# An Emerging Adeno-Associated Viral Vector Pipeline for Cardiac Gene Therapy

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# Abstract

The naturally occurring adeno-associated virus (AAV) isolates display diverse tissue tropisms in different hosts. Robust cardiac transduction in particular has been reported for certain AAV strains. Successful applications of these AAV strains in preclinical and clinical settings with a focus on treating cardiovascular disease continue to be reported. At the same time, these studies have highlighted challenges such as cross-species variability in AAV tropism, transduction efficiency, and immunity. Continued progress in our understanding of AAV capsid structure and biology has provided the rationale for designing improved vectors that can possibly address these concerns. The current report provides an overview of cardiotropic AAV, existing gaps in our knowledge, and newly engineered AAV strains that are viable candidates for the cardiac gene therapy clinic.

# Recombinant Adeno-Associated Virus Vectors in Cardiac Gene Transfer: A Historical Perspective

DENO-ASSOCIATED VIRUSES (AAV) are nonpathogenic, Ahelper-dependent parvoviruses with a 4.7kb singlestranded DNA genome. The icosahedral (T=1) virion shell is 25 nm in diameter and comprises 60 copies of viral capsid protein (VP) subunits. The biology of host cell entry, antigenicity, and tissue tropisms displayed in different hosts are determined by clusters of amino acid residues, interdigitating loops, surface topologies, and the three-dimensional structure observed for different AAV capsids (Bowles et al., 2006). Since the discovery of the first AAV strain (AAV2) in the 1960s, several other serotypes and new AAV variants have been isolated. A summary of current knowledge pertaining to the biology, preclinical studies, and clinical applications of the different AAV serotypes and pertinent literature has been reviewed elsewhere (Agbandje-McKenna and Kleinschmidt, 2011; Mingozzi and High, 2011). The focus of the current review is to provide a historical perspective of AAV as a reagent for cardiac gene transfer, outline the biology of various cardiotropic AAV strains, their evaluation in preclinical studies as well as clinical trials focused on cardiac gene therapy, and provide examples of newly engineered AAV strains available for clinical translation.

One of the earliest studies demonstrating that recombinant AAV vectors can be utilized for gene transfer in mammalian hearts was carried out using AAV serotype 2 (Kaplitt et al., 1996). Long-term expression of the lacZ reporter was observed after direct intramyocardial injections in the rat heart for 2 months and up to 6 months after intracoronary infusion in adult pigs. Later studies reported significantly higher transduction efficiencies after intracoronary artery infusions of recombinant AAV2 vectors in adult mice (Svensson et al., 1999). These pilots were rapidly followed by preclinical studies evaluating AAV2mediated cardiac delivery of therapeutic transgenes such as vascular endothelial growth factor (VEGF) in mice (Su et al., 2000, 2002, 2004); delta-sarcoglycan in a hamster model of dilated cardiomyopathy (Kawada *et al.*, 2002; Li *et al.*, 2003); heme oxygenase-1 and superoxide dismutase in a rat model of ischemia-induced myocardial injury (Melo et al., 2002; Agrawal et al., 2004); human growth hormone under the myosin heavy chain promoter in mice (Aikawa *et al.*, 2002); acid alpha-1,4 glucosidase in a mouse model of Pompe disease (Fraites et al., 2002); phospholamban in mouse, rat, and hamster models of heart failure (Hoshijima et al., 2002; Champion et al., 2003; Iwanaga et al., 2004); dominantnegative suppressor of cytokine signaling-1 in a model of enterovirus-mediated cardiac injury (Yasukawa et al., 2003); and microdystrophin delivery in the *mdx* mouse heart (Yue et al., 2003). In addition to these studies, continued validation of AAV2 as a tool for cardiac gene transfer in large animal models, including pigs (Kaspar et al., 2005), dogs (Ferrarini et al., 2006), and baboons (McTiernan et al., 2007), was carried out by several other groups.

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### AAV VECTORS FOR CARDIAC GENE THERAPY

Against this backdrop of these promising preclinical studies with AAV2, evaluation of new AAV serotypes/isolates for cardiac gene transfer began about a decade ago. In these early comparative studies, AAV1, which was isolated as a contaminant in primate adenovirus stocks, emerged as the lead candidate for cardiac gene transfer (Du et al., 2004). However, at the wake of these studies, robust cardiac transduction was also reported after direct myocardial injections of AAV6, AAV7, and AAV8, all nonhuman primate isolates (Kawamoto et al., 2005; Palomeque et al., 2007); intravenous administration of AAV8 (Wang et al., 2005; Zhu et al., 2005; Palomeque et al., 2007); and intravenous administration of AAV9, a human tissue isolate (Inagaki et al., 2006; Pacak et al., 2006) in various small animal models. Efficacy testing of these new AAV serotypes in different animal models of cardiac disease/heart failure was carried out over the next few years (Su et al., 2006, 2008; Pleger et al., 2007; Townsend *et al.*, 2007; Andino *et al.*, 2008; Bish *et al.*, 2008b,c; Bostick et al., 2008; Byrne et al., 2008; Kawase et al., 2008; Odom et al., 2008; Raake et al., 2008).

After over a decade of evaluating recombinant AAV vectors as prospective tools for cardiac gene transfer, the first phase I/II clinical trial for treatment of heart failure using AAV1 vectors was designed. This study involved intracoronary infusion of AAV1 vectors packaging the *SERCA2a* gene, which encodes a major cardiac calcium cycling protein (Hajjar *et al.*, 2008). Progress and updates pertaining to this clinical trial have been reported in detail (Hajjar, 2013). In the meantime, the validation of cardiotropic AAV serotypes in animal models of cardiac disease has continued over the past 5 years. These specific applications of recombinant AAV vectors in cardiac gene therapy have been reviewed elsewhere (Pacak and Byrne, 2011; Lai and Duan, 2012; Tang *et al.*, 2012; Hajjar, 2013; Scimia *et al.*, 2013).

# Cardiotropic AAV Serotypes: Vector Biology and Species Differences

Recombinant AAV vectors utilize a diverse array of receptors for host cell binding and entry. These early events in the infectious pathway of AAV capsids have a profound impact on the blood circulation profile, biodistribution, tissue uptake and clearance, as well as subsequent downstream events such as intracellular trafficking. Further, variations in capsid structure have been shown to affect AAV tissue tropism, antigenicity, host receptor recognition, and efficiencies of capsid uncoating. When combined with genetic variation in different preclinical animal models and human beings, AAV biology presents a complex challenge toward achieving effective clinical translation. Thus, a thorough understanding of the molecular and cellular factors that dictate AAV cardiotropism in different hosts is essential.

### AAV1

Alpha-2,3 and alpha-2,6-linked sialic acids (SA) have been identified as glycans essential for cell surface binding by AAV1 (Wu *et al.*, 2006b). Coreceptors for AAV1 capsids are currently not known. Cross-species variability in SA linkage is well documented with human beings preferentially expressing alpha-2,6-linked SA, while other preclinical animal models generally overexpress alpha-2,3-linked SA (Altheide *et al.*, 2006; Varki and Schauer, 2009; Cohen and Varki, 2010). In addition,

humans possess an inactivating mutation in the CMP N-Acetyl neuraminic acid hydroxylase gene, which results in the loss of synthesis of glycolylated SA or Neu5Gc and the overexpression of acetylated SA or Neu5Ac (Altheide et al., 2006; Varki and Schauer, 2009; Cohen and Varki, 2010). Since AAV1 was isolated as a contaminant from primate adenovirus stocks, it is conceivable that AAV1 might have evolved to recognize Neu5Gc and SA linkage commonly found in primates. Despite these potential caveats and although no direct comparisons have been made to date, cardiac transduction by AAV1 in different large animal models appears to be quite robust. For instance, AAV1 has been proven effective for cardiac gene transfer through intracoronary infusion in a sheep model of ischemic heart failure (Fargnoli et al., 2013). Another study carried out in a porcine model demonstrated that coadministration of nitroglycerin, a vasodilator, increases AAV1 uptake and mRNA expression in cardiac tissue (Karakikes *et al.*, 2012). These results support the notion that AAV1 does not readily traverse the vascular wall and there is room for improving cardiac gene transfer efficiency with AAV1 vectors. It is also interesting to note that such treatment with vasodilators did not result in increased uptake of AAV1 in lung or liver tissue. These observations are consistent with the notion that AAV1 only appears to transduce tissues in the immediate vicinity of the site of administration. Therefore, both intramyocardial (intramuscular) and intracoronary routes appear optimal for AAV1 administration. In contrast, intravenous injections of AAV1 vectors appear to largely result in liver sequestration. This phenomenon can possibly be attributed to binding of AAV1 capsids by certain serum factors (see the next section on AAV6) that could alter the biodistribution and consequently tissue tropism. These factors should be taken into account while evaluating AAV1 as a lead candidate for cardiac gene therapy trials.

# AAV6

Similar to AAV1, AAV6 is known to utilize alpha2,3- or alpha2,6-linked SA as receptors for cell surface binding (Wu et al., 2006b). However, AAV6 has the distinction of being the only known naturally occurring strain capable of recognizing two glycan receptors-SA and heparan sulfate (HS). Further, epidermal growth factor receptor is a known coreceptor for AAV6 host cell entry (Weller *et al.*, 2010). Of the six amino acid residues that differ between AAV6 and AAV1, a single lysine (K531) has been shown to be impart HS binding ability to AAV6 (Wu et al., 2006a; Ng et al., 2010; Xie et al., 2011). Three other surface-exposed residues are thought to play a critical role in other interactions between the AAV6 capsid and host cells. Whether the ability of AAV6 capsids to bind dual glycan receptors (SA and HS) confers the ability to mediate robust and long-term myocardial gene expression has not been directly examined. In one comparative study, intracoronary injections in mice revealed higher transgene expression levels in the heart with AAV6 vectors in comparison with AAV1, 7, 8, or 9 (Zincarelli et al., 2010). In another study comparing different AAV serotypes 1-8 after intramyocardial injection in rats, AAV1 and AAV6 were found be equally robust, but less efficient than AAV8 in transducing the heart (Palomeque et al., 2007). Further, both AAV1 and AAV6 displayed identical transduction profiles after intrapericardial administration in murine hearts (Bish et al., 2008b). In general, AAV6 appears to have emerged as a superior vector that can achieve highly effective cardiac gene transfer after transendocardial or intracoronary injections in large animal models such as rhesus macaques, dogs, pigs, and sheep (White *et al.*, 2011; Gao *et al.*, 2011b; Bish *et al.*, 2012; Raake *et al.*, 2013). However, it should also be noted that intravenous administration of AAV6 vectors results in significant levels of transgene expression in the liver and skeletal muscle. Thus, similar to AAV1, intravenous administration of AAV6 does not appear to be optimal for cardiac-specific gene transfer applications. Further, coadministration of vasodilators such as VEGF can improve the transduction efficiency of AAV6, corroborating the potential for generating mutants with an improved cardiac transduction profile (Gregorevic *et al.*, 2004).

More recently, both AAV1 and AAV6 have been shown to interact with canine and human galectin 3 binding protein (G3BP), a soluble scavenger receptor (Denard *et al.*, 2012). This interaction is potentiated by the K531 residue unique to AAV6. Interestingly, both AAV1 and AAV6 do not interact with murine or macaque G3BP. Further, both AAV strains have been shown to bind murine C-reactive protein, but not the human counterpart (Denard et al., 2013). These findings highlight the potential for variability in species-specific interactions between AAV capsids and host proteins in general. Whether these interactions (or lack thereof) could affect the biodistribution and transduction profile of AAV6 in patients remains to be determined. Further, it should be noted that preexisting humoral immunity to AAV6 (and AAV1) is higher than that observed for AAV8 or AAV9 in both human beings and different animal models [reviewed recently by Rapti *et al.* (2012) and Louis Jeune *et al.* (2013)]. These studies demonstrate that immunoglobulin and nonimmunoglobulin neutralizing factors affecting AAV6 transduction were particularly high in canine models.

# AAV9

Some of the biology of AAV9, a human isolate, has been resolved over the past two years. Terminal galactose is the primary cell surface receptor for AAV9 (Bell et al., 2011; Shen et al., 2011). Coreceptors for AAV9 are currently unknown. Comparative studies evaluating the transduction efficiencies of different AAV serotypes after intrapericardial or intramyocardial injections have revealed higher transduction by AAV9 in the mouse and rat hearts compared with AAV1, AAV5, AAV6, AAV7, or AAV8 after direct intramyocardial administration (Bish et al., 2008a; Qi et al., 2010; Prasad et al., 2011a,b; Fang et al., 2012). In contrast, transendocardial administration of AAV6, AAV8, and AAV9 in canines revealed that AAV9 is less efficient than AAV6 (Bish et al., 2008c). These results have since been corroborated by another comprehensive study in adult rhesus macaques, wherein AAV9 vectors were found to mediate less efficient cardiac gene transfer when compared with AAV6 and AAV8 after transendocardial injection (Gao et al., 2011a). Despite these findings, recent preclinical studies have demonstrated effective cardiac gene transfer after intracoronary administration of AAV9 vectors in porcine models of heart failure (Pleger et al., 2011; Fish et al., 2013). However, it should be noted that unlike AAV6, AAV9 vectors are less cardiac-specific and display broad biodistribution in off-target organs after administration. Taken together, there appears to be a lack of correlation in the cardiac transduction profile of AAV9 observed in rodents and large animal models. Such cross-species variability can likely be attributed in part to the propensity for AAV9 to rapidly spread to multiple organs after injection into any tissue type. Studies in our lab and others have demonstrated that the prolonged blood circulation profile of AAV9 vectors (Kotchey et al., 2011; Shen et al., 2012) and low glycan binding avidity of this serotype profoundly affect the cardiac transduction profile (Shen et al., 2012). Whether galactose or glycan expression levels in different organs of human and animal origin can serve as an indicator of the cardiac gene transfer efficiency of AAV serotypes in general remains to be determined. It is important to note that despite these drawbacks, AAV9 is more effective than AAV1 or AAV6 for achieving cardiac gene transfer when administered through the intravenous route. Further, preexisting humoral immunity to AAV9 is lower than that observed for AAV1 or AAV6 in both human beings and different animal models [reviewed recently by Rapti et al. (2012) and Louis Jeune et al. (2013)]. It is critical to consider these factors before advancing AAV9 into the cardiac gene transfer clinic.

# Engineered AAV Strains: New Vectors for the Cardiac Gene Transfer Clinic

As discussed above, several naturally occurring AAV serotypes show promise for cardiac gene transfer. AAV1 and AAV6 appear more suitable for cardiac gene transfer through intramyocardial, intrapericardial, or intracoronary routes, while AAV8 and AAV9 can achieve efficient cardiac transduction when administered intravenously. However, these preclinical and clinical studies have also highlighted critical challenges for each vector: (a) variability among different species, (b) transduction of off-target organs such as the liver, and (c) neutralization caused by preexisting humoral immunity and non-immunoglobulin-based serum factors. Novel mutant and chimeric AAV strains displaying improved transduction profiles have since been engineered to address some of these challenges. Several examples are reviewed in detail below, and a comparative analysis of natural and engineered cardiotropic AAV strains is outlined in Table 1.

### Synthetic AAV2-derived strains

The earliest examples of mutant AAV vectors with an improved cardiotropic profile were engineered using AAV2 capsids as a template (Kern et al., 2003; Muller et al., 2006; Raake et al., 2008). These modified AAV2 strains were generated by ablating binding of AAV2 capsids to HS through site-directed mutagenesis of critical arginine residues (R484 and/or R585). The resulting heparin binding-deficient mutants displayed decreased liver tropism and continued cardiac transduction after intravenous administration. The cardiac transduction efficiency of liver-detargeted AAV2 mutants could be potentiated by coadministration of vasodilators such as VEGF (Raake et al., 2008). Subsequent studies in our labs engineered a hybrid liver-detargeted strain, AAV2i8, which is capable of traversing the blood vessel barrier and transducing cardiac and skeletal muscle tissue with high efficiency (Asokan et al., 2010). Since then, we have successfully carried out systemic studies resulting in robust gene expression in primates (Asokan, Samulski and Tarantal, unpublished). More recently, we have engineered novel

	TABLE 1. CC	omparative Analysis of Natu Their Biolo	ral and Engineere ogy, Tissue Tropism	ed Cardiotropic Adei 48, and Antigenicity	NO-ASSOCIATED	Virus Strains,	
AAV strain	Reference	Origin	Glycan receptor usage	Optimal routes of administration	Liver- detargeted?	Transduction in noncardiac tissues	Human NAb prevalence
AAV1	See main text	Primate isolate	SA	Intramyocardial/	No	Low liver,	High
AAV6	See main text	Primate isolate	SA and HS	Intracoronary Intramyocardial/	No	vasculature Liver, skeletal	High
AAV8	See main text	Primate isolate	Unknown	Intravenous	No	Liver, skeletal	Moderate
AAV9	See main text	Human isolate	Gal	Intravenous	No	Inuscie, partereas Liver, skeletal	Moderate
AAVM41	Yang <i>et al.</i> (2009)	DNA shuffling/ directed evolution	Unknown	Intravenous	Yes	muscle, brain Skeletal muscle	Unknown
AAV2- psvsvrp	Ying et al. (2010)	Peptide display/ combinatorial screenino	Unknown; HS-deficient	Intravenous	Yes	Lung, pancreas	Unknown
AAV2- VNICTRLD	Ying et al. (2010)	Peptide display/	Unknown; HS doficiont	Intravenous	Yes	Lung, pancreas	Unknown
AAV2/R585E AAV2i8	Kern <i>et al.</i> (2003) Asokan	Rational mutagenesis Receptor footprint	HS-deficient HS-deficient	Intravenous Intravenous	Yes Yes	Skeletal muscle Skeletal muscle	High Unknown
AAV2i8G9	<i>et al.</i> (2010) Shen <i>et al.</i> (2013)	engmeering Receptor footprint	HS-deficient;	Intravenous	Yes	Skeletal muscle	Unknown
AAV2.5	Bowles et al. (2012)	enguieering Rational mutagenesis	HS	Intramyocardial/	No	Liver	Low, NAb escape
AAV2/265	Li et al. (2012)	Rational mutagenesis	HS	Intramyocardial	No	Liver	Low, NAb escape
AAV3/ cacto	Piacentino	Rational mutagenesis	HS	Intramyocardial	Unknown	Not reported	Unknown
AAV1.9-6	Kotchey	Domain swapping	Gal	Intravenous	No	Liver	Unknown
AAV9.24/ AAV9.45	Pulicherla $et al. (2011)$	Random mutagenesis/ combinatorial screening	Gal-deficient	Intravenous	Yes	Skeletal muscle, brain	Unknown

AAV, adeno-associated virus; Gal, galactose; HS, heparan sulfate; NAb, neutralizing antibody; SA, sialic acid.

chimeric AAV strains by engrafting the galactose receptor footprint from AAV9 onto AAV2i8. The resulting AAV2i8G9 strain can mediate robust cardiac gene expression comparable to AAV9 after intravenous injection (Shen *et al.*, 2013). More importantly, AAV2i8G9 shows 50–1000-fold higher and preferential transduction of cardiac tissue over other major off-target organs such as liver, kidney, and spleen.

Another AAV2 mutant, dubbed AAV2.5, was the first example of a hybrid AAV vector to proceed to clinical trials. The AAV2.5 vector is a rationally engineered AAV strain designed to graft the muscle tropism determinants of AAV1 onto parental AAV2 (Bowles et al., 2012). As shown in preclinical studies and in a phase I clinical trial of Duchenne muscular dystrophy, AAV2.5 is capable of robust gene transfer in skeletal muscle. More recently, AAV2.5 and related mutants thereof were shown to display significantly different humoral immune profiles when compared with the AAV2 parent backbone. The ability to confer altered antigenicity has since been narrowed down to a single amino acid at position 265 and appears to mediate decreased recognition by antisera when administered in mice (Li et al., 2012). In an effort to test the importance of this domain in alternative AAV backbones, a series of capsid variants have been generated (AAV 1-9) and determined to mediate robust transgene expression in numerous murine tissues. Interestingly, a subclass of these mutants appears to preferentially transduce the murine heart after intramyocardial injection (Warischalk and Samulski, unpublished observations). Another related chimera, dubbed AAV3-SASTG, demonstrated robust cardiac transduction in mice higher than AAV2.5 and other related mutants, AAV1 as well as AAV9 vectors, after intramyocardial administration (Piacentino et al., 2012). Evaluation of these novel AAV1/AAV2/AAV3-derived mutant strains in large animal models is forthcoming and likely to provide further insight into the biology of AAVcardiac tissue interactions in different hosts and improved reagents for cardiac gene transfer.

### Synthetic AAV9-derived strains

Nakai and others generated a chimeric AAV1 strain capable of robust cardiac transduction in mice after intravenous administration (Kotchey et al., 2011). The AAV1.9-6 mutant was generated by swapping a 37 amino acid domain (of which 11 residues differ) from the C-terminal region of the AAV9 VP subunit onto AAV1. The mechanisms underlying the enhanced cardiac and liver transduction of this vector remain to be determined. Using a random mutagenesis approach, our lab discovered several novel liver-detargeted AAV9 mutants capable of robust cardiac transduction at levels similar to the parental AAV9 strain after intravenous administration (Pulicherla et al., 2011). The AAV9.24, AAV9.45, and 9.61 mutants harbored 1-2 point mutations in residues within or adjacent to the galactose-binding region and displayed 10-25-fold higher and preferential cardiac transduction over liver and other off-target organs. Since then, we have successfully carried out systemic studies resulting in robust cardiac gene expression in a porcine model of heart failure (Hammond and Asokan, unpublished). Zhong, Srivastava, and others have recently developed a series of tyrosine-mutant AAV vectors that display improved gene transfer efficiency in a wide variety of organs, including liver, muscle,

and eye (Zhong *et al.*, 2008; Petrs-Silva *et al.*, 2011a,b; Qiao *et al.*, 2012). However, it appears that single tyrosine mutations in the context of AAV9 capsids were unable to enhance cardiac transduction efficiency in two different strains of mice (Qiao *et al.*, 2012).

### Synthetic AAV strains from combinatorial libraries

Synthetic cardiotropic AAV strains have also been obtained from combinatorial AAV-based peptide display libraries (Ying et al., 2010). These libraries were generated by insertion of random peptide sequences at the N587/R588 position on the AAV2 VP template. After intravenous injection of the AAV peptide library in mice, hearts were excised at 3 days after injection and subjected to super-infection with human adenovirus 5 as organotypic cultures. Replicating AAV strains were subjected to further rounds of PCR amplification, and screening yielded two new cardiotropic AAV strains. Both AAV2-PSVSPRP and AAV2-VNSTRLP yielded 50-100-fold higher and preferential cardiac transduction over off-target organs such as the liver and kidney. In addition, these strains were found more effective than wild-type AAV2, the liverdetargeted AV2/R585E mutant, and AAV9 vectors after intravenous administration. Additional work in preclinical large animal models will be needed to determine whether these targeting strategies can translate across multiple species.

A myocardium-tropic AAV strain, AAVM41, was recently obtained by subjected DNA-shuffled libraries to directed evolution in mice (Yang et al., 2009). The resulting chimeric AAV capsid was derived from largely from AAV1 and 6 interrupted by an ~20 amino acid residue stretch from AAV8 and ~200 amino acid domain derived from AAV7. AAVM41 was shown to be more efficient than AAV6 in transducing the murine heart and as efficient as AAV9 after intravenous administration. In addition, the mutant also demonstrated >10fold attenuated tropism for liver, skeletal muscle, and other off-target organs. Efficient rescue of cardiac function was also demonstrated after intravenous administration of AAVM41 vectors delivering delta-sarcoglycan in a hamster cardiomyopathy model. Further evaluation of this chimeric AAV portfolio in large animal models would unequivocally establish their position in the clinical pipeline.

Similar directed evolution and combinatorial engineering strategies are likely to provide new and improved vector candidates that can evade preexisting humoral immunity. Early examples of such efforts include the AAV2-derived mutants, AAV2.15 and AAV2.4, both of which contain mutations at critical antigenic sites, thereby capable of evading neutralizing antibodies in human serum (Maheshri et al., 2006). Another approach is to mutate previously mapped immunogenic epitopes on AAV capsids to engineer neutralizing antibody escape mutants (Maersch et al., 2010). The recent mapping of surface-exposed antigenic epitopes using cryo-EM (Gurda et al., 2012, 2013; Harbison et al., 2012; Lerch et al., 2012) is likely to enable structure-driven genetic manipulation of different cardiotropic AAV serotypes to generate novel, neutralizing antibody escape variants suitable for administration in the presence of preexisting humoral immunity. When combined with mutations that enhance cardiotropism and/or cardiac gene transfer efficiency, these next-generation AAV strains are likely to provide the cardiovascular community with improved tools for clinical gene transfer.

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