, G.V., Ling, C., Zhong, L., Gao, G., Yoder, M.C., Ling, C., et al. (2013). High-efficiency transduction of primary human hematopoietic stem cells and erythroid lineage-restricted expression by optimized AAV6 serotype vectors in vitro and in a murine xenograft model in vivo. PLoS One 8, e58757.
- 127. Handa, A., Muramatsu, S.I., Qiu, J., Mizukami, H., and Brown, K.E. (2000). Adenoassociated virus (AAV)-3-based vectors transduce haematopoietic cells not susceptible to transduction with AAV-2-based vectors. J. Gen. Virol. 81, 2077–2084.
- 128. Biswas, M., Marsic, D., Li, N., Zou, C., Gonzalez-Aseguinolaza, G., Zolotukhin, I., Kumar, S.R.P., Rana, J., Butterfield, J.S.S., Kondratov, O., et al. (2020). Engineering and in vitro selection of a novel AAV3B variant with high hepatocyte tropism and reduced seroreactivity. Mol. Ther. Methods Clin. Dev. 19, 347–361.
- 129. Purohit, N., Jain, A., Mathews, V., and Jayandharan, G.R. (2019). Molecular characterization of novel Adeno-associated virus variants infecting human tissues. Virus Res. 272, 197716.
- 130. Ito, M., Takino, N., Nomura, T., Kan, A., and Muramatsu, S.I. (2021). Engineered adeno-associated virus 3 vector with reduced reactivity to serum antibodies. Sci. Rep. 11, 9322.
- 131. Yin, L., Keeler, G.D., Zhang, Y., Hoffman, B.E., Ling, C., Qing, K., and Srivastava, A. (2021). AAV3-miRNA vectors for growth suppression of human hepatocellular carcinoma cells in vitro and human liver tumors in a murine xenograft model in vivo. Gene Ther. 28, 422–434.
- 132. Martin, R.M., Ikeda, K., Cromer, M.K., Uchida, N., Nishimura, T., Romano, R., Tong, A.J., Lemgart, V.T., Camarena, J., Pavel-Dinu, M., et al. (2019). Highly efficient and marker-free genome editing of human pluripotent stem cells by CRISPR-Cas9 RNP and AAV6 donor-mediated homologous recombination. Cell Stem Cell 24, 821–828.e5.
- 133. Houghton, B.C., Panchal, N., Haas, S.A., Chmielewski, K.O., Hildenbeutel, M., Whittaker, T., Mussolino, C., Cathomen, T., Thrasher, A.J., and Booth, C. (2022). Genome editing with TALEN, CRISPR-Cas9 and CRISPR-Cas12a in combination with AAV6 homology donor restores T cell function for XLP. Front. Genome Ed. 4, 828489.

- 134. Haltalli, M.L.R., Wilkinson, A.C., Rodriguez-Fraticelli, A., and Porteus, M. (2022). Hematopoietic stem cell gene editing and expansion: state-of-the-art technologies and recent applications. Exp. Hematol. 107, 9–13.
- 135. Cromer, M.K., Vaidyanathan, S., Ryan, D.E., Curry, B., Lucas, A.B., Camarena, J., Kaushik, M., Hay, S.R., Martin, R.M., Steinfeld, I., et al. (2018). Global transcriptional response to CRISPR/Cas9-AAV6-Based genome editing in CD34+ hematopoietic stem and progenitor cells. Mol. Ther. 26, 2431–2442.
- 136. Wang, J., Exline, C.M., DeClercq, J.J., Llewellyn, G.N., Hayward, S.B., Li, P.W.L., Shivak, D.A., Surosky, R.T., Gregory, P.D., Holmes, M.C., et al. (2015). Homology-driven genome editing in hematopoietic stem and progenitor cells using ZFN mRNA and AAV6 donors. Nat. Biotechnol. 33, 1256–1263.
- 137. Yang, H., Qing, K., Keeler, G.D., Yin, L., Mietzsch, M., Ling, C., Hoffman, B.E., Agbandje-McKenna, M., Tan, M., Wang, W., et al. (2020). Enhanced transduction of human hematopoietic stem cells by AAV6 vectors: implications in gene therapy and genome editing. Mol. Ther. Nucleic Acids 20, 451–458.
- 138. Wilkinson, A.C., Dever, D.P., Baik, R., Camarena, J., Hsu, I., Charlesworth, C.T., Morita, C., Nakauchi, H., and Porteus, M.H. (2021). Cas9-AAV6 gene correction of beta-globin in autologous HSCs improves sickle cell disease erythropoiesis in mice. Nat. Commun. 12, 686.
- 139. Bak, R.O., Dever, D.P., Reinisch, A., Cruz Hernandez, D., Majeti, R., and Porteus, M.H. (2017). Multiplexed genetic engineering of human hematopoietic stem and progenitor cells using CRISPR/Cas9 and AAV6. Elife 6, e27873.
- 140. Dudek, A.M., and Porteus, M.H. (2019). AAV6 is superior to clade F AAVs in stimulating homologous recombination-based genome editing in human HSPCs. Mol. Ther. 27, 1701–1705.
- 141. Romero, Z., Lomova, A., Said, S., Miggelbrink, A., Kuo, C.Y., Campo-Fernandez, B., Hoban, M.D., Masiuk, K.E., Clark, D.N., Long, J., et al. (2019). Editing the sickle cell disease mutation in human hematopoietic stem cells: comparison of endonucleases and homologous donor templates. Mol. Ther. 27, 1389–1406.
- 142. Vercauteren, K., Hoffman, B.E., Zolotukhin, I., Keeler, G.D., Xiao, J.W., Basner-Tschakarjan, E., High, K.A., Ertl, H.C., Rice, C.M., Srivastava, A., et al. (2016). Superior in vivo transduction of human hepatocytes using engineered AAV3 capsid. Mol. Ther. 24, 1042–1049.
- 143. Brown, H.C., Doering, C.B., Herzog, R.W., Ling, C., Markusic, D.M., Spencer, H.T., Srivastava, A., and Srivastava, A. (2020). Development of a clinical candidate AAV3 vector for gene therapy of Hemophilia B. Hum. Gene Ther. 31, 1114–1123.
- 144. Kumar, S.R.P., Xie, J., Hu, S., Ko, J., Huang, Q., Brown, H.C., Srivastava, A., Markusic, D.M., Doering, C.B., Spencer, H.T., et al. (2021). Coagulation factor IX gene transfer to non-human primates using engineered AAV3 capsid and hepatic optimized expression cassette. Mol. Ther. Methods Clin. Dev. 23, 98–107.
- 145. Ling, C., Bhukhai, K., Yin, Z., Tan, M., Yoder, M.C., Leboulch, P., Payen, E., and Srivastava, A. (2016). High-efficiency transduction of primary human hematopoietic stem/progenitor cells by AAV6 vectors: strategies for overcoming donor-variation and implications in genome editing. Sci. Rep. 6, 35495.
- 146. Yang, H., Qing, K., Keeler, G.D., Yin, L., Mietzsch, M., Ling, C., Hoffman, B.E., Agbandje-McKenna, M., Tan, M., Wang, W., et al. (2020). Enhanced transduction of human hematopoietic stem cells by AAV6 vectors: implications in gene therapy and genome editing. Mol. Ther. Nucleic Acids 20, 451–458.
- 147. Blacklow, N.R., Hoggan, M.D., Sereno, M.S., Brandt, C.D., Kim, H.W., Parrott, R.H., and Chanock, R.M. (1971). A seroepidemiologic study of Adenovirus-associated virus infection in infants and children. Am. J. Epidemiol. 94, 359–366.
- 148. Zaiss, A.K., Cotter, M.J., White, L.R., Clark, S.A., Wong, N.C.W., Holers, V.M., Bartlett, J.S., and Muruve, D.A. (2008). Complement is an essential component of the immune response to adeno-associated virus vectors. J. Virol. 82, 2727–2740.
- 149. Sender, R., Fuchs, S., and Milo, R. (2016). Revised estimates for the number of human and bacteria cells in the body. PLoS Biol. 14, e1002533.
- 150. https://www.genengnews.com/topics/genome-editing/looking-toward-the-future-of-cell-gene-therapies/.