A METHOD OF DETECTING AND/OR IDENTIFYING ADENO-ASSOCIATED VIRUS (AAV) SEQUENCES AND ISOLATING NOVEL SEQUENCES IDENTIFIED THEREBY

BACKGROUND OF THE INVENTION

Adeno-associated virus (AAV), a member of the Parvovirus family, is a small nonenveloped, icosahedral virus with single-stranded linear DNA genomes of 4.7 kilobases (kb) to 6 kb. AAV is assigned to the genus, Dependovirus, because the virus was discovered as a contaminant in purified adenovirus stocks. AAV's life cycle includes a latent phase at which AAV genomes, after infection, are site specifically integrated into host chromosomes and an infectious phase in which, following either adenovirus or herpes simplex virus infection, the integrated genomes are subsequently rescued, replicated, and packaged into infectious viruses. The properties of non-pathogenicity, broad host range of infectivity, including non-dividing cells, and potential site-specific chromosomal integration make AAV an attractive tool for gene transfer.

Recent studies suggest that AAV vectors may be the preferred vehicle for gene therapy. To date, there have been 6 different serotypes of AAVs isolated from human or non-human primates (NHP) and well characterized. Among them, human serotype 2 is the first AAV that was developed as a gene transfer vector; it has been widely used for efficient gene transfer experiments in different target tissues and animal models. Clinical trials of the experimental application of AAV2 based vectors to some human disease models are in progress, and include such diseases as cystic fibrosis and hemophilia B.

What are desirable are AAV-based constructs for gene delivery.

SUMMARY OF THE INVENTION

In one aspect, the invention provides a novel method of detecting and identifying AAV sequences from cellular DNAs of various human and non-human primate (NHP) tissues using bioinformatics analysis, PCR based gene amplification and cloning technology, based on the nature of latency and integration of AAVs in the absence of helper virus co-infection.

In another aspect, the invention provides method of isolating novel AAV sequences detected using the above described method of the invention. The invention further comprises methods of generating vectors based upon these novel AAV serotypes, for serology and gene

transfer studies solely based on availability of capsid gene sequences and structure of rep/cap gene junctions.

In still another aspect, the invention provides a novel method for performing studies of serology, epidemiology, biodistribution and mode of transmission, using reagents according to the invention, which include generic sets of primers/probes and quantitative real time PCR.

In yet another aspect, the invention provides a method of isolating complete and infectious genomes of novel AAV serotypes from cellular DNA of different origins using RACE and other molecular techniques.

In a further aspect, the invention provides a method of rescuing novel serotypes of AAV genomes from human and NHP cell lines using adenovirus helpers of different origins.

In still a further aspect, the invention provides novel AAV serotypes, vectors containing same, and methods of using same.

These and other aspects of the invention will be readily apparent from the following detailed description of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A through 1AAAR provide an alignment of the nucleic acid sequences encoding at least the cap proteins for the AAV serotypes. The full-length sequences including the ITRs, the rep region, and the capsid region are provided for novel AAV serotype 7 [SEQ ID NO:1], and for previously published AAV1 [SEQ IN NO:6], AAV2 [SEQ ID NO:7]; and AAV3 [SEQ ID NO:8]. Novel AAV serotypes AAV8 [SEQ ID NO:4] and AAV9 [SEQ ID NO:5] are the subject of co-filed applications. The other novel clones of the invention provided in this alignment include: 42-2 [SEQ ID NO:9], 42-8 [SEQ ID NO:27], 42-15 [SEQ ID NO:28], 42-5b [SEQ ID NO: 29], 42-1b [SEQ ID NO:30]; 42-13 [SEQ ID NO: 31], 42-3a [SEQ ID NO: 32], 42-4 [SEQ ID NO:33], 42-5a [SEQ ID NO: 34], 42-10 [SEQ ID NO:35], 42-3b [SEQ ID NO: 36], 42-11 [SEQ ID NO: 37], 42-6b [SEQ ID NO:38], 43-1 [SEQ ID NO: 39], 43-5 [SEQ ID NO: 40], 43-12 [SEQ ID NO:41], 43-20 [SEQ ID NO:42], 43-21 [SEQ ID NO: 43], 43-23 [SEQ ID NO:44], 43-25 [SEQ ID NO: 45], 44.1 [SEQ ID NO:47], 44.5 [SEQ ID NO:47], 223.10 [SEQ ID NO:48], 223.2 [SEQ ID NO:49], 223.4 [SEQ ID NO:50], 223.5 [SEQ ID NO: 51], 223.6 [SEQ ID NO: 52], 223.7 [SEQ ID NO: 53], A3.4 [SEQ ID NO: 54], A3.5 [SEQ ID NO:55], A3.7 [SEQ ID NO: 56], A3.3 [SEQ ID NO:57], 42.12 [SEQ ID NO: 58], 44.2 [SEQ ID NO: 59]. The nucleotide sequences of the signature regions of AAV10 [SEQ ID NO: 117], AAV11 [SEQ ID NO:

118] and AAV12 [SEQ ID NO:119] are provided in this figure. Critical landmarks in the structures of AAV genomes are shown. Gaps are demonstrated by dots. The 3' ITR of AAV1 [SEQ ID NO:6] is shown in the same configuration as in the published sequences. TRS represents terminal resolution site. Notice that AAV7 is the only AAV reported that uses GTG as the initiation codon for VP3.

Figs. 2A through 2F are an alignment of the amino acid sequences of the proteins of the vp1 capsid proteins of previously published AAV serotypes 1 [SEQ ID NO:64], AAV2 [SEQ ID NO:70], AAV3 [SEQ ID NO: 71], AAV4 [SEQ ID NO:63], AAV5 [SEQ ID NO:114], and AAV6 [SEQ ID NO:65] and novel AAV sequences of the invention, including: C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67], A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO:102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-3B [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO:111], 42-6B [SEQ ID NO: 112], 42-12 [SEQ ID NO: 113]. Novel serotypes AAV8 [SEQ ID NO:95] and AAV9 [SEQ ID NO:100] are the subject of co-filed patent applications.

Figs. 3A through 3C provide the amino acid sequences of the AAV7 rep proteins [SEQ ID NO:3].

DETAILED DESCRIPTION OF THE INVENTION

In the present invention, the inventors have found a method which takes advantage of the ability of adeno-associated virus (AAV) to penetrate the nucleus, and, in the absence of a helper virus co-infection, to integrate into cellular DNA and establish a latent infection. This method utilizes a polymerase chain reaction (PCR)-based strategy for detection, identification and/or isolation of sequences of AAVs from DNAs from tissues of human and non-human primate origin as well as from other sources. Advantageously, this method is

also suitable for detection, identification and/or isolation of other integrated viral and non-viral sequences, as described below.

The invention further provides nucleic acid sequences identified according to the methods of the invention. One such adeno-associated virus is of a novel serotype, termed herein serotype 7 (AAV7). Other novel adeno-associated virus serotypes provided herein include AAV10, AAV11, and AAV12. Still other novel AAV serotypes identified according to the methods of the invention are provided in the present specification. See, Figures and Sequence Listing, which is incorporated by reference.

Also provided are fragments of these AAV sequences. Among particularly desirable AAV fragments are the cap proteins, including the vp1, vp2, vp3, the hypervariable regions, the rep proteins, including rep 78, rep 68, rep 52, and rep 40, and the sequences encoding these proteins. Each of these fragments may be readily utilized in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a vector contains the AAV cap and/or rep sequences of the invention.

As described herein, alignments are performed using any of a variety of publicly or commercially available Multiple Sequence Alignment Programs, such as "Clustal W", accessible through Web Servers on the internet. Alternatively, Vector NTI utilities are also used. There are also a number of algorithms known in the art which can be used to measure nucleotide sequence identity, including those contained in the programs described above. As another example, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1, herein incorporated by reference. Similar programs are available for amino acid sequences, e.g., the "Clustal X" program. Generally, any of these programs are used at default settings, although one of skill in the art can alter these settings as needed. Alternatively, one of skill in the art can utilize another algorithm or computer program which provides at least the level of identity or alignment as that provided by the referenced algorithms and programs.

The term "substantial homology" or "substantial similarity," when referring to a nucleic acid, or fragment thereof, indicates that, when optimally aligned with appropriate

nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or an open reading frame thereof, or another suitable fragment which is at least 15 nucleotides in length. Examples of suitable fragments are described herein.

The term "substantial homology" or "substantial similarity," when referring to amino acids or fragments thereof, indicates that, when optimally aligned with appropriate amino acid insertions or deletions with another amino acid, there is amino acid sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or a protein thereof, e.g., a cap protein, a rep protein, or a fragment thereof which is at least 8 amino acids, or more desirably, at least 15 amino acids in length. Examples of suitable fragments are described herein.

By the term "highly conserved" is meant at least 80% identity, preferably at least 90% identity, and more preferably, over 97% identity. Identity is readily determined by one of skill in the art by resort to algorithms and computer programs known by those of skill in the art.

The term "percent sequence identity" or "identical" in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length of the genome, the full-length of a gene coding sequence, or a fragment of at least about 500 to 5000 nucleotides, is desired. However, identity among smaller fragments, e.g. of at least about nine nucleotides, usually at least about 20 to 24 nucleotides, at least about 28 to 32 nucleotides, at least about 36 or more nucleotides, may also be desired. Similarly, "percent sequence identity" may be readily determined for amino acid sequences, over the full-length of a protein, or a fragment thereof. Suitably, a fragment is at least about 8 amino acids in length, and may be up to about 700 amino acids. Examples of suitable fragments are described herein.

The AAV sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors. The invention further provides nucleic acid molecules, gene delivery vectors, and host cells which contain the AAV sequences of the invention.

As described herein, the vectors of the invention containing the AAV capsid proteins of the invention are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors of the invention are particularly advantageous in rAAV readministration and repeat gene therapy.

These and other embodiments and advantages of the invention are described in more detail below. As used throughout this specification and the claims, the terms "comprising" and "including" and their variants are inclusive of other components, elements, integers, steps and the like. Conversely, the term "consisting" and its variants is exclusive of other components, elements, integers, steps and the like.

I. Methods of the Invention

A. Detection of Sequences Via Molecular Cloning

In one aspect, the invention provides a method of detecting and/or identifying target nucleic acid sequences in a sample. This method is particularly well suited for detection of viral sequences which are integrated into the chromosome of a cell, e.g., adeno-associated viruses (AAV) and retroviruses, among others. The specification makes reference to AAV, which is exemplified herein. However, based on this information, one of skill in the art may readily perform the methods of the invention on retroviruses [e.g., feline leukemia virus (FeLV), HTLVI and HTLVII], and lentivirinae [e.g., human immunodeficiency virus (HIV), simian immunodeficiency virus (SIV), feline immunodeficiency virus (FIV), equine infectious anemia virus, and spumavirinal)], among others. Further, the method of the invention may also be used for detection of other viral and non-viral sequences, whether integrated or non-integrated into the genome of the host cell.

As used herein, a sample is any source containing nucleic acids, e.g., tissue, tissue culture, cells, cell culture, and biological fluids including, without limitation, urine and blood. These nucleic acid sequences may be DNA or RNA from plasmids, natural DNA or RNA from any source, including bacteria, yeast, viruses, and higher organisms such as plants or animals. DNA or RNA is extracted from the sample by a variety of techniques known to those of skill in the art, such as those described by Sambrook, Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory). The origin of the sample and the method by which the nucleic acids are obtained for application of the method of the

invention is not a limitation of the present invention. Optionally, the method of the invention can be performed directly on the source of DNA, or on nucleic acids obtained (e.g., extracted) from a source.

The method of the invention involves subjecting a sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers specific for a first region of double-stranded nucleic acid sequences, thereby obtaining amplified sequences.

As used herein, each of the "regions" is predetermined based upon the alignment of the nucleic acid sequences of at least two serotypes (e.g., AAV) or strains (e.g., lentiviruses), and wherein each of said regions is composed of sequences having a 5' end which is highly conserved, a middle which is preferably, but necessarily, variable, and a 3' end which is highly conserved, each of these being conserved or variable relative to the sequences of the at least two aligned AAV serotypes. Preferably, the 5' and/or 3' end is highly conserved over at least about 9, and more preferably, at least 18 base pairs (bp). However, one or both of the sequences at the 5' or 3' end may be conserved over more than 18 bp, more than 25 bp, more than 30 bp, or more than 50 bp at the 5' end. With respect to the variable region, there is no requirement for conserved sequences, these sequences may be relatively conserved, or may have less than 90, 80, or 70% identity among the aligned serotypes or strains.

Each of the regions may span about 100 bp to about 10 kilobase pairs in length. However, it is particularly desirable that one of the regions is a "signature region", i.e., a region which is sufficiently unique to positively identify the amplified sequence as being from the target source. For example, in one embodiment, the first region is about 250 bp in length, and is sufficiently unique among known AAV sequences, that it positively identifies the amplified region as being of AAV origin. Further, the variable sequences within this region are sufficiently unique that can be used to identify the serotype from which the amplified sequences originate. Once amplified (and thereby detected), the sequences can be identified by performing conventional restriction digestion and comparison to restriction digestion patterns for this region in any of AAV1, AAV2, AAV3, AAV4, AAV5, or AAV6, or that of AAV7, AAV10, AAV11, AAV12, or any of the other novel serotypes identified by the invention, which is predetermined and provided by the present invention.

Given the guidance provided herein, one of skill in the art can readily identify such regions among other integrated viruses to permit ready detection and identification of these sequences. Thereafter, an optimal set of generic primers located

within the highly conserved ends can be designed and tested for efficient amplification of the selected region from samples. This aspect of the invention is readily adapted to a diagnostic kit for detecting the presence of the target sequence (e.g., AAV) and for identifying the AAV serotype, using standards which include the restriction patterns for the AAV serotypes described herein or isolated using the techniques described herein. For example, quick identification or molecular serotyping of PCR products can be accomplished by digesting the PCR products and comparing restriction patterns.

Thus, in one embodiment, the "signature region" for AAV spans about bp 2800 to about 3200 of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2, AAV3, AAV4, AAV5, and AAV6. More desirably, the region is about 250 bp, located within bp 2886 to about 3143 bp of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2 [SEQ ID NO:7], AAV3 [SEQ ID NO8], and other AAV serotypes. See, Fig. 1. To permit rapid detection of AAV in the sample, primers which specifically amplify this signature region are utilized. However, the present invention is not limited to the exact sequences identified herein for the AAV signature region, as one of skill in the art may readily alter this region to encompass a shorter fragment, or a larger fragment of this signature region.

The PCR primers are generated using techniques known to those of skill in the art. Each of the PCR primer sets is composed of a 5' primer and a 3' primer. See, e.g., Sambrook et al, cited herein. The term "primer" refers to an oligonucleotide which acts as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced. The primer is preferably single stranded. However, if a double stranded primer is utilized, it is treated to separate its strands before being used to prepare extension products. The primers may be about 15 to 25 or more nucleotides, and preferably at least 18 nucleotides. However, for certain applications shorter nucleotides, e.g., 7 to 15 nucleotides are utilized.

The primers are selected to be sufficiently complementary to the different strands of each specific sequence to be amplified to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the region being amplified. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being completely complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient

complementarity with the sequence of the strand to be amplified to hybridize therewith and form a template for synthesis of the extension product of the other primer.

The PCR primers for the signature region according to the invention are based upon the highly conserved sequences of two or more aligned sequences (e.g., two or more AAV serotypes). The primers can accommodate less than exact identity among the two or more aligned AAV serotypes at the 5' end or in the middle. However, the sequences at the 3' end of the primers correspond to a region of two or more aligned AAV serotypes in which there is exact identity over at least five, preferably, over at least nine base pairs, and more preferably, over at least 18 base pairs at the 3' end of the primers. Thus, the 3' end of the primers is composed of sequences with 100% identity to the aligned sequences over at least five nucleotides. However, one can optionally utilize one, two, or more degenerate nucleotides at the 3' end of the primer.

For example, the primer set for the signature region of AAV was designed based upon a unique region within the AAV capsid, as follows. The 5' primer was based upon nt 2867-2891 of AAV2 [SEQ ID NO:7], 5'-GGTAATTCCTCCGGAAATTGGCATT3'. See, Fig. 1. The 3' primer was designed based upon nt 3096-3122 of AAV2 [SEQ ID NO:7], 5'-GACTCATCAACAACAACTGGGGATTC-3'. However, one of skill in the art may have readily designed the primer set based upon the corresponding regions of AAV 1, AAV3, AAV4, AAV5, AAV6, or based upon the information provided herein, AAV7, AAV10, AAV11, AAV12, or another novel AAV of the invention. In addition, still other primer sets can be readily designed to amplify this signature region, using techniques known to those of skill in the art.

B. Isolation of Target Sequences

As described herein, the present invention provides a first primer set which specifically amplifies the signature region of the target sequence, e.g., an AAV serotype, in order to permit detection of the target. In a situation in which further sequences are desired, e.g., if a novel AAV serotype is identified, the signature region may be extended. Thus, the invention may further utilize one or more additional primer sets.

Suitably, these primer sets are designed to include either the 5' or 3' primer of the first primer set and a second primer unique to the primer set, such that the primer set amplifies a region 5' or 3' to the signature region which anneals to either the 5' end or the 3' end of the signature region. For example, a first primer set is composed of a 5' primer, P1

and a 3' primer P2 to amplify the signature region. In order to extend the signature region on its 3' end, a second primer set is composed of primer P1 and a 3' primer P4, which amplifies the signature region and contiguous sequences downstream of the signature region. In order to extend the signature region on its 5' end, a third primer set is composed of a 5' primer, P5, and primer P2, such that the signature region and contiguous sequences upstream of the signature region are amplified. These extension steps are repeated (or performed at the same time), as needed or desired. Thereafter, the products results from these amplification steps are fused using conventional steps to produce an isolated sequence of the desired length.

The second and third primer sets are designed, as with the primer set for the signature region, to amplify a region having highly conserved sequences among the aligned sequences. Reference herein to the term "second" or "third" primer set is for each of discussion only, and without regard to the order in which these primers are added to the reaction mixture, or used for amplification. The region amplified by the second primer set is selected so that upon amplification it anneals at its 5' end to the 3' end of the signature region. Similarly, the region amplified by the third primer set is selected so that upon amplification it anneals at its 3' end anneals to the 5' end of the signature region. Additional primer sets can be designed such that the regions which they amplify anneal to the either the 5' end or the 3' end of the extension products formed by the second or third primer sets, or by subsequent primer sets.

For example, where AAV is the target sequence, a first set of primers (P1 and P2) are used to amplify the signature region from the sample. In one desirable embodiment, this signature region is located within the AAV capsid. A second set of primers (P1 and P4) is used to extend the 3' end of the signature region to a location in the AAV sequence which is just before the AAV 3' ITR, i.e., providing an extension product containing the entire 3' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P4 primer corresponds to nt 4435 to 4462 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.6 kb, which contains the 0.25 kb signature region. A third set of primers (P3 and P2) is used to extend the 5' end of signature region to a location in the AAV sequences which is in the 3' end of the rep genes, i.e., providing an extension product containing the entire 5' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P3 primer corresponds to nt 1384 to 1409 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.7

kb, which contains the 0.25 kb signature region. Optionally, a fourth set of primers are used to further extend the extension product containing the entire 5' end of the AAV capsid to also include the rep sequences. In one embodiment, the primer designated P5 corresponds to nt 108 to 133 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes and is used in conjunction with the P2 primer.

Following completion of the desired number of extension steps, the various extension products are fused, making use of the signature region as an anchor or marker, to construct an intact sequence. In the example provided herein, AAV sequences containing, at a minimum, an intact AAV cap gene are obtained. Larger sequences may be obtained, depending upon the number of extension steps performed.

Suitably, the extension products are assembled into an intact AAV sequence using methods known to those of skill in the art. For example, the extension products may be digested with DraIII, which cleaves at the DraIII site located within the signature region, to provide restriction fragments which are re-ligated to provide products containing (at a minimum) an intact AAV cap gene. However, other suitable techniques for assembling the extension products into an intact sequence may be utilized. See, generally, Sambrook et al, cited herein.

As an alternative to the multiple extension steps described above, another embodiment of the invention provides for direct amplification of a 3.1 kb fragment which allows isolation of full-length cap sequences. To directly amplify a 3.1 kb full-length cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene is utilized (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGTTCAACTGAAACGA 3', SEQ ID NO: 7) for amplification of AAV sequences including the full-length AAV cap. Typically, following amplification, the products are cloned and sequence analysis is performed with an accuracy of $\geq$ 99.9%. Using this method, the inventors have isolated at least 50 capsid clones which have subsequently been characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1 – rh.37), 6 clones from cynomologous macaques (cy.1 – cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1 – ch.5). These clones are identified

elsewhere in the specification, together with the species of animal from which they were identified and the tissues in that animal these novel sequences have been located.

C. Alternative method for isolating novel AAV

In another aspect, the invention provides an alternative method for isolating novel AAV from a cell. This method involves infecting the cell with a vector which provides helper functions to the AAV; isolating infectious clones containing AAV; sequencing the isolated AAV; and comparing the sequences of the isolated AAV to known AAV serotypes, whereby differences in the sequences of the isolated AAV and known AAV serotypes indicates the presence of a novel AAV.

In one embodiment, the vector providing helper functions provides essential adenovirus functions, including, e.g., E1a, E1b, E2a, E4ORF6. In one embodiment, the helper functions are provided by an adenovirus. The adenovirus may be a wild-type adenovirus, and may be of human or non-human origin, preferably non-human primate (NHP) origin. The DNA sequences of a number of adenovirus types are available from Genbank, including type Ad5 [Genbank Accession No. M73260]. The adenovirus sequences may be obtained from any known adenovirus serotype, such as serotypes 2, 3, 4, 7, 12 and 40, and further including any of the presently identified human types [see, e.g., Horwitz, cited above]. Similarly adenoviruses known to infect non-human animals (e.g., chimpanzees) may also be employed in the vector constructs of this invention. See, e.g., US Patent No. 6,083,716. In addition to wild-type adenoviruses, recombinant viruses or non-viral vectors (e.g., plasmids, episomes, etc.) carrying the necessary helper functions may be utilized. Such recombinant viruses are known in the art and may be prepared according to published techniques. See, e.g., US Patent No. 5,871,982 and US Patent 6,251,677, which describe a hybrid Ad/AAV virus. The selection of the adenovirus type is not anticipated to limit the following invention. A variety of adenovirus strains are available from the American Type Culture Collection, Manassas, Virginia, or available by request from a variety of commercial and institutional sources. Further, the sequences of many such strains are available from a variety of databases including, e.g., PubMed and GenBank.

In another alternative, infectious AAV may be isolated using genome walking technology (Siebert *et al.*, 1995, *Nucleic Acid Research*, 23:1087-1088, Friezner-Degen *et al.*, 1986, *J. Biol. Chem.* **261**:6972-6985, BD Biosciences Clontech, Palo Alto, CA). Genome walking is particularly well suited for identifying and isolating the sequences adjacent to the novel sequences identified according to the method of the invention. For

example, this technique may be useful for isolating inverted terminal repeat (ITRs) of the novel AAV serotype, based upon the novel AAV capsid and/or rep sequences identified using the methods of the invention. This technique is also useful for isolating sequences adjacent to other AAV and non-AAV sequences identified and isolated according to the present invention. See, Examples 3 and 4.

The methods of the invention may be readily used for a variety of epidemiology studies, studies of biodistribution, monitoring of gene therapy via AAV vectors and vector derived from other integrated viruses. Thus, the methods are well suited for use in pre-packaged kits for use by clinicians, researchers, and epidemiologists.

II. Diagnostic Kit

In another aspect, the invention provides a diagnostic kit for detecting the presence of a known or unknown adeno-associated virus (AAV) in a sample. Such a kit may contain a first set of 5' and 3' PCR primers specific for a signature region of the AAV nucleic acid sequence. Alternatively, or additionally, such a kit can contain a first set of 5' and 3' PCR primers specific for the 3.1 kb fragment which includes the full-length AAV capsid nucleic acid sequence identified herein (e.g., the AV1ns and AV2cas primers.) Optionally, a kit of the invention may further contain two or more additional sets of 5' and 3' primers, as described herein, and/or PCR probes. These primers and probes are used according to the present invention amplify signature regions of each AAV serotype, e.g., using quantitative PCR.

The invention further provides a kit useful for identifying an AAV serotype detected according to the method of the invention and/or for distinguishing novel AAV from known AAV. Such a kit may further include one or more restriction enzymes, standards for AAV serotypes providing their "signature restriction enzyme digestions analyses", and/or other means for determining the serotype of the AAV detected.

In addition, kits of the invention may include, instructions, a negative and/or positive control, containers, diluents and buffers for the sample, indicator charts for signature comparisons, disposable gloves, decontamination instructions, applicator sticks or containers, and sample preparator cups, as well as any desired reagents, including media, wash reagents and concentration reagents. Such reagents may be readily selected from among the reagents described herein, and from among conventional concentration reagents. In one desirable embodiment, the wash reagent is an isotonic saline solution which has been

buffered to physiologic pH, such as phosphate buffered saline (PBS); the elution reagent is PBS containing 0.4 M NaCl, and the concentration reagents and devices. For example, one of skill in the art will recognize that reagents such as polyethylene glycol (PEG), or NH_4SO_4 may be useful, or that devices such as filter devices. For example, a filter device with a 100 K membrane would concentrate rAAV.

The kits provided by the present invention are useful for performing the methods described herein, and for study of biodistribution, epidemiology, mode of transmission of novel AAV serotypes in human and NHPs.

Thus, the methods and kits of the invention permit detection, identification, and isolation of target viral sequences, particularly integrated viral sequences. The methods and kits are particularly well suited for use in detection, identification and isolation of AAV sequences, which may include novel AAV serotypes.

In one notable example, the method of the invention facilitated analysis of cloned AAV sequences by the inventors, which revealed heterogeneity of proviral sequences between cloned fragments from different animals, all of which were distinct from the known six AAV serotypes, with the majority of the variation localized to hypervariable regions of the capsid protein. Surprising divergence of AAV sequences was noted in clones isolated from single tissue sources, such as lymph node, from an individual rhesus monkey. This heterogeneity is best explained by apparent evolution of AAV sequence within individual animals due, in part, to extensive homologous recombination between a limited number of co-infecting parenteral viruses. These studies suggest sequence evolution of widely disseminated virus during the course of a natural AAV infection that presumably leads to the formation of swarms of quasispecies which differ from one another in the array of capsid hypervariable regions. This is the first example of rapid molecular evolution of a DNA virus in a way that formerly was thought to be restricted to RNA viruses.

Sequences of several novel AAV serotypes identified by the method of the invention and characterization of these serotypes is provided.

III. Novel AAV Serotypes

A. Nucleic Acid Sequences

Nucleic acid sequences of novel AAV serotypes identified by the methods of the invention are provided. See, SEQ ID NO:1, 9 – 59, and 117 – 120, which are incorporated by reference herein. See also, Fig. 1 and the sequence listing.

For novel serotype AAV7, the full-length sequences, including the AAV 5' ITRs, capsid, rep, and AAV 3' ITRs are provided in SEQ ID NO:1.

For other novel AAV serotypes of the invention, the approximately 3.1 kb fragment isolated according to the method of the invention is provided. This fragment contains sequences encoding full-length capsid protein and all or part of the sequences encoding the rep protein. These sequences include the clones identified below.

For still other novel AAV serotypes, the signature region encoding the capsid protein is provided. For example, the AAV10 nucleic acid sequences of the invention include those illustrated in Fig. 1 [See, SEQ ID NO:117, which spans 255 bases]. The AAV11 nucleic acid sequences of the invention include the DNA sequences illustrated in Fig. 1 [See, SEQ ID NO:118 which spans 258 bases]. The AAV12 nucleic acid sequences of the invention include the DNA sequences illustrated in Fig. 1 [See, SEQ ID NO:119, which consists of 255 bases]. Using the methodology described above, further AAV10, AAV11 and AAV12 sequences can be readily identified and used for a variety of purposes, including those described for AAV7 and the other novel serotypes herein.

Figure 1 provides the non-human primate (NHP) AAV nucleic acid sequences of the invention in an alignment with the previously published AAV serotypes, AAV 1 [SEQ ID NO:6], AAV2 [SEQ ID NO:7], and AAV3 [SEQ ID NO:8]. These novel NHP sequences include those provided in the following Table I, which are identified by clone number:

Table 1

AAV Cap Sequence	Clone Number	Source		
		Species	Tissue	SEQ ID NO (DNA)
Rh.1	Clone 9 (AAV9)	Rhesus	Heart	5
Rh.2	Clone 43.1	Rhesus	MLN	39
Rh.3	Clone 43.5	Rhesus	MLN	40
Rh.4	Clone 43.12	Rhesus	MLN	41
Rh.5	Clone 43.20	Rhesus	MLN	42
Rh.6	Clone 43.21	Rhesus	MLN	43
Rh.7	Clone 43.23	Rhesus	MLN	44

Table 1 (cont'd)

Rh.8	Clone 43.25	Rhesus	MLN	45
Rh.9	Clone 44.1	Rhesus	Liver	46
Rh.10	Clone 44.2	Rhesus	Liver	59
Rh.11	Clone 44.5	Rhesus	Liver	47
Rh.12	Clone 42.1B	Rhesus	MLN	30
Rh.13	42.2	Rhesus	MLN	9
Rh.14	Clone 42.3A	Rhesus	MLN	32
Rh.15	Clone 42.3B	Rhesus	MLN	36
Rh.16	Clone 42.4	Rhesus	MLN	33
Rh.17	Clone 42.5A	Rhesus	MLN	34
Rh.18	Clone 42.5B	Rhesus	MLN	29
Rh.19	Clone 42.6B	Rhesus	MLN	38
Rh.20	Clone 42.8	Rhesus	MLN	27
Rh.21	Clone 42.10	Rhesus	MLN	35
Rh.22	Clone 42.11	Rhesus	MLN	37
Rh.23	Clone 42.12	Rhesus	MLN	58
Rh.24	Clone 42.13	Rhesus	MLN	31
Rh.25	Clone 42.15	Rhesus	MLN	28
Rh.26	Clone 223.2	Rhesus	Liver	49
Rh.27	Clone 223.4	Rhesus	Liver	50
Rh.28	Clone 223.5	Rhesus	Liver	51
Rh.29	Clone 223.6	Rhesus	Liver	52
Rh.30	Clone 223.7	Rhesus	Liver	53
Rh.31	Clone 223.10	Rhesus	Liver	48
Rh.32	Clone C1	Rhesus	Spleen, Duo, Kid & Liver	19
Rh.33	Clone C3	Rhesus		20
Rh.34	Clone C5	Rhesus		21
Rh.35	Clone F1	Rhesus	Liver	22
Rh.36	Clone F3	Rhesus		23
Rh.37	Clone F5	Rhesus		24
Cy.1	Clone 1.3	Cyno	Blood	14
Cy.2	Clone 13.3B	Cyno	Blood	15
Cy.3	Clone 24.1	Cyno	Blood	16
Cy.4	Clone 27.3	Cyno	Blood	17
Cy.5	Clone 7.2	Cyno	Blood	18
Cy.6	Clone 16.3	Cyno	Blood	10

Table 1 (cont'd)

bb.1	Clone 29.3	Baboon	Blood	11
bb.2	Clone 29.5	Baboon	Blood	13
Ch.1	Clone A3.3	Chimp	Blood	57
Ch.2	Clone A3.4	Chimp	Blood	54
Ch.3	Clone A3.5	Chimp	Blood	55
Ch.4	Clone A3.7	Chimp	Blood	56

A novel NHP clone was made by splicing capsids fragments of two chimp adenoviruses into an AAV2 rep construct. This new clone, A3.1, is also termed Ch.5 [SEQ ID NO:20]. Additionally, the present invention includes two human AAV sequences, termed H6 [SEQ ID NO:25] and H2 [SEQ ID NO:26].

The AAV nucleic acid sequences of the invention further encompass the strand which is complementary to the strands provided in the sequences provided in Fig. 1 and the Sequence Listing [SEQ ID NO:1, 9 – 59, 117 –120], nucleic acid sequences, as well as the RNA and cDNA sequences corresponding to the sequences provided in Fig. 1 and the Sequence Listing [SEQ ID NO:1, 9 – 59, 117-120], and their complementary strands. Also included in the nucleic acid sequences of the invention are natural variants and engineered modifications of the sequences of Fig1 and the Sequence Listing [SEQ ID NO:1, 9 – 59, 117-120], and their complementary strands. Such modifications include, for example, labels which are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with a degenerate nucleotide.

Further included in this invention are nucleic acid sequences which are greater than 85%, preferably at least about 90%, more preferably at least about 95%, and most preferably at least about 98 to 99% identical or homologous to the sequences of the invention, including Fig. 1 and the Sequence Listing [SEQ ID NO:1, 9 – 59, 117-120]. These terms are as defined herein.

Also included within the invention are fragments of the novel AAV sequences identified by the method described herein. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments, i.e., fragments which are of biological interest. In one embodiment, these fragments are fragments of the novel sequences of Fig. 1 and the Sequence Listing [SEQ ID NO:1, 9 – 59, 117-120], their complementary strands, cDNA and RNA complementary thereto.

Examples of suitable fragments are provided with respect to the location of these fragments on AAV1, AAV2, or AAV7. However, using the alignment provided herein (obtained using the Clustal W program at default settings), or similar techniques for

generating an alignment with other novel serotypes of the invention, one of skill in the art can readily identify the precise nucleotide start and stop codons for desired fragments.

Examples of suitable fragments include the sequences encoding the three variable proteins (vp) of the AAV capsid which are alternative splice variants: vp1 [e.g., nt 825 to 3049 of AAV7, SEQ ID NO: 1]; vp2 [e.g., nt 1234 - 3049 of AAV7, SEQ ID NO: 1]; and vp 3 [e.g., nt 1434 - 3049 of AAV7, SEQ ID NO:1]. It is notable that AAV7 has an unusual GTG start codon. With the exception of a few house-keeping genes, such a start codon has not previously been reported in DNA viruses. The start codons for vp1, vp2 and vp3 for other AAV serotypes have been believed to be such that they permit the cellular mechanism of the host cell in which they reside to produce vp1, vp2 and vp3 in a ratio of 10%:10%:80%, respectively, in order to permit efficient assembly of the virion. However, the AAV7 virion has been found to assemble efficiently even with this rare GTG start codon. Thus, the inventors anticipate this it is desirable to alter the start codon of the vp3 of other AAV serotypes to contain this rare GTG start codon, in order to improve packaging efficiency, to alter the virion structure and/or to alter location of epitopes (e.g., neutralizing antibody epitopes) of other AAV serotypes. The start codons may be altered using conventional techniques including, e.g., site directed mutagenesis. Thus, the present invention encompasses altered AAV virions of any selected serotype, composed of a vp 3, and/or optionally, vp 1 and/or vp2 having start codons altered to GTG.

Other suitable fragments of AAV, include a fragment containing the start codon for the AAV capsid protein [e.g., nt 468 to 3090 of AAV7, SEQ ID NO:1, nt 725 to 3090 of AAV7, SEQ ID NO: 1, and corresponding regions of the other AAV serotypes]. Still other fragments of AAV7 and the other novel AAV serotypes identified using the methods described herein include those encoding the rep proteins, including *rep* 78 [e.g., initiation codon 334 of Fig 1 for AAV7], *rep* 68 [initiation codon nt 334 of Fig. 1 for AAV7], *rep* 52 [initiation codon 1006 of Fig. 1 for AAV7], and *rep* 40 [initiation codon 1006 of Fig. 1 for AAV7] Other fragments of interest may include the AAV 5' inverted terminal repeats ITRs, [nt 1 to 107 of Fig. 1 for AAV7]; the AAV 3' ITRs [nt 4704 to 4721 of Fig. 1 for AAV7], P19 sequences, AAV P40 sequences, the rep binding site, and the terminal resolute site (TRS). Still other suitable fragments will be readily apparent to those of skill in the art. The corresponding regions in the other novel serotypes of the invention can be readily determined by reference to Figure 1, or by utilizing conventional alignment techniques with the sequences provided herein.

In addition to including the nucleic acid sequences provided in the figures and Sequence Listing, the present invention includes nucleic acid molecules and sequences which are designed to express the amino acid sequences, proteins and peptides of the AAV serotypes of the invention. Thus, the invention includes nucleic acid sequences which encode the following novel AAV amino acid sequences: C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67], A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO:102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-3B [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO:111], 42-6B [SEQ ID NO: 112], and/or 42-12 [SEQ ID NO: 113], and artificial AAV serotypes generated using these sequences and/or unique fragments thereof.

As used herein, artificial AAV serotypes include, without limitation, AAV with a non-naturally occurring capsid protein. Such an artificial capsid may be generated by any suitable technique, using a novel AAV sequence of the invention (e.g., a fragment of a vp1 capsid protein) in combination with heterologous sequences which may be obtained from another AAV serotype (known or novel), non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source. An artificial AAV serotype may be, without limitation, a chimeric AAV capsid, a recombinant AAV capsid, or a "humanized" AAV capsid.

B. AAV Amino Acid Sequences, Proteins and Peptides

The invention provides proteins and fragments thereof which are encoded by the nucleic acid sequences of the novel AAV serotypes identified herein, including, e.g., AAV7 [nt 825 to 3049 of AAV7, SEQ ID NO: 1] the other novel serotypes provided herein. Thus, the capsid proteins of the novel serotypes of the invention, including: H6 [SEQ ID NO: 25], H2 [SEQ ID NO: 26], 42-2 [SEQ ID NO:9], 42-8 [SEQ ID NO:27], 42-15 [SEQ ID NO:28], 42-5b [SEQ ID NO: 29], 42-1b [SEQ ID NO:30]; 42-13 [SEQ ID NO: 31], 42-3a

[SEQ ID NO: 32], 42-4 [SEQ ID NO:33], 42-5a [SEQ ID NO: 34], 42-10 [SEQ ID NO:35], 42-3b [SEQ ID NO: 36], 42-11 [SEQ ID NO: 37], 42-6b [SEQ ID NO:38], 43-1 [SEQ ID NO: 39], 43-5 [SEQ ID NO: 40], 43-12 [SEQ ID NO:41], 43-20 [SEQ ID NO:42], 43-21 [SEQ ID NO: 43], 43-23 [SEQ ID NO:44], 43-25 [SEQ ID NO: 45], 44.1 [SEQ ID NO:47], 44.5 [SEQ ID NO:47], 223.10 [SEQ ID NO:48], 223.2 [SEQ ID NO:49], 223.4 [SEQ ID NO:50], 223.5 [SEQ ID NO: 51], 223.6 [SEQ ID NO: 52], 223.7 [SEQ ID NO: 53], A3.4 [SEQ ID NO: 54], A3.5 [SEQ ID NO:55], A3.7 [SEQ ID NO: 56], A3.3 [SEQ ID NO:57], 42.12 [SEQ ID NO: 58], and 44.2 [SEQ ID NO: 59], can be readily generated using conventional techniques from the open reading frames provided for the above-listed clones.

The invention further encompasses AAV serotypes generated using sequences of the novel AAV serotypes of the invention, which are generated using synthetic, recombinant or other techniques known to those of skill in the art. The invention is not limited to novel AAV amino acid sequences, peptides and proteins expressed from the novel AAV nucleic acid sequences of the invention and encompasses amino acid sequences, peptides and proteins generated by other methods known in the art, including, e.g., by chemical synthesis, by other synthetic techniques, or by other methods. For example, the sequences of any of C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67], A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO:102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-3B [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO:111], 42-6B [SEQ ID NO: 112], and/or 42-12 [SEQ ID NO: 113] by be readily generated using a variety of techniques.

Suitable production techniques are well known to those of skill in the art. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (Cold Spring Harbor, NY). Alternatively, peptides can also be synthesized by the well known solid phase peptide synthesis methods (Merrifield, *J. Am. Chem. Soc.*, 85:2149

(1962); Stewart and Young, Solid Phase Peptide Synthesis (Freeman, San Francisco, 1969) pp. 27-62). These and other suitable production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

Particularly desirable proteins include the AAV capsid proteins, which are encoded by the nucleotide sequences identified above. The sequences of many of the capsid proteins of the invention are provided in an alignment in Fig. 2 and/or in the Sequence Listing, SEQ ID NO: 2 and 60 to 115, which is incorporated by reference herein. The AAV capsid is composed of three proteins, vp1, vp2 and vp3, which are alternative splice variants. The full-length sequence provided in these figures is that of vp1. Based on the numbering of the AAV7 capsid [SEQ ID NO:2], the sequences of vp2 span amino acid 138 - 737 of AAV7 and the sequences of vp3 span amino acids 203 - 737 of AAV7. With this information, one of skill in the art can readily determine the location of the vp2 and vp3 proteins for the other novel serotypes of the invention.

Other desirable proteins and fragments of the capsid protein include the constant and variable regions, located between hypervariable regions (HPV) and the sequences of the HPV regions themselves. An algorithm developed to determine areas of sequence divergence in AAV2 has yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the four previously described variable regions. [Chiorini *et al, J. Virol*, 73:1309-19 (1999); Rutledge *et al, J. Virol.*, 72:309-319] Using this algorithm and/or the alignment techniques described herein, the HVR of the novel AAV serotypes are determined. For example, with respect to the number of the AAV2 vp1 [SEQ ID NO:70], the HVR are located as follows: HVR1, aa 146-152; HVR2, aa 182-186; HVR3, aa 262-264; HVR4, aa 381-383; HVR5, aa 450-474; HVR6, aa 490-495; HVR7, aa500-504; HVR8, aa 514-522; HVR9, aa 534-555; HVR10, aa 581-594; HVR11, aa 658-667; and HVR12, aa 705-719. Utilizing an alignment prepared in accordance with conventional methods and the novel sequences provided herein [See, e.g., Figure 2], one can readily determine the location of the HVR in the novel AAV serotypes of the invention. For example, utilizing Figure 2, one can readily determine that for AAV7 [SEQ ID NO:2]. HVR1 is located at aa 146 – 152; HVR2 is located at 182-187; HVR3 is located at aa 263-266, HVR4 is located at aa 383-385, HVR5 is located at aa 451-475; HVR6 is located at aa 491-496 of AAV7; HVR7 is located at aa 501-505; HVR8 is located at aa 513-521; HVR9 is located at 533-554; HVR10 is located at aa 583-596; HVR11 is located at aa 660-669; HVR12 is located at aa 707-721. Using the

information provided herein, the HVRs for the other novel serotypes of the invention can be readily determined.

In addition, within the capsid, amino acid cassettes of identity have been identified. These cassettes are of particular interest, as they are useful in constructing artificial serotypes, e.g., by replacing a HVR1 cassette of a selected serotype with an HVR1 cassette of another serotype. Certain of these cassettes of identity are noted in Fig. 2. See, Fig. 2, providing the Clustal X alignment, which has a ruler is displayed below the sequences, starting at 1 for the first residue position. The line above the ruler is used to mark strongly conserved positions. Three characters (*, : , .) are used. "*" indicates positions which have a single, fully conserved residue. ":" indicates that a "strong" group is fully conserved "." Indicates that a "weaker" group is fully conserved. These are all the positively scoring groups that occur in the Gonnet Pam250 matrix. The strong groups are defined as a strong score >0.5 and the weak groups are defined as weak score <0.5.

Additionally, examples of other suitable fragments of AAV capsids include, with respect to the numbering of AAV2 [SEQ ID NO:70], aa 24 – 42, aa 25 – 28; aa 81 – 85; aa133-165; aa 134 – 165; aa 137-143; aa 154-156; aa 194-208; aa 261-274; aa 262-274; aa 171-173; aa 413-417; aa 449-478; aa 494-525; aa 534-571; aa 581-601; aa 660-671; aa 709-723. Still other desirable fragments include, for example, in AAV7, amino acids 1 to 184 of SEQ ID NO:2, amino acids 199 to 259; amino acids 274 to 446; amino acids 603 to 659; amino acids 670 to 706; amino acids 724 to 736; aa 185 to 198; aa 260 to 273; aa447 to 477; aa495 to 602; aa660 to 669; and aa707 to 723. Still other desirable regions, based on the numbering of AAV7 [SEQ ID NO:2], are selected from among the group consisting of aa 185 to 198; aa 260 to 273; aa447 to 477;aa495 to 602; aa660 to 669; and aa707 to 723. Using the alignment provided herein performed using the Clustal X program at default settings, or using other commercially or publicly available alignment programs at default settings, one of skill in the art can readily determine corresponding fragments of the novel AAV capsids of the invention.

Other desirable proteins are the AAV rep proteins [aa 1 to 623 of SEQ ID NO:3 for AAV7] and functional fragments thereof, including, e.g., aa 1 to 171, aa 172 to 372, aa 373 to 444, aa 445 to 623 of SEQ ID NO:3, among others. Suitably, such fragments are at least 8 amino acids in length. See, Fig. 3. Comparable regions can be identified in the proteins of the other novel AAV of the invention, using the techniques described herein and those which are known in the art. In addition, fragments of other desired lengths may be

readily utilized. Such fragments may be produced recombinantly or by other suitable means, e.g., chemical synthesis.

The sequences, proteins, and fragments of the invention may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

IV. Production of rAAV with novel AAV capsids

The invention encompasses novel, wild-type AAV serotypes identified by the invention, the sequences of which wild-type AAV serotypes are free of DNA and/or cellular material with these viruses are associated in nature. In another aspect, the present invention provides molecules which utilize the novel AAV sequences of the invention, including fragments thereof, for production of molecules useful in delivery of a heterologous gene or other nucleic acid sequences to a target cell.

The molecules of the invention which contain sequences of a novel AAV serotype of the invention include any genetic element (vector) which may be delivered to a host cell, e.g., naked DNA, a plasmid, phage, transposon, cosmid, episome, a protein in a non-viral delivery vehicle (e.g., a lipid-based carrier), virus, etc. which transfer the sequences carried thereon. The selected vector may be delivered by any suitable method, including transfection, electroporation, liposome delivery, membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, NY.

In one embodiment, the vectors of the invention contain sequences encoding a novel AAV capsid of the invention (e.g., AAV7 capsid, AAV 44-2 (rh.10), an AAV10 capsid, an AAV11 capsid, an AAV12 capsid), or a fragment of one or more of these AAV capsids. Alternatively, the vectors may contain the capsid protein, or a fragment thereof, itself.

Optionally, vectors of the invention may contain sequences encoding AAV rep proteins. Such *rep* sequences may be from the same AAV serotype which is providing the cap sequences. Alternatively, the present invention provides vectors in which the *rep* sequences are from an AAV serotype which differs from that which is providing the *cap*

sequences. In one embodiment, the *rep* and *cap* sequences are expressed from separate sources (e.g., separate vectors, or a host cell and a vector). In another embodiment, these *rep* sequences are expressed from the same source as the *cap* sequences. In this embodiment, the *rep* sequences may be fused in frame to *cap* sequences of a different AAV serotype to form a chimeric AAV vector. Optionally, the vectors of the invention further contain a minigene comprising a selected transgene which is flanked by AAV 5' ITR and AAV 3' ITR.

Thus, in one embodiment, the vectors described herein contain nucleic acid sequences encoding an intact AAV capsid which may be from a single AAV serotype (e.g., AAV7 or another novel AAV). Alternatively, these vectors contain sequences encoding artificial capsids which contain one or more fragments of the AAV7 (or another novel AAV) capsid fused to heterologous AAV or non-AAV capsid proteins (or fragments thereof). These artificial capsid proteins are selected from non-contiguous portions of the AAV7 (or another novel AAV) capsid or from capsids of other AAV serotypes. For example, it may be desirable to modify the coding regions of one or more of the AAV vp1, e.g., in one or more of the hypervariable regions (i.e., HPV1-12), or vp2, and/or vp3. In another example, it may be desirable to alter the start codon of the vp3 protein to GTG. These modifications may be to increase expression, yield, and/or to improve purification in the selected expression systems, or for another desired purpose (e.g., to change tropism or alter neutralizing antibody epitopes).

The vectors described herein, e.g., a plasmid, are useful for a variety of purposes, but are particularly well suited for use in production of a rAAV containing a capsid comprising AAV sequences or a fragment thereof. These vectors, including rAAV, their elements, construction, and uses are described in detail herein.

In one aspect, the invention provides a method of generating a recombinant adeno-associated virus (AAV) having an AAV serotype 7 (or another novel AAV) capsid, or a portion thereof. Such a method involves culturing a host cell which contains a nucleic acid sequence encoding an adeno-associated virus (AAV) serotype 7 (or another novel AAV) capsid protein, or fragment thereof, as defined herein; a functional rep gene; a minigene composed of, at a minimum, AAV inverted terminal repeats (ITRs) and a transgene; and sufficient helper functions to permit packaging of the minigene into the AAV7 (or another novel AAV) capsid protein.

The components required to be cultured in the host cell to package an AAV minigene in an AAV capsid may be provided to the host cell in *trans*. Alternatively, any one or more

of the required components (e.g., minigene, *rep* sequences, *cap* sequences, and/or helper functions) may be provided by a stable host cell which has been engineered to contain one or more of the required components using methods known to those of skill in the art. Most suitably, such a stable host cell will contain the required component(s) under the control of an inducible promoter. However, the required component(s) may be under the control of a constitutive promoter. Examples of suitable inducible and constitutive promoters are provided herein, in the discussion of regulatory elements suitable for use with the transgene. In still another alternative, a selected stable host cell may contain selected component(s) under the control of a constitutive promoter and other selected component(s) under the control of one or more inducible promoters. For example, a stable host cell may be generated which is derived from 293 cells (which contain E1 helper functions under the control of a constitutive promoter), but which contains the rep and/or cap proteins under the control of inducible promoters. Still other stable host cells may be generated by one of skill in the art.

The minigene, *rep* sequences, *cap* sequences, and helper functions required for producing the rAAV of the invention may be delivered to the packaging host cell in the form of any genetic element which transfer the sequences carried thereon. The selected genetic element may be delivered by any suitable method, including those described herein. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, NY. Similarly, methods of generating rAAV virions are well known and the selection of a suitable method is not a limitation on the present invention. See, e.g., K. Fisher et al, J. Virol., 70:520-532 (1993) and US Patent 5,478,745.

A. The Minigene

The minigene is composed of, at a minimum, a transgene and its regulatory sequences, and 5' and 3' AAV inverted terminal repeats (ITRs). It is this minigene which is packaged into a capsid protein and delivered to a selected host cell.

1. The transgene

The transgene is a nucleic acid sequence, heterologous to the vector sequences flanking the transgene, which encodes a polypeptide, protein, or other product, of interest. The nucleic acid coding sequence is operatively linked to regulatory

components in a manner which permits transgene transcription, translation, and/or expression in a host cell.

The composition of the transgene sequence will depend upon the use to which the resulting vector will be put. For example, one type of transgene sequence includes a reporter sequence, which upon expression produces a detectable signal. Such reporter sequences include, without limitation, DNA sequences encoding β-lactamase, β-galactosidase (LacZ), alkaline phosphatase, thymidine kinase, green fluorescent protein (GFP), chloramphenicol acetyltransferase (CAT), luciferase, membrane bound proteins including, for example, CD2, CD4, CD8, the influenza hemagglutinin protein, and others well known in the art, to which high affinity antibodies directed thereto exist or can be produced by conventional means, and fusion proteins comprising a membrane bound protein appropriately fused to an antigen tag domain from, among others, hemagglutinin or Myc.

These coding sequences, when associated with regulatory elements which drive their expression, provide signals detectable by conventional means, including enzymatic, radiographic, colorimetric, fluorescence or other spectrographic assays, fluorescent activating cell sorting assays and immunological assays, including enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and immunohistochemistry. For example, where the marker sequence is the LacZ gene, the presence of the vector carrying the signal is detected by assays for beta-galactosidase activity. Where the transgene is green fluorescent protein or luciferase, the vector carrying the signal may be measured visually by color or light production in a luminometer.

However, desirably, the transgene is a non-marker sequence encoding a product which is useful in biology and medicine, such as proteins, peptides, RNA, enzymes, or catalytic RNAs. Desirable RNA molecules include tRNA, dsRNA, ribosomal RNA, catalytic RNAs, and antisense RNAs. One example of a useful RNA sequence is a sequence which extinguishes expression of a targeted nucleic acid sequence in the treated animal.

The transgene may be used to correct or ameliorate gene deficiencies, which may include deficiencies in which normal genes are expressed at less than normal levels or deficiencies in which the functional gene product is not expressed. A preferred type of transgene sequence encodes a therapeutic protein or polypeptide which is expressed in a host cell. The invention further includes using multiple transgenes, e.g., to correct or ameliorate a gene defect caused by a multi-subunit protein. In certain situations, a

different transgene may be used to encode each subunit of a protein, or to encode different peptides or proteins. This is desirable when the size of the DNA encoding the protein subunit is large, e.g., for an immunoglobulin, the platelet-derived growth factor, or a dystrophin protein. In order for the cell to produce the multi-subunit protein, a cell is infected with the recombinant virus containing each of the different subunits. Alternatively, different subunits of a protein may be encoded by the same transgene. In this case, a single transgene includes the DNA encoding each of the subunits, with the DNA for each subunit separated by an internal ribozyme entry site (IRES). This is desirable when the size of the DNA encoding each of the subunits is small, e.g., the total size of the DNA encoding the subunits and the IRES is less than five kilobases. As an alternative to an IRES, the DNA may be separated by sequences encoding a 2A peptide, which self-cleaves in a post-translational event. See, e.g., M.L. Donnelly, *et al, J. Gen. Virol.*, 78(Pt 1):13-21 (Jan 1997); Furler, S., *et al, Gene Ther.*, 8(11):864-873 (June 2001); Klump H., *et al.*, *Gene Ther.*, 8(10):811-817 (May 2001). This 2A peptide is significantly smaller than an IRES, making it well suited for use when space is a limiting factor. However, the selected transgene may encode any biologically active product or other product, e.g., a product desirable for study.

Suitable transgenes may be readily selected by one of skill in the art. The selection of the transgene is not considered to be a limitation of this invention.

2. Regulatory Elements

In addition to the major elements identified above for the minigene, the vector also includes conventional control elements necessary which are operably linked to the transgene in a manner which permits its transcription, translation and/or expression in a cell transfected with the plasmid vector or infected with the virus produced by the invention. As used herein, "operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in *trans* or at a distance to control the gene of interest.

Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. A great number of expression control

sequences, including promoters which are native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

Examples of constitutive promoters include, without limitation, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, e.g., Boshart *et al*, *Cell*, **41**:521-530 (1985)], the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1α promoter [Invitrogen].

Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, e.g., acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech and Ariad. Many other systems have been described and can be readily selected by one of skill in the art. Examples of inducible promoters regulated by exogenously supplied promoters include the zinc-inducible sheep metallothionine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system [WO 98/10088]; the ecdysone insect promoter [No *et al*, *Proc. Natl. Acad. Sci. USA*, **93**:3346-3351 (1996)], the tetracycline-repressible system [Gossen *et al*, *Proc. Natl. Acad. Sci. USA*, **89**:5547-5551 (1992)], the tetracycline-inducible system [Gossen *et al*, *Science*, **268**:1766-1769 (1995), see also Harvey *et al*, *Curr. Opin. Chem. Biol.*, **2**:512-518 (1998)], the RU486-inducible system [Wang *et al*, *Nat. Biotech.*, **15**:239-243 (1997) and Wang *et al*, *Gene Ther.*, **4**:432-441 (1997)] and the rapamycin-inducible system [Magari *et al*, *J. Clin. Invest.*, **100**:2865-2872 (1997)]. Still other types of inducible promoters which may be useful in this context are those which are regulated by a specific physiological state, e.g., temperature, acute phase, a particular differentiation state of the cell, or in replicating cells only.

In another embodiment, the native promoter for the transgene will be used. The native promoter may be preferred when it is desired that expression of the transgene should mimic the native expression. The native promoter may be used when expression of the transgene must be regulated temporally or developmentally, or in a tissue-specific manner, or in response to specific transcriptional stimuli. In a further embodiment,

other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

Another embodiment of the transgene includes a transgene operably linked to a tissue-specific promoter. For instance, if expression in skeletal muscle is desired, a promoter active in muscle should be used. These include the promoters from genes encoding skeletal β-actin, myosin light chain 2A, dystrophin, muscle creatine kinase, as well as synthetic muscle promoters with activities higher than naturally-occurring promoters (see Li *et al.*, *Nat. Biotech.*, **17**:241-245 (1999)). Examples of promoters that are tissue-specific are known for liver (albumin, Miyatake *et al.*, *J. Virol.*, **71**:5124-32 (1997); hepatitis B virus core promoter, Sandig *et al.*, *Gene Ther.*, **3**:1002-9 (1996); alpha-fetoprotein (AFP), Arbuthnot *et al.*, *Hum. Gene Ther.*, 7:1503-14 (1996)), bone osteocalcin (Stein *et al.*, *Mol. Biol. Rep.*, **24**:185-96 (1997)); bone sialoprotein (Chen *et al.*, *J. Bone Miner. Res.*, **11**:654-64 (1996)), lymphocytes (CD2, Hansal *et al.*, *J. Immunol.*, **161**:1063-8 (1998); immunoglobulin heavy chain; T cell receptor α chain), neuronal such as neuron-specific enolase (NSE) promoter (Andersen *et al.*, *Cell. Mol. Neurobiol.*, **13**:503-15 (1993)), neurofilament light-chain gene (Piccioli *et al.*, *Proc. Natl. Acad. Sci. USA*, **88**:5611-5 (1991)), and the neuron-specific vgf gene (Piccioli *et al.*, *Neuron*, **15**:373-84 (1995)), among others.

Optionally, plasmids carrying therapeutically useful transgenes may also include selectable markers or reporter genes may include sequences encoding geneticin, hygromicin or purimycin resistance, among others. Such selectable reporters or marker genes (preferably located outside the viral genome to be rescued by the method of the invention) can be used to signal the presence of the plasmids in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication. Selection of these and other promoters and vector elements are conventional and many such sequences are available [see, e.g., Sambrook et al, and references cited therein].

The combination of the transgene, promoter/enhancer, and 5' and 3' ITRs is referred to as a "minigene" for ease of reference herein. Provided with the teachings of this invention, the design of such a minigene can be made by resort to conventional techniques.

3. Delivery of the Minigene to a Packaging Host Cell

The minigene can be carried on any suitable vector, e.g., a plasmid, which is delivered to a host cell. The plasmids useful in this invention may be

engineered such that they are suitable for replication and, optionally, integration in prokaryotic cells, mammalian cells, or both. These plasmids (or other vectors carrying the 5' AAV ITR-heterologous molecule-3'ITR) contain sequences permitting replication of the minigene in eukaryotes and/or prokaryotes and selection markers for these systems. Selectable markers or reporter genes may include sequences encoding geneticin, hygromicin or purimycin resistance, among others. The plasmids may also contain certain selectable reporters or marker genes that can be used to signal the presence of the vector in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication and an amplicon, such as the amplicon system employing the Epstein Barr virus nuclear antigen. This amplicon system, or other similar amplicon components permit high copy episomal replication in the cells. Preferably, the molecule carrying the minigene is transfected into the cell, where it may exist transiently. Alternatively, the minigene (carrying the 5' AAV ITR-heterologous molecule-3' ITR) may be stably integrated into the genome of the host cell, either chromosomally or as an episome. In certain embodiments, the minigene may be present in multiple copies, optionally in head-to-head, head-to-tail, or tail-to-tail concatamers. Suitable transfection techniques are known and may readily be utilized to deliver the minigene to the host cell.

Generally, when delivering the vector comprising the minigene by transfection, the vector is delivered in an amount from about 5 μg to about 100 μg DNA, and preferably about 10 to about 50 μg DNA to about 1 x 10^4 cells to about 1 x 10^{13} cells, and preferably about 10^5 cells. However, the relative amounts of vector DNA to host cells may be adjusted, taking into consideration such factors as the selected vector, the delivery method and the host cells selected.

B. *Rep* and *Cap* Sequences

In addition to the minigene, the host cell contains the sequences which drive expression of the novel AAV capsid protein (e.g., AAV7 or other novel AAV capsid or an artificial capsid protein comprising a fragment of one or more of these capsids) in the host cell and rep sequences of the same serotype as the serotype of the AAV ITRs found in the minigene. The AAV *cap* and *rep* sequences may be independently obtained from an AAV source as described above and may be introduced into the host cell in any manner known to one in the art as described above. Additionally, when pseudotyping a novel AAV capsid of the invention, the sequences encoding each of the essential rep proteins may be supplied by the same AAV serotype, or the sequences encoding the rep proteins may

be supplied by different AAV serotypes (e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, or one of the novel serotypes identified herein). For example, the *rep*78/68 sequences may be from AAV2, whereas the *rep*52/40 sequences may from AAV1.

In one embodiment, the host cell stably contains the capsid protein under the control of a suitable promoter, such as those described above. Most desirably, in this embodiment, the capsid protein is expressed under the control of an inducible promoter. In another embodiment, the capsid protein is supplied to the host cell in *trans*. When delivered to the host cell in *trans*, the capsid protein may be delivered via a plasmid which contains the sequences necessary to direct expression of the selected capsid protein in the host cell. Most desirably, when delivered to the host cell in *trans*, the plasmid carrying the capsid protein also carries other sequences required for packaging the rAAV, e.g., the *rep* sequences.

In another embodiment, the host cell stably contains the *rep* sequences under the control of a suitable promoter, such as those described above. Most desirably, in this embodiment, the essential rep proteins are expressed under the control of an inducible promoter. In another embodiment, the rep proteins are supplied to the host cell in *trans*. When delivered to the host cell in *trans*, the rep proteins may be delivered via a plasmid which contains the sequences necessary to direct expression of the selected rep proteins in the host cell. Most desirably, when delivered to the host cell in *trans*, the plasmid carrying the capsid protein also carries other sequences required for packaging the rAAV, e.g., the *rep* and *cap* sequences.

Thus, in one embodiment, the *rep* and *cap* sequences may be transfected into the host cell on a single nucleic acid molecule and exist stably in the cell as an episome. In another embodiment, the *rep* and *cap* sequences are stably integrated into the genome of the cell. Another embodiment has the *rep* and *cap* sequences transiently expressed in the host cell. For example, a useful nucleic acid molecule for such transfection comprises, from 5' to 3', a promoter, an optional spacer interposed between the promoter and the start site of the *rep* gene sequence, an AAV *rep* gene sequence, and an AAV *cap* gene sequence.

Optionally, the *rep* and/or *cap* sequences may be supplied on a vector that contains other DNA sequences that are to be introduced into the host cells. For instance, the vector may contain the rAAV construct comprising the minigene. The vector may

comprise one or more of the genes encoding the helper functions, e.g., the adenoviral proteins E1, E2a, and E4ORF6, and the gene for VAI RNA.

Preferably, the promoter used in this construct may be any of the constitutive, inducible or native promoters known to one of skill in the art or as discussed above. In one embodiment, an AAV P5 promoter sequence is employed. The selection of the AAV to provide any of these sequences does not limit the invention.

In another preferred embodiment, the promoter for *rep* is an inducible promoter, as are discussed above in connection with the transgene regulatory elements. One preferred promoter for *rep* expression is the T7 promoter. The vector comprising the *rep* gene regulated by the T7 promoter and the *cap* gene, is transfected or transformed into a cell which either constitutively or inducibly expresses the T7 polymerase. See WO 98/10088, published March 12, 1998.

The spacer is an optional element in the design of the vector. The spacer is a DNA sequence interposed between the promoter and the *rep* gene ATG start site. The spacer may have any desired design; that is, it may be a random sequence of nucleotides, or alternatively, it may encode a gene product, such as a marker gene. The spacer may contain genes which typically incorporate start/stop and polyA sites. The spacer may be a non-coding DNA sequence from a prokaryote or eukaryote, a repetitive non-coding sequence, a coding sequence without transcriptional controls or a coding sequence with transcriptional controls. Two exemplary sources of spacer sequences are the λ phage ladder sequences or yeast ladder sequences, which are available commercially, e.g., from Gibco or Invitrogen, among others. The spacer may be of any size sufficient to reduce expression of the *rep*78 and *rep*68 gene products, leaving the *rep*52, *rep*40 and *cap* gene products expressed at normal levels. The length of the spacer may therefore range from about 10 bp to about 10.0 kbp, preferably in the range of about 100 bp to about 8.0 kbp. To reduce the possibility of recombination, the spacer is preferably less than 2 kbp in length; however, the invention is not so limited.

Although the molecule(s) providing *rep* and *cap* may exist in the host cell transiently (i.e., through transfection), it is preferred that one or both of the *rep* and *cap* proteins and the promoter(s) controlling their expression be stably expressed in the host cell, e.g., as an episome or by integration into the chromosome of the host cell. The methods employed for constructing embodiments of this invention are conventional genetic engineering or recombinant engineering techniques such as those described in the references

above. While this specification provides illustrative examples of specific constructs, using the information provided herein, one of skill in the art may select and design other suitable constructs, using a choice of spacers, P5 promoters, and other elements, including at least one translational start and stop signal, and the optional addition of polyadenylation sites.

In another embodiment of this invention, the rep or cap protein may be provided stably by a host cell.

C. The Helper Functions

The packaging host cell also requires helper functions in order to package the rAAV of the invention. Optionally, these functions may be supplied by a herpesvirus. Most desirably, the necessary helper functions are each provided from a human or non-human primate adenovirus source, such as those described above and/or are available from a variety of sources, including the American Type Culture Collection (ATCC), Manassas, VA (US). In one currently preferred embodiment, the host cell is provided with and/or contains an E1a gene product, an E1b gene product, an E2a gene product, and/or an E4 ORF6 gene product. The host cell may contain other adenoviral genes such as VAI RNA, but these genes are not required. In a preferred embodiment, no other adenovirus genes or gene functions are present in the host cell.

By "adenoviral DNA which expresses the E1a gene product", it is meant any adenovirus sequence encoding E1a or any functional E1a portion. Adenoviral DNA which expresses the E2a gene product and adenoviral DNA which expresses the E4 ORF6 gene products are defined similarly. Also included are any alleles or other modifications of the adenoviral gene or functional portion thereof. Such modifications may be deliberately introduced by resort to conventional genetic engineering or mutagenic techniques to enhance the adenoviral function in some manner, as well as naturally occurring allelic variants thereof. Such modifications and methods for manipulating DNA to achieve these adenovirus gene functions are known to those of skill in the art.

The adenovirus E1a, E1b, E2a, and/or E4ORF6 gene products, as well as any other desired helper functions, can be provided using any means that allows their expression in a cell. Each of the sequences encoding these products may be on a separate vector, or one or more genes may be on the same vector. The vector may be any vector known in the art or disclosed above, including plasmids, cosmids and viruses. Introduction into the host cell of the vector may be achieved by any means known in the art or as disclosed above, including transfection, infection, electroporation, liposome delivery,

membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion, among others. One or more of the adenoviral genes may be stably integrated into the genome of the host cell, stably expressed as episomes, or expressed transiently. The gene products may all be expressed transiently, on an episome or stably integrated, or some of the gene products may be expressed stably while others are expressed transiently. Furthermore, the promoters for each of the adenoviral genes may be selected independently from a constitutive promoter, an inducible promoter or a native adenoviral promoter. The promoters may be regulated by a specific physiological state of the organism or cell (i.e., by the differentiation state or in replicating or quiescent cells) or by exogenously-added factors, for example.

D. Host Cells And Packaging Cell Lines

The host cell itself may be selected from any biological organism, including prokaryotic (e.g., bacterial) cells, and eukaryotic cells, including, insect cells, yeast cells and mammalian cells. Particularly desirable host cells are selected from among any mammalian species, including, without limitation, cells such as A549, WEHI, 3T3, 10T1/2, BHK, MDCK, COS 1, COS 7, BSC 1, BSC 40, BMT 10, VERO, WI38, HeLa, 293 cells (which express functional adenoviral E1), Saos, C2C12, L cells, HT1080, HepG2 and primary fibroblast, hepatocyte and myoblast cells derived from mammals including human, monkey, mouse, rat, rabbit, and hamster. The selection of the mammalian species providing the cells is not a limitation of this invention; nor is the type of mammalian cell, i.e., fibroblast, hepatocyte, tumor cell, etc. The most desirable cells do not carry any adenovirus gene other than E1, E2a and/or E4 ORF6; nor do they contain any other virus gene which could result in homologous recombination of a contaminating virus during the production of rAAV; and it is capable of infection or transfection of DNA and expression of the transfected DNA. In a preferred embodiment, the host cell is one that has *rep* and *cap* stably transfected in the cell.

One host cell useful in the present invention is a host cell stably transformed with the sequences encoding rep and cap, and which is transfected with the adenovirus E1, E2a, and E4ORF6 DNA and a construct carrying the minigene as described above. Stable *rep* and/or *cap* expressing cell lines, such as B-50 (PCT/US98/19463), or those described in U.S. Patent No. 5,658,785, may also be similarly employed. Another desirable host cell contains the minimum adenoviral DNA which is sufficient to express E4 ORF6. Yet other cell lines can be constructed using the novel AAV *rep* and/or novel AAV *cap* sequences of the invention.

The preparation of a host cell according to this invention involves techniques such as assembly of selected DNA sequences. This assembly may be accomplished utilizing conventional techniques. Such techniques include cDNA and genomic cloning, which are well known and are described in Sambrook et al., cited above, use of overlapping oligonucleotide sequences of the adenovirus and AAV genomes, combined with polymerase chain reaction, synthetic methods, and any other suitable methods which provide the desired nucleotide sequence.

Introduction of the molecules (as plasmids or viruses) into the host cell may also be accomplished using techniques known to the skilled artisan and as discussed throughout the specification. In preferred embodiment, standard transfection techniques are used, e.g., $CaPO_4$ transfection or electroporation, and/or infection by hybrid adenovirus/AAV vectors into cell lines such as the human embryonic kidney cell line HEK 293 (a human kidney cell line containing functional adenovirus E1 genes which provides *trans*-acting E1 proteins).

These novel AAV-based vectors which are generated by one of skill in the art are beneficial for gene delivery to selected host cells and gene therapy patients since no neutralization antibodies to AAV7 have been found in the human population. Further, early studies show no neutralizing antibodies in cyno monkey and chimpanzee populations, and less than 15% cross-reactivity of AAV 7 in rhesus monkeys, the species from which the serotype was isolated. One of skill in the art may readily prepare other rAAV viral vectors containing the AAV7 capsid proteins provided herein using a variety of techniques known to those of skill in the art. One may similarly prepare still other rAAV viral vectors containing AAV7 sequence and AAV capsids of another serotype. Similar advantages are conferred by the vectors based on the other novel AAV of the invention.

Thus, one of skill in the art will readily understand that the AAV7 sequences of the invention can be readily adapted for use in these and other viral vector systems for *in vitro, ex vivo or in vivo* gene delivery. Similarly, one of skill in the art can readily select other fragments of the novel AAV genome of the invention for use in a variety of rAAV and non-rAAV vector systems. Such vectors systems may include, e.g., lentiviruses, retroviruses, poxviruses, vaccinia viruses, and adenoviral systems, among others. Selection of these vector systems is not a limitation of the present invention.

Thus, the invention further provides vectors generated using the nucleic acid and amino acid sequences of the novel AAV of the invention. Such vectors are

useful for a variety of purposes, including for delivery of therapeutic molecules and for use in vaccine regimens. Particularly desirable for delivery of therapeutic molecules are recombinant AAV containing capsids of the novel AAV of the invention. These, or other vector constructs containing novel AAV sequences of the invention may be used in vaccine regimens, e.g., for co-delivery of a cytokine, or for delivery of the immunogen itself.

V. Recombinant Viruses And Uses Thereof

Using the techniques described herein, one of skill in the art may generate a rAAV having a capsid of a novel serotype of the invention, or a novel capsid containing one or more novel fragments of an AAV serotype identified by the method of the invention. In one embodiment, a full-length capsid from a single serotype, e.g., AAV7 [SEQ ID NO: 2] can be utilized. In another embodiment, a full-length capsid may be generated which contains one or more fragments of a novel serotype of the invention fused in frame with sequences from another selected AAV serotype. For example, a rAAV may contain one or more of the novel hypervariable region sequences of an AAV serotype of the invention. Alternatively, the unique AAV serotypes of the invention may be used in constructs containing other viral or non-viral sequences.

It will be readily apparent to one of skill in the art one embodiment, that certain serotypes of the invention will be particularly well suited for certain uses. For example, vectors based on AAV7 capsids of the invention are particularly well suited for use in muscle; whereas vectors based on rh.10 (44-2) capsids of the invention are particularly well suited for use in lung. Uses of such vectors are not so limited and one of skill in the art may utilize these vectors for delivery to other cell types, tissues or organs. Further, vectors based upon other capsids of the invention may be used for delivery to these or other cells, tissues or organs.

A. Delivery of Transgene

In another aspect, the present invention provides a method for delivery of a transgene to a host which involves transfecting or infecting a selected host cell with a vector generated with the sequences of the AAV of the invention. Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

In one desirable embodiment, the invention provides a method for AAV-mediated delivery of a transgene to a host. This method involves transfecting or infecting a

selected host cell with a recombinant viral vector containing a selected transgene under the control of sequences which direct expression thereof and AAV capsid proteins.

Optionally, a sample from the host may be first assayed for the presence of antibodies to a selected AAV serotype. A variety of assay formats for detecting neutralizing antibodies are well known to those of skill in the art. The selection of such an assay is not a limitation of the present invention. See, e.g., Fisher et al, *Nature Med.*, 3(3):306-312 (March 1997) and W. C. Manning et al, *Human Gene Therapy*, 9:477-485 (March 1, 1998). The results of this assay may be used to determine which AAV vector containing capsid proteins of a particular serotype are preferred for delivery, e.g., by the absence of neutralizing antibodies specific for that capsid serotype.

In one aspect of this method, the delivery of vector with a selected AAV capsid proteins may precede or follow delivery of a gene via a vector with a different serotype AAV capsid protein. Similarly, the delivery of vector with other novel AAV capsid proteins of the invention may precede or follow delivery of a gene via a vector with a different serotype AAV capsid protein. Thus, gene delivery via rAAV vectors may be used for repeat gene delivery to a selected host cell. Desirably, subsequently administered rAAV vectors carry the same transgene as the first rAAV vector, but the subsequently administered vectors contain capsid proteins of serotypes which differ from the first vector. For example, if a first vector has AAV7 capsid proteins [SEQ ID NO:2], subsequently administered vectors may have capsid proteins selected from among the other serotypes, including AAV1, AAV2, AAV3A, AAV3B, AAV4, AAV6, AAV10, AAV11, and AAV12, or any of the other novel AAV capsids identified herein including, without limitation: A3.1, H2, H6, C1, C2, C5, A3-3, A3-7, A3-4, A3-5, 3.3b, 223.4, 223-5, 223-10, 223-2, 223-7, 223-6, 44-1, 44-5, 44-2, 42-15, 42-8, 42-13, 42-3A, 42-4, 42-5A, 42-1B, 42-5B, 43-1, 43-12, 43-5, 43-21, 43-25, 43-20, 24.1, 42.2, 7.2, 27.3, 16.3, 42.10, 42-3B, 42-11, F1, F5, F3, 42-6B, and/or 42-12.

The above-described recombinant vectors may be delivered to host cells according to published methods. The rAAV, preferably suspended in a physiologically compatible carrier, may be administered to a human or non-human mammalian patient. Suitable carriers may be readily selected by one of skill in the art in view of the indication for which the transfer virus is directed. For example, one suitable carrier includes saline, which may be formulated with a variety of buffering solutions (e.g., phosphate buffered saline). Other exemplary carriers include sterile saline, lactose, sucrose, calcium phosphate,

gelatin, dextran, agar, pectin, peanut oil, sesame oil, and water. The selection of the carrier is not a limitation of the present invention.

Optionally, the compositions of the invention may contain, in addition to the rAAV and carrier(s), other conventional pharmaceutical ingredients, such as preservatives, or chemical stabilizers. Suitable exemplary preservatives include chlorobutanol, potassium sorbate, sorbic acid, sulfur dioxide, propyl gallate, the parabens, ethyl vanillin, glycerin, phenol, and parachlorophenol. Suitable chemical stabilizers include gelatin and albumin.

The viral vectors are administered in sufficient amounts to transfect the cells and to provide sufficient levels of gene transfer and expression to provide a therapeutic benefit without undue adverse effects, or with medically acceptable physiological effects, which can be determined by those skilled in the medical arts. Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, direct delivery to the selected organ (e.g., intraportal delivery to the liver), oral, inhalation (including intranasal and intratracheal delivery), intraocular, intravenous, intramuscular, subcutaneous, intradermal, and other parental routes of administration. Routes of administration may be combined, if desired.

Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective human dosage of the viral vector is generally in the range of from about 1 ml to about 100 ml of solution containing concentrations of from about 1×10^9 to 1×10^{16} genomes virus vector. A preferred human dosage may be about 1×10^{13} to 1×10^{16} AAV genomes. The dosage will be adjusted to balance the therapeutic benefit against any side effects and such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed. The levels of expression of the transgene can be monitored to determine the frequency of dosage resulting in viral vectors, preferably AAV vectors containing the minigene. Optionally, dosage regimens similar to those described for therapeutic purposes may be utilized for immunization using the compositions of the invention.

Examples of therapeutic products and immunogenic products for delivery by the AAV-containing vectors of the invention are provided below. These vectors may be used for a variety of therapeutic or vaccinal regimens, as described herein. Additionally, these vectors may be delivered in combination with one or more other vectors or active ingredients in a desired therapeutic and/or vaccinal regimen.

B. Therapeutic Transgenes

Useful therapeutic products encoded by the transgene include hormones and growth and differentiation factors including, without limitation, insulin, glucagon, growth hormone (GH), parathyroid hormone (PTH), growth hormone releasing factor (GRF), follicle stimulating hormone (FSH), luteinizing hormone (LH), human chorionic gonadotropin (hCG), vascular endothelial growth factor (VEGF), angiopoietins, angiostatin, granulocyte colony stimulating factor (GCSF), erythropoietin (EPO), connective tissue growth factor (CTGF), basic fibroblast growth factor (bFGF), acidic fibroblast growth factor (aFGF), epidermal growth factor (EGF), transforming growth factor α (TGFα), platelet-derived growth factor (PDGF), insulin growth factors I and II (IGF-I and IGF-II), any one of the transforming growth factor β superfamily, including TGF β, activins, inhibins, or any of the bone morphogenic proteins (BMP) BMPs 1-15, any one of the heregluin/neuregulin/ARIA/neu differentiation factor (NDF) family of growth factors, nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), neurotrophins NT-3 and NT-4/5, ciliary neurotrophic factor (CNTF), glial cell line derived neurotrophic factor (GDNF), neurturin, agrin, any one of the family of semaphorins/collapsins, netrin-1 and netrin-2, hepatocyte growth factor (HGF), ephrins, noggin, sonic hedgehog and tyrosine hydroxylase.

Other useful transgene products include proteins that regulate the immune system including, without limitation, cytokines and lymphokines such as thrombopoietin (TPO), interleukins (IL) IL-1 through IL-25 (including, IL-2, IL-4, IL-12, and IL-18), monocyte chemoattractant protein, leukemia inhibitory factor, granulocyte-macrophage colony stimulating factor, Fas ligand, tumor necrosis factors α and β, interferons α, β, and γ, stem cell factor, flk-2/flt3 ligand. Gene products produced by the immune system are also useful in the invention. These include, without limitations, immunoglobulins IgG, IgM, IgA, IgD and IgE, chimeric immunoglobulins, humanized antibodies, single chain antibodies, T cell receptors, chimeric T cell receptors, single chain T cell receptors, class I and class II MHC molecules, as well as engineered immunoglobulins and MHC molecules. Useful gene products also include complement regulatory proteins such as complement regulatory proteins, membrane cofactor protein (MCP), decay accelerating factor (DAF), CR1, CF2 and CD59.

Still other useful gene products include any one of the receptors for the hormones, growth factors, cytokines, lymphokines, regulatory proteins and immune system

proteins. The invention encompasses receptors for cholesterol regulation, including the low density lipoprotein (LDL) receptor, high density lipoprotein (HDL) receptor, the very low density lipoprotein (VLDL) receptor, and the scavenger receptor. The invention also encompasses gene products such as members of the steroid hormone receptor superfamily including glucocorticoid receptors and estrogen receptors, Vitamin D receptors and other nuclear receptors. In addition, useful gene products include transcription factors such as *jun*, *fos*, max, mad, serum response factor (SRF), AP-1, AP2, *myb*, MyoD and myogenin, ETS-box containing proteins, TFE3, E2F, ATF1, ATF2, ATF3, ATF4, ZF5, NFAT, CREB, HNF-4, C/EBP, SP1, CCAAT-box binding proteins, interferon regulation factor (IRF-1), Wilms tumor protein, ETS-binding protein, STAT, GATA-box binding proteins, e.g., GATA-3, and the forkhead family of winged helix proteins.

Other useful gene products include, carbamoyl synthetase I, ornithine transcarbamylase, arginosuccinate synthetase, arginosuccinate lyase, arginase, fumarylacetacetate hydrolase, phenylalanine hydroxylase, alpha-1 antitrypsin, glucose-6-phosphatase, porphobilinogen deaminase, factor VIII, factor IX, cystathione beta-synthase, branched chain ketoacid decarboxylase, albumin, isovaleryl-coA dehydrogenase, propionyl CoA carboxylase, methyl malonyl CoA mutase, glutaryl CoA dehydrogenase, insulin, beta-glucosidase, pyruvate carboxylate, hepatic phosphorylase, phosphorylase kinase, glycine decarboxylase, H-protein, T-protein, a cystic fibrosis transmembrane regulator (CFTR) sequence, and a dystrophin cDNA sequence. Still other useful gene products include enzymes such as may be useful in enzyme replacement therapy, which is useful in a variety of conditions resulting from deficient activity of enzyme. For example, enzymes that contain mannose-6-phosphate may be utilized in therapies for lysosomal storage diseases (e.g., a suitable gene includes that encoding β-glucuronidase (GUSB)).

Other useful gene products include non-naturally occurring polypeptides, such as chimeric or hybrid polypeptides having a non-naturally occurring amino acid sequence containing insertions, deletions or amino acid substitutions. For example, single-chain engineered immunoglobulins could be useful in certain immunocompromised patients. Other types of non-naturally occurring gene sequences include antisense molecules and catalytic nucleic acids, such as ribozymes, which could be used to reduce overexpression of a target.

Reduction and/or modulation of expression of a gene is particularly desirable for treatment of hyperproliferative conditions characterized by hyperproliferating cells, as

are cancers and psoriasis. Target polypeptides include those polypeptides which are produced exclusively or at higher levels in hyperproliferative cells as compared to normal cells. Target antigens include polypeptides encoded by oncogenes such as myb, myc, fyn, and the translocation gene bcr/abl, ras, src, P53, neu, trk and EGRF. In addition to oncogene products as target antigens, target polypeptides for anti-cancer treatments and protective regimens include variable regions of antibodies made by B cell lymphomas and variable regions of T cell receptors of T cell lymphomas which, in some embodiments, are also used as target antigens for autoimmune disease. Other tumor-associated polypeptides can be used as target polypeptides such as polypeptides which are found at higher levels in tumor cells including the polypeptide recognized by monoclonal antibody 17-1A and folate binding polypeptides.

Other suitable therapeutic polypeptides and proteins include those which may be useful for treating individuals suffering from autoimmune diseases and disorders by conferring a broad based protective immune response against targets that are associated with autoimmunity including cell receptors and cells which produce "self"-directed antibodies. T cell mediated autoimmune diseases include Rheumatoid arthritis (RA), multiple sclerosis (MS), Sjögren's syndrome, sarcoidosis, insulin dependent diabetes mellitus (IDDM), autoimmune thyroiditis, reactive arthritis, ankylosing spondylitis, scleroderma, polymyositis, dermatomyositis, psoriasis, vasculitis, Wegener's granulomatosis, Crohn's disease and ulcerative colitis. Each of these diseases is characterized by T cell receptors (TCRs) that bind to endogenous antigens and initiate the inflammatory cascade associated with autoimmune diseases.

C. Immunogenic Transgenes

Alternatively, or in addition, the vectors of the invention may contain AAV sequences of the invention and a transgene encoding a peptide, polypeptide or protein which induces an immune response to a selected immunogen. For example, immunogens may be selected from a variety of viral families. Example of desirable viral families against which an immune response would be desirable include, the picornavirus family, which includes the genera rhinoviruses, which are responsible for about 50% of cases of the common cold; the genera enteroviruses, which include polioviruses, coxsackieviruses, echoviruses, and human enteroviruses such as hepatitis A virus; and the genera apthoviruses, which are responsible for foot and mouth diseases, primarily in non-human animals. Within the picornavirus family of viruses, target antigens include the VP1, VP2, VP3, VP4, and VPG. Another viral

family includes the calcivirus family, which encompasses the Norwalk group of viruses, which are an important causative agent of epidemic gastroenteritis. Still another viral family desirable for use in targeting antigens for inducing immune responses in humans and non-human animals is the togavirus family, which includes the genera alphavirus, which include Sindbis viruses, RossRiver virus, and Venezuelan, Eastern & Western Equine encephalitis, and rubivirus, including Rubella virus. The flaviviridae family includes dengue, yellow fever, Japanese encephalitis, St. Louis encephalitis and tick borne encephalitis viruses. Other target antigens may be generated from the Hepatitis C or the coronavirus family, which includes a number of non-human viruses such as infectious bronchitis virus (poultry), porcine transmissible gastroenteric virus (pig), porcine hemagglutinating encephalomyelitis virus (pig), feline infectious peritonitis virus (cats), feline enteric coronavirus (cat), canine coronavirus (dog), and human respiratory coronaviruses, which may cause the common cold and/or non-A, B or C hepatitis. Within the coronavirus family, target antigens include the E1 (also called M or matrix protein), E2 (also called S or Spike protein), E3 (also called HE or hemagglutin-elterose) glycoprotein (not present in all coronaviruses), or N (nucleocapsid). Still other antigens may be targeted against the rhabdovirus family, which includes the genera vesiculovirus (e.g., Vesicular Stomatitis Virus), and the general lyssavirus (e.g., rabies). Within the rhabdovirus family, suitable antigens may be derived from the G protein or the N protein. The family filoviridae, which includes hemorrhagic fever viruses such as Marburg and Ebola virus may be a suitable source of antigens. The paramyxovirus family includes parainfluenza Virus Type 1, parainfluenza Virus Type 3, bovine parainfluenza Virus Type 3, rubulavirus (mumps virus, parainfluenza Virus Type 2, parainfluenza virus Type 4, Newcastle disease virus (chickens), rinderpest, morbillivirus, which includes measles and canine distemper, and pneumovirus, which includes respiratory syncytial virus. The influenza virus is classified within the family orthomyxovirus and is a suitable source of antigen (e.g., the HA protein, the N1 protein). The bunyavirus family includes the genera bunyavirus (California encephalitis, La Crosse), phlebovirus (Rift Valley Fever), hantavirus (puremala is a hemahagin fever virus), nairovirus (Nairobi sheep disease) and various unassigned bungaviruses. The arenavirus family provides a source of antigens against LCM and Lassa fever virus. The reovirus family includes the genera reovirus, rotavirus (which causes acute gastroenteritis in children), orbiviruses, and cultivirus (Colorado Tick fever, Lebombo (humans), equine encephalosis, blue tongue).

The retrovirus family includes the sub-family oncorivirinal which encompasses such human and veterinary diseases as feline leukemia virus, HTLVI and HTLVII, lentivirinal (which includes human immunodeficiency virus (HIV), simian immunodeficiency virus (SIV), feline immunodeficiency virus (FIV), equine infectious anemia virus, and spumavirinal). Between the HIV and SIV, many suitable antigens have been described and can readily be selected. Examples of suitable HIV and SIV antigens include, without limitation the gag, pol, Vif, Vpx, VPR, Env, Tat and Rev proteins, as well as various fragments thereof. In addition, a variety of modifications to these antigens have been described. Suitable antigens for this purpose are known to those of skill in the art. For example, one may select a sequence encoding the gag, pol, Vif, and Vpr, Env, Tat and Rev, amongst other proteins. See, e.g., the modified gag protein which is described in US Patent 5,972,596. See, also, the HIV and SIV proteins described in D.H. Barouch et al, J. Virol., 75(5):2462-2467 (March 2001), and R.R. Amara, et al, Science, 292:69-74 (6 April 2001). These proteins or subunits thereof may be delivered alone, or in combination via separate vectors or from a single vector.

The papovavirus family includes the sub-family polyomaviruses (BKU and JCU viruses) and the sub-family papillomavirus (associated with cancers or malignant progression of papilloma). The adenovirus family includes viruses (EX, AD7, ARD, O.B.) which cause respiratory disease and/or enteritis. The parvovirus family feline parvovirus (feline enteritis), feline panleucopeniavirus, canine parvovirus, and porcine parvovirus. The herpesvirus family includes the sub-family alphaherpesvirinae, which encompasses the genera simplexvirus (HSVI, HSVII), varicellovirus (pseudorabies, varicella zoster) and the sub-family betaherpesvirinae, which includes the genera cytomegalovirus (HCMV, muromegalovirus) and the sub-family gammaherpesvirinae, which includes the genera lymphocryptovirus, EBV (Burkitts lymphoma), infectious rhinotracheitis, Marek's disease virus, and rhadinovirus. The poxvirus family includes the sub-family chordopoxvirinae, which encompasses the genera orthopoxvirus (Variola (Smallpox) and Vaccinia (Cowpox)), parapoxvirus, avipoxvirus, capripoxvirus, leporipoxvirus, suipoxvirus, and the sub-family entomopoxvirinae. The hepadnavirus family includes the Hepatitis B virus. One unclassified virus which may be suitable source of antigens is the Hepatitis delta virus. Still other viral sources may include avian infectious bursal disease virus and porcine respiratory and reproductive syndrome virus. The alphavirus family includes equine arteritis virus and various Encephalitis viruses.

The present invention may also encompass immunogens which are useful to immunize a human or non-human animal against other pathogens including bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or from a cancer cell or tumor cell. Examples of bacterial pathogens include pathogenic gram-positive cocci include pneumococci; staphylococci; and streptococci. Pathogenic gram-negative cocci include meningococcus; gonococcus. Pathogenic enteric gram-negative bacilli include enterobacteriaceae; pseudomonas, acinetobacteria and eikenella; melioidosis; salmonella; shigella; haemophilus; moraxella; *H. ducreyi* (which causes chancroid); brucella; *Franisella tularensis* (which causes tularemia); yersinia (pasteurella); streptobacillus moniliformis and spirillum; Gram-positive bacilli include listeria monocytogenes; erysipelothrix rhusiopathiae; *Corynebacterium diphtheria* (diphtheria); cholera; *B. anthracis* (anthrax); donovanosis (granuloma inguinale); and bartonellosis. Diseases caused by pathogenic anaerobic bacteria include tetanus; botulism; other clostridia; tuberculosis; leprosy; and other mycobacteria. Pathogenic spirochetal diseases include syphilis; treponematoses: yaws, pinta and endemic syphilis; and leptospirosis. Other infections caused by higher pathogen bacteria and pathogenic fungi include actinomycosis; nocardiosis; cryptococcosis, blastomycosis, histoplasmosis and coccidioidomycosis; candidiasis, aspergillosis, and mucormycosis; sporotrichosis; paracoccidiodomycosis, petriellidiosis, torulopsosis, mycetoma and chromomycosis; and dermatophytosis. Rickettsial infections include Typhus fever, Rocky Mountain spotted fever, Q fever, and Rickettsialpox. Examples of mycoplasma and chlamydial infections include: mycoplasma pneumoniae; lymphogranuloma venereum; psittacosis; and perinatal chlamydial infections. Pathogenic eukaryotes encompass pathogenic protozoans and helminths and infections produced thereby include: amebiasis; malaria; leishmaniasis; trypanosomiasis; toxoplasmosis; *Pneumocystis carinii*; *Trichans*; *Toxoplasma gondii*; babesiosis; giardiasis; trichinosis; filariasis; schistosomiasis; nematodes; trematodes or flukes; and cestode (tapeworm) infections.

Many of these organisms and/or toxins produced thereby have been identified by the Centers for Disease Control [(CDC), Department of Heath and Human Services, USA], as agents which have potential for use in biological attacks. For example, some of these biological agents, include, *Bacillus anthracis* (anthrax), *Clostridium botulinum* and its toxin (botulism), *Yersinia pestis* (plague), variola major (smallpox), *Francisella tularensis* (tularemia), and viral hemorrhagic fever, all of which are currently classified as

Category A agents; *Coxiella burnetti* (Q fever); Brucella species (brucellosis), *Burkholderia mallei* (glanders), *Ricinus communis* and its toxin (ricin toxin), *Clostridium perfringens* and its toxin (epsilon toxin), *Staphylococcus* species and their toxins (enterotoxin B), all of which are currently classified as Category B agents; and Nipan virus and hantaviruses, which are currently classified as Category C agents. In addition, other organisms, which are so classified or differently classified, may be identified and/or used for such a purpose in the future. It will be readily understood that the viral vectors and other constructs described herein are useful to deliver antigens from these organisms, viruses, their toxins or other by-products, which will prevent and/or treat infection or other adverse reactions with these biological agents.

Administration of the vectors of the invention to deliver immunogens against the variable region of the T cells elicit an immune response including CTLs to eliminate those T cells. In rheumatoid arthritis (RA), several specific variable regions of T cell receptors (TCRs) which are involved in the disease have been characterized. These TCRs include V-3, V-14, V-17 and Vα-17. Thus, delivery of a nucleic acid sequence that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in RA. In multiple sclerosis (MS), several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-7 and Vα-10. Thus, delivery of a nucleic acid sequence that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in MS. In scleroderma, several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-6, V-8, V-14 and Vα-16, Vα-3C, Vα-7, Vα-14, Vα-15, Vα-16, Vα-28 and Vα-12. Thus, delivery of a nucleic acid molecule that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in scleroderma.

Optionally, vectors containing AAV sequences of the invention may be delivered using a prime-boost regimen. A variety of such regimens have been described in the art and may be readily selected. See, e.g., WO 00/11140, published March 2, 2000, incorporated by reference.

Such prime-boost regimens typically involve the administration of a DNA (e.g., plasmid) based vector to prime the immune system to second, booster, administration with a traditional antigen, such as a protein or a recombinant virus carrying the sequences encoding such an antigen. In one embodiment, the invention provides a method of priming

and boosting an immune response to a selected antigen by delivering a plasmid DNA vector carrying said antigen, followed by boosting, e.g., with a vector containing AAV sequences of the invention.

In one embodiment, the prime-boost regimen involves the expression of multiproteins from the prime and/or the boost vehicle. See, e.g., R.R. Amara, Science, 292:69-74 (6 April 2001) which describes a multiprotein regimen for expression of protein subunits useful for generating an immune response against HIV and SIV. For example, a DNA prime may deliver the Gag, Pol, Vif, VPX and Vpr and Env, Tat, and Rev from a single transcript. Alternatively, the SIV Gag, Pol and HIV-1 Env is delivered.

However, the prime-boost regimens are not limited to immunization for HIV or to delivery of these antigens. For example, priming may involve delivering with a first chimp vector of the invention followed by boosting with a second chimp vector, or with a composition containing the antigen itself in protein form. In one or example, the prime-boost regimen can provide a protective immune response to the virus, bacteria or other organism from which the antigen is derived. In another desired embodiment, the prime-boost regimen provides a therapeutic effect that can be measured using convention assays for detection of the presence of the condition for which therapy is being administered.

The priming vaccine may be administered at various sites in the body in a dose dependent manner, which depends on the antigen to which the desired immune response is being targeted. The invention is not limited to the amount or situs of injection(s) or to the pharmaceutical carrier. Rather, the priming step encompasses treatment regimens which include a single dose or dosage which is administered hourly, daily, weekly or monthly, or yearly. As an example, the mammals may receive one or two priming injection containing between about 10 μg to about 50 μg of plasmid in carrier. A desirable priming amount or dosage of the priming DNA vaccine composition ranges between about 1 μg to about 10,000 μg of the DNA vaccine. Dosages may vary from about 1 μg to 1000 μg DNA per kg of subject body weight. The amount or site of injection is desirably selected based upon the identity and condition of the mammal being vaccinated.

The dosage unit of the DNA vaccine suitable for delivery of the antigen to the mammal is described herein. The DNA vaccine is prepared for administration by being suspended or dissolved in a pharmaceutically or physiologically acceptable carrier such as isotonic saline, isotonic salts solution or other formulations which will be apparent to those skilled in such administration. The appropriate carrier will be evident to those skilled in the

art and will depend in large part upon the route of administration. The compositions of the invention may be administered to a mammal according to the routes described above, in a sustained release formulation using a biodegradable biocompatible polymer, or by on-site delivery using micelles, gels and liposomes.

Optionally, the priming step of this invention also includes administering with the priming DNA vaccine composition, a suitable amount of an adjuvant, such as are defined herein.

Preferably, a boosting composition is administered about 2 to about 27 weeks after administering the priming DNA vaccine to the mammalian subject. The administration of the boosting composition is accomplished using an effective amount of a boosting vaccine composition containing or capable of delivering the same antigen as administered by the priming DNA vaccine. The boosting composition may be composed of a recombinant viral vector derived from the same viral source or from another source. Alternatively, the "boosting composition" can be a composition containing the same antigen as encoded in the priming DNA vaccine, but in the form of a protein or peptide, which composition induces an immune response in the host. In another embodiment, the boosting vaccine composition includes a composition containing a DNA sequence encoding the antigen under the control of a regulatory sequence directing its expression in a mammalian cell, e.g., vectors such as well-known bacterial or viral vectors. The primary requirements of the boosting vaccine composition are that the antigen of the vaccine composition is the same antigen, or a cross-reactive antigen, as that encoded by the DNA vaccine.

Suitably, the vectors of the invention are also well suited for use in regimens which use non-AAV vectors as well as proteins, peptides, and/or other biologically useful therapeutic or immunogenic compounds. These regimens are particularly well suited to gene delivery for therapeutic poses and for immunization, including inducing protective immunity. Such uses will be readily apparent to one of skill in the art.

Further, a vector of the invention provides an efficient gene transfer vehicle which can deliver a selected transgene to a selected host cell *in vivo or ex vivo* even where the organism has neutralizing antibodies to one or more AAV serotypes. In one embodiment, the vector (e.g., an rAAV) and the cells are mixed *ex vivo;* the infected cells are cultured using conventional methodologies; and the transduced cells are re-infused into the patient. Further, the vectors of the invention may also be used for production of a desired gene product *in vitro.* For *in vitro* production, a desired product (e.g., a protein) may be

obtained from a desired culture following transfection of host cells with a rAAV containing the molecule encoding the desired product and culturing the cell culture under conditions which permit expression. The expressed product may then be purified and isolated, as desired. Suitable techniques for transfection, cell culturing, purification, and isolation are known to those of skill in the art.

The present invention also provides any one of the embodiments disclosed below and indicated with the numbers 1 to 23.

1. A method of detecting adeno-associated virus (AAV) sequences in a sample, said method comprising the steps of:

(a) subjecting a sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers which specifically amplify a first region of AAV nucleic acid sequences;

(b) optionally subjecting the DNA to further amplification using a second set of primers which specifically amplify a second region which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;

(c) optionally subjecting the DNA to further amplification using a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained,

wherein each of said regions is predetermined based upon the alignment of the nucleic acid sequences of at least two AAV serotypes and each of said regions comprises nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of the at least two aligned AAV serotypes; and

wherein each of the sets of primers consist of a 5' primer and a 3' primer;

wherein the presence of amplified sequences indicates the presence of an AAV in the sample.

2. A method according to claim 1, wherein steps (b) and (c) are performed, and further comprising the step of :

(d) using the amplified sequences to construct a sequence comprising a partial and/or complete AAV gene, thereby isolating an AAV gene sequence from the sample.

3. The method according to claim 2, wherein the first region is in the AAV capsid, the second region extends to the 3' end of the rep genes, and the third region extends to 5' of the AAV 3' ITR, such that step (d) permits the construction of AAV gene sequences comprising the complete AAV capsid gene.

4. The method according to claim 2, further comprising the step of subjecting the DNA to amplification with a fourth set of primers which specifically amplifies a fourth region which extend 5' to the third region.

5. The method according to claim 4, wherein the fourth region extends to 3' of the AAV 5' ITR, such that step (d) permits the construction of AAV gene sequences comprising the complete AAV rep and cap genes.

6. The method according to claim 1 or claim 2, wherein said sample comprises cellular or genomic DNA.

7. The method according to claim 1 or claim 2, wherein said DNA has been extracted from the group consisting of cells, cell culture, tissue, tissue culture, and biological fluids.

8. The method according to claim 1 or claim 2, wherein the first region is about 250 base pairs in length.

9. The method according to claim 1 or 2, wherein the first region is highly conserved over at least about 25 base pairs at the 5' and/or 3' end of the region.

10. The method according to claim 1or 2, wherein the first region is highly conserved over at least about 30 base pairs at the 5' and/or 3' end of the region.

11. The method according to claim 1 or claim 2, wherein the highly conserved sequences of the first region have at least 80% identity among the aligned AAV serotypes at the 5' and/or 3' end of the region.

12. The method according claim 11, wherein the highly conserved sequences of the first region have at least 90% identity among the aligned AAV serotypes at the 5' and/or 3' end of the region.

13. The method according to claim 1 or claim 2, wherein the variable sequences in the middle of the first region have less than 70% identity among the aligned AAV serotypes.

14. The method according to claim 1 or claim 2, wherein the first region spans about bp 2800 to about 3200 of AAV 1, SEQ ID NO:6, and corresponding base pairs in other AAV serotypes.

15. The method according to claim 14, wherein the first region is 257 bp spanning bp 2886 to about 3143 bp of AAV 1, SEQ ID NO:6, and corresponding base pairs in other AAV serotypes.

16. The method according to claim 1, wherein the primers are AV1ns and AV2cas.

17. A method of identifying the serotype of adeno-associated virus (AAV) sequences in a sample as known or unknown, said method comprising the steps of:

(a) obtaining an enzymatic digestion analysis of a sample containing DNA molecules comprising AAV sequences which span all or a portion of bp 2886 to 3143 of AAV1, SEQ ID NO:1, and corresponding regions of other AAV serotypes; and

(b) comparing the enzymatic digestion analysis from the sample to enzymatic digestion analysis for corresponding regions of one or more AAV serotypes,

thereby identifying the AAV sequences in the sample as being from one of the one or more AAV serotypes or from an unknown serotype.

18. The method according to claim 17, wherein the AAV sequences were obtained by the method of claim 1.

19. A diagnostic kit for detecting the presence of an unknown adeno-associated virus (AAV) in a sample, said kit comprising:

(a) a first set of primers which specifically amplify a first region of AAV nucleic acid sequences;

(b) optionally a second set of primers specific for a second region of the AAV nucleic acid sequences which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;

(c) optionally a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained,

wherein each of said regions is predetermined based upon the alignment of the nucleic acid sequences of at least two AAV serotypes and each of said regions comprises nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of the at least two aligned AAV serotypes

wherein each of the sets of primers consist of a 5' primer and a 3' primer.

20. A method for isolating novel adeno-associated viruses (AAV) from a cell, said method comprising the steps of: (a) infecting the cell with a virus which provides helper functions to said AAV; (b) isolating infectious clones containing AAV; (c) sequencing the isolated AAV; and (d) comparing the sequences of the isolated AAV to known AAV serotypes, whereby differences in the sequences of the isolated AAV and known AAV

serotypes indicates the presence of a novel AAV.

21. The method according to claim 20, wherein said virus is an adenovirus.

22. The method according to claim 21, wherein said adenovirus is of human or non-human primate origin.

23. A novel adeno-associated virus (AAV) serotype identified by a method according to claim 2 or claim 20.

The following examples illustrate several aspects and embodiments of the invention.

EXAMPLES

Example 1: PCR amplification, cloning and characterization of novel AAV sequences.

Tissues from nonhuman primates were screened for AAV sequences using a PCR method based on oligonucleotides to highly conserved regions of known AAVs. A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which a hypervariable region of the capsid protein (Cap) that is unique to each known AAV serotype, which is termed herein a "signature region," is flanked by conserved sequences. In later analysis, this signature region was shown to be located between conserved residues spanning hypervariable region 3.

An initial survey of peripheral blood of a number of nonhuman primate species revealed detectable AAV in a subset of animals from species such as rhesus macaques, cynomologous macaques, chimpanzees and baboons. However, there were no AAV sequences detected in some other species tested, including Japanese macaques, pig-tailed macaques and squirrel monkeys. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

A. *Amplification of an AAV signature region*

DNA sequences of AAV1-6 and AAVs isolated from Goose and Duck were aligned to each other using "Clustal W" at default settings. The alignment for AAV1-6, and

including the information for the novel AAV7, is provided in Fig. 1. Sequence similarities among AAVs were compared.

In the line of study, a 257 bp region spanning 2886 bp to 3143 bp of AAV 1 [SEQ ID NO: 6], and the corresponding region in the genomes of AAV 2-6 genomes [See, Fig. 1], was identified by the inventors. This region is located with the AAV capsid gene and has highly conserved sequences among at both 5' and 3' ends and is relatively variable sequence in the middle. In addition, this region contains a DraIII restriction enzyme site (CACCACGTC, SEQ ID NO:15) . The inventors have found that this region serves as specific signature for each known type of AAV DNA. In other words, following PCR reactions, digestion with endonucleases that are specific to each known serotypes and gel electrophoresis analysis, this regions can be used to definitively identify amplified DNA as being from serotype 1, 2, 3, 4, 5, 6, or another serotype.

The primers were designed, validated and PCR conditions optimized with AAV1, 2 and 5 DNA controls. The primers were based upon the sequences of AAV2: 5' primer, 1S: bp 2867-2891 of AAV2 (SEQ ID NO:7) and 3' primer, 18as, bp 3095-3121 of AAV2 (SEQ ID NO:7).

Cellular DNAs from different tissues including blood, brain, liver, lung, testis, etc. of different rhesus monkeys were studied utilizing the strategy described above. The results revealed that DNAs from different tissues of these monkeys gave rise to strong PCR amplifications. Further restriction analyses of PCR products indicated that they were amplified from AAV sequences different from any published AAV sequences.

PCR products (about 255 bp in size) from DNAs of a variety of monkey tissues have been cloned and sequenced. Bioinformatics study of these novel AAV sequences indicated that they are novel AAV sequences of capsid gene and distinct from each other. Fig. 1 includes in the alignment the novel AAV signature regions for AAV10-12 [SEQ ID NO:117, 118 and 119, respectively]. Multiple sequence alignment analysis was performed using the Clustal W (1.81) program. The percentage of sequence identity between the signature regions of AAV 1-7 and AAV 10-12 genomes is provided below.

Table 1. Sequences for Analysis

Sequence #	AAV Serotype	Size (bp)
1	AAV1	258
2	AAV2	255
3	AAV3	255
4	AAV4	246
5	AAV5	258
6	AAV6	258
7	AAV7	258
10	AAV10	255
11	AAV11	258
12	AAV12	255

Table 3. Pairwise Alignment (Percentage of Identity)

	AAV2	AAV3	AAV4	AAV5	AAV6	AAV7	AAV10	AAV11	AAV12
AAV1	90	90	81	76	97	91	93	94	93
AAV2		93	79	78	90	90	93	93	92
AAV3			80	76	90	92	92	92	92
AAV4				76	81	84	82	81	79
AAV5					75	78	79	79	76
AAV6						91	92	94	94
AAV7							94	92	92
AAV10								95	93
AAV11									94

Over 300 clones containing novel AAV serotype sequences that span the selected 257 bp region were isolated and sequenced. Bioinformatics analysis of these 300+ clones suggests that this 257 bp region is critical in serving as a good land marker or signature sequence for quick isolation and identification of novel AAV serotype.

B. *Use of the signature region for PCR amplification.*

The 257 bp signature region was used as a PCR anchor to extend PCR amplifications to 5' of the genome to cover the junction region of rep and cap genes (1398 bp – 3143 bp, SEQ ID NO:6) and 3' of the genome to obtain the entire cap gene sequence (2866 bp – 4600 bp, SEQ ID NO:6). PCR amplifications were carried out using the standard conditions, including denaturing at 95°C for 0.5-1 min, annealing at 60-65°C for 0.5-1 min and extension at 72° C for 1 min per kb with a total number of amplification cycles ranging from 28 to 42.

Using the aligned sequences as described in "A", two other relative conserved regions were identified in the sequence located in 3' end of rep genes and 5' to the

257 bp region and in the sequence down stream of the 257 bp fragment but before the AAV' 3 ITR. Two sets of new primers were designed and PCR conditions optimized for recovery of entire capsid and a part of rep sequences of novel AAV serotypes. More specifically, for the 5' amplification, the 5' primer, AV1Ns, was GCTGCGTCAACTGGACCAATGAGAAC [nt 1398-1423 of AAV1, SEQ ID NO:6] and the 3' primer was 18as, identified above. For the 3' amplification, the 5' primer was 1s, identified above, and the 3' primer was AV2Las, TCGTTTCAGTTGAACTTTGGTCTCTGCG [nt 4435-4462 of AAV2, SEQ ID NO:7].

In these PCR amplifications, the 257 bp region was used as a PCR anchor and land marker to generate overlapping fragments to construct a complete capsid gene by fusion at the DraIII site in the signature region following amplification of the 5' and 3' extension fragments obtained as described herein. More particularly, to generate the intact AAV7 cap gene, the three amplification products (a) the sequences of the signature region; (b) the sequences of the 5' extension; and (c) the sequences of the 3' extension were cloned into a pCR4-Topo [Invitrogen] plasmid backbone according to manufacturer's instructions. Thereafter, the plasmids were digested with DraIII and recombined to form an intact cap gene.

In this line of work, about 80 % of capsid sequences of AAV7 and AAV 8 were isolated and analyzed. Another novel serotype, AAV9, was also discovered from Monkey #2.

Using the PCR conditions described above, the remaining portion of the rep gene sequence for AAV7 is isolated and cloned using the primers that amplify 108 bp to 1461 bp of AAV genome (calculated based on the numbering of AAV2, SEQ ID NO:7). This clone is sequenced for construction of a complete AAV7 genome without ITRs.

C. Direct Amplification of 3.1 kb Cap fragment

To directly amplify a 3.1 kb full-length Cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene was selected (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt 1398-1423 of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGTTCAACTGAAACGA 3', SEQ ID NO:7) for amplification of full-length cap fragments. The PCR products were Topo-cloned according to manufacturer's directions (Invitrogen) and sequence analysis was performed by

Qiagengenomics (Qiagengenomics, Seattle, WA) with an accuracy of ≥ 99.9%. A total of 50 capsid clones were isolated and characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1 – rh.37), 6 clones from cynomologous macaques (cy.1 – cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1 – ch.5).

To rule out the possibility that sequence diversity within the novel AAV family was not an artifact of the PCR, such as PCR-mediated gene splicing by overlap extension between different partial DNA templates with homologous sequences, or the result of recombination process in bacteria, a series of experiments were performed under identical conditions for VP1 amplification using total cellular DNAs. First, intact AAV7 and AAV8 plasmids were mixed at an equal molar ratio followed by serial dilutions. The serially diluted mixtures were used as templates for PCR amplification of 3.1 kb VP1 fragments using universal primers and identical PCR conditions to that were used for DNA amplifications to see whether any hybrid PCR products were generated. The mixture was transformed into bacteria and isolated transformants to look for hybrid clones possibly derived from recombination process in bacterial cells. In a different experiment, we restricted AAV7 and AAV8 plasmids with Msp I, Ava I and HaeI, all of which cut both genomes multiple times at different positions, mixed the digestions in different combinations and used them for PCR amplification of VP1 fragments under the same conditions to test whether any PCR products could be generated through overlap sequence extension of partial AAV sequences. In another experiment, a mixture of gel purified 5' 1.5 kb AAV7 VP1 fragment and 3' 1.7 kb AAV8 VP1 fragment with overlap in the signature region was serially diluted and used for PCR amplification in the presence and absence of 200 ng cellular DNA extracted from a monkey cell line that was free of AAV sequences by TaqMan analysis. None of these experiments demonstrated efficient PCR-mediated overlap sequence production under the conditions of the genomic DNA Cap amplification (data not shown). As a further confirmation, 3 pairs of primers were designed, which were located at different HVRs, and were sequence specific to the variants of clone 42s from Rhesus macaque F953, in different combinations to amplify shorter fragments from mesenteric lymph node (MLN) DNA from F953 from which clone 42s were isolated. All sequence variations identified in full-length Cap clones were found in these short fragments (data not shown).

Example 2: Adeno-Associated Viruses Undergo Substantial Evolution in Primates During Natural Infections

Sequence analysis of selected AAV isolates revealed divergence throughout the genome that is most concentrated in hypervariable regions of the capsid proteins. Epidemiologic data indicate that all known serotypes are endemic to primates, although isolation of clinical isolates has been restricted to AAV2 and AAV3 from anal and throat swabs of human infants and AAV5 from a human condylomatous wart. No known clinical sequalae have been associated with AAV infection.

In an attempt to better understand the biology of AAV, nonhuman primates were used as models to characterize the sequlae of natural infections. Tissues from nonhuman primates were screened for AAV sequences using the PCR method of the invention based on oligonucleotides to highly conserved regions of known AAVs (see Example 1). A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which conserved sequences are flanked by a hypervariable region that is unique to each known AAV serotype, termed herein a "signature region."

An initial survey of peripheral blood of a number of nonhuman primate species including rhesus monkeys, cynomologous monkeys, chimpanzees, and baboons revealed detectable AAV in a subset of animals from all species. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

The amplified signature sequences were subcloned into plasmids and individual transformants were subjected to sequence analysis. This revealed substantial variation in nucleotide sequence of clones derived from different animals. Variation in the signature sequence was also noted in clones obtained within individual animals. Tissues harvested from two animals in which unique signature sequences were identified (i.e., colon from 98E044 and heart from 98E056) were further characterized by expanding the sequence amplified by PCR using oligonucleotides to highly conserved sequences. In this way, complete proviral structures were reconstructed for viral genomes from both tissues as described herein. These proviruses differ from the other known AAVs with the greatest sequence divergence noted in regions of the Cap gene.

Additional experiments were performed to confirm that AAV sequences resident to the nonhuman primate tissue represented proviral genomes of infectious virus that is capable

of being rescued and form virions. Genomic DNA from liver tissue of animal 98E056, from which AAV8 signature sequence was detected, was digested with an endonuclease that does not have a site within the AAV sequence and transfected into 293 cells with a plasmid containing an E1 deleted genome of human adenovirus serotype 5 as a source of helper functions. The resulting lysate was passaged on 293 cells once and the lysate was recovered and analyzed for the presence of AAV Cap proteins using a broadly reacting polyclonal antibody to Cap proteins and for the presence and abundance of DNA sequences from the PCR amplified AAV provirus from which AAV8 was derived. Transfection of endonuclease restricted heart DNA and the adenovirus helper plasmid yielded high quantities of AAV8 virus as demonstrated by the detection of Cap proteins by Western blot analysis and the presence of 10^4 AAV8 vector genomes per 293 cell. Lysates were generated from a large-scale preparation and the AAV was purified by cesium sedimentation. The purified preparation demonstrated 26 nm icosohedral structures that look identical to those of AAV serotype 2. Transfection with the adenovirus helper alone did not yield AAV proteins or genomes, ruling out contamination as a source of the rescued AAV.

To further characterize the inter and intra animal variation of AAV signature sequence, selected tissues were subjected to extended PCR to amplify entire Cap open reading frames.

The resulting fragments were cloned into bacterial plasmids and individual transformants were isolated and fully sequenced. This analysis involved mesenteric lymph nodes from three rhesus monkeys (Tulane/V223 – 6 clones; Tulane/T612 – 7 clones; Tulane/F953 – 14 clones), liver from two rhesus monkeys (Tulane/V251 – 3 clones; Penn/00E033 – 3 clones), spleen from one rhesus monkey (Penn/97E043 – 3 clones), heart from one rhesus monkey (IHGT/98E046- 1 clone) and peripheral blood from one chimpanzee (New Iberia/X133 – 5 clones), six cynomologous macaques (Charles River/A1378, A3099, A3388, A3442, A2821, A3242 – 6 clones total) and one Baboon (SFRB/8644 – 2 clones). Of the 50 clones that were sequenced from 15 different animals, 30 were considered non-redundant based on the finding of at least 7 amino acid differences from one another. The non-redundant VP1 clones are numbered sequentially as they were isolated, with a prefix indicating the species of non-human primate from which they were derived. The structural relationships between these 30 non-redundant clones and the previously described 8 AAV serotypes were determined using the SplitsTree program [Huson, D. H. SplitsTree: analyzing and visualizing evolutionary data. *Bioinformatics* **14**,

68-73 (1998)] with implementation of the method of split decomposition. The analysis depicts homoplasy between a set of sequences in a tree-like network rather than a bifurcating tree. The advantage is to enable detection of groupings that are the result of convergence and to exhibit phylogenetic relationships even when they are distorted by parallel events. Extensive phylogenetic research will be required in order to elucidate the AAV evolution, whereas the intention here only is to group the different clones as to their sequence similarity.

To confirm that the novel VP1 sequences were derived from infectious viral genomes, cellular DNA from tissues with high abundance of viral DNA was restricted with an endonuclease that should not cleave within AAV and transfected into 293 cells, followed by infection with adenovirus. This resulted in rescue and amplification of AAV genomes from DNA of tissues from two different animals (data not shown).

VP1 sequences of the novel AAVs were further characterized with respect to the nature and location of amino acid sequence variation. All 30 VP1 clones that were shown to differ from one another by greater than 1% amino acid sequence were aligned and scored for variation at each residue. An algorithm developed to determine areas of sequence divergence yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the 4 previously described variable regions [Kotin, cited above; Rutledge, cited above]. The three-fold-proximal peaks contain most of the variability (HVR5-10). Interestingly the loops located at the 2 and 5 fold axis show intense variation as well. The HVRs 1 and 2 occur in the N-terminal portion of the capsid protein that is not resolved in the X-ray structure suggesting that the N-terminus of the VP1 protein is exposed on the surface of the virion.

Real-time PCR was used to quantify AAV sequences from tissues of 21 rhesus monkeys using primers and probes to highly conserved regions of Rep (one set) and Cap (two sets) of known AAVs. Each data point represents analysis from tissue DNA from an individual animal. This confirmed the wide distribution of AAV sequences, although the quantitative distribution differed between individual animals. The source of animals and previous history or treatments did not appear to influence distribution of AAV sequences in rhesus macaques. The three different sets of primers and probes used to quantify AAV yielded consistent results. The highest levels of AAV were found consistently in mesenteric lymph nodes at an average of 0.01 copies per diploid genome for 13 animals that were positive. Liver and spleen also contained high abundance of virus DNA. There were examples of very high AAV, such as in heart of rhesus macaque 98E056, spleen of rhesus

macaque 97E043 and liver of rhesus macaque RQ4407, which demonstrated 1.5, 3 and 20 copies of AAV sequence per diploid genome respectively. Relatively low levels of virus DNA were noted in peripheral blood mononuclear cells, suggesting the data in tissue are not due to resident blood components (data not shown). It should be noted that this method would not necessarily capture all AAVs resident to the nonhuman primates since detection requires high homology to both the oligonucleotides and the real time PCR probe. Tissues from animals with high abundance AAV DNA was further analyzed for the molecular state of the DNA, by DNA hybridization techniques, and its cellular distribution, by *in situ* hybridization.

The kind of sequence variation revealed in AAV proviral fragments isolated from different animals and within tissues of the same animals is reminiscent of the evolution that occurs for many RNA viruses during pandemics or even within the infection of an individual. In some situations the notion of a wild-type virus has been replaced by the existence of swarms of quasispecies that evolve as a result of rapid replication and mutations in the presence of selective pressure. One example is infection by HIV, which evolves in response to immunologic and pharmacologic pressure. Several mechanisms contribute to the high rate of mutations in RNA viruses, including low fidelity and lack of proof reading capacity of reverse transcriptase and non-homologous and homologous recombination.

Evidence for the formation of quasispecies of AAV was illustrated in this study by the systematic sequencing of multiple cloned proviral fragments. In fact, identical sequences could not be found within any extended clones isolated between or within animals. An important mechanism for this evolution of sequence appears to be a high rate of homologous recombination between a more limited number of parenteral viruses. The net result is extensive swapping of hypervariable regions of the Cap protein leading to an array of chimeras that could have different tropisms and serologic specificities (i.e., the ability to escape immunologic responses especially as it relates to neutralizing antibodies). Mechanisms by which homologous recombination could occur are unclear. One possibility is that + and – strands of different single stranded AAV genomes anneal during replication as has been described during high multiplicity of infections with AAV recombinants. It is unclear if other mechanisms contribute to sequence evolution in AAV infections. The overall rate of mutation that occurs during AAV replication appears to be relatively low and the data do not suggest high frequencies of replication errors. However, substantial rearrangements of the AAV genome have been described during lytic infection leading to the

formation of defective interfering particles. Irrespective of the mechanisms that lead to sequence divergence, with few exceptions , vp1 structures of the quasispecies remained intact without frameshifts or nonsense mutations suggesting that competitive selection of viruses with the most favorable profile of fitness contribute to the population dynamics.

These studies have implications in several areas of biology and medicine. The concept of rapid virus evolution, formerly thought to be a property restricted to RNA viruses, should be considered in DNA viruses, which classically have been characterized by serologic assays. It will be important in terms of parvoviruses to develop a new method for describing virus isolates that captures the complexity of its structure and biology, such as with HIV, which are categorized as general families of similar structure and function called Clades. An alternative strategy is to continue to categorize isolates with respect to serologic specificity and develop criteria for describing variants within serologic groups.

Example 3: Vectorology of recombinant AAV genomes equipped with AAV2 ITRs using chimeric plasmids containing AAV2 rep and novel AAV cap genes for serological and gene transfer studies in different animal models.

Chimeric packaging constructs are generated by fusing AAV2 rep with cap sequences of novel AAV serotypes. These chimeric packaging constructs are used, initially, for pseudotyping recombinant AAV genomes carrying AAV2 ITRs by triple transfection in 293 cell using Ad5 helper plasmid. These pseudotyped vectors are used to evaluate performance in transduction-based serological studies and evaluate gene transfer efficiency of novel AAV serotypes in different animal models including NHP and rodents, before intact and infectious viruses of these novel serotypes are isolated.

A. *pAAV2GFP*

The AAV2 plasmid which contains the AAV2 ITRs and green fluorescent protein expressed under the control of a constitutitive promoter. This plasmid contains the following elements: the AAV2 ITRs, a CMV promoter, and the GFP coding sequences.

B. *Cloning of trans* plasmid

To construct the chimeric trans-plasmid for production of recombinant pseudotyped AAV7 vectors, p5E18 plasmid (Xiao *et al.*, 1999, *J. Virol* 73:3994-4003) was partially digested with Xho I to linearize the plasmid at the Xho I site at the position of 3169 bp only. The Xho I cut ends were then filled in and ligated back. This modified p5E18 plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2

cap gene sequence and replaced with a 2267 bp Spe I/Xho I fragment containing the AAV7 cap gene which was isolated from pCRAAV7 6-5+15-4 plasmid.

The resulting plasmid contains the AAV2 rep sequences for Rep78/68 under the control of the AAV2 P5 promoter, and the AAV2 rep sequences for Rep52/40 under the control of the AAV2 P19 promoter. The AAV7 capsid sequences are under the control of the AAV2 P40 promoter, which is located within the Rep sequences. This plasmid further contains a spacer 5' of the rep ORF.

C. *Production of Pseudotyped rAAV*

The rAAV particles (AAV2 vector in AAV7 capsid) are generated using an adenovirus-free method. Briefly, the cis plasmid (pAAV2.1 lacZ plasmid containing AAV2 ITRs), and the trans plasmid pCRAAV7 6-5+15-4 (containing the AAV2 rep and AAV7 cap) and a helper plasmid, respectively, were simultaneously co-transfected into 293 cells in a ratio of 1:1:2 by calcium phosphate precipitation.

For the construction of the pAd helper plasmids, pBG10 plasmid was purchased from Microbix (Canada). A RsrII fragment containing L2 and L3 was deleted from pBHG10, resulting in the first helper plasmid, pAdΔF13. Plasmid AdΔ F1 was constructed by cloning Asp700/SalI fragment with a PmeI/SgfI deletion, isolating from pBHG10, into Bluescript. MLP, L2, L2 and L3 were deleted in the pAdΔF1. Further deletions of a 2.3 kb NruI fragment and, subsequently, a 0.5 kb RsrII/NruI fragment generated helper plasmids pAdΔF5 and pAdΔF6, respectively. The helper plasmid, termed pΔF6, provides the essential helper functions of E2a and E4 ORF6 not provided by the E1-expressing helper cell, but is deleted of adenoviral capsid proteins and functional E1 regions).

Typically, 50 μg of DNA (cis:trans:helper) was transfected onto a 150 mm tissue culture dish. The 293 cells were harvested 72 hours post-transfection, sonicated and treated with 0.5% sodium deoxycholate (37°C for 10 min.) Cell lysates were then subjected to two rounds of a CsCl gradient. Peak fractions containing rAAV vector are collected, pooled and dialyzed against PBS.

Example 4: Creation of infectious clones carrying intact novel AAV serotypes for study of basic virology in human and NHP derived cell lines and evaluation of pathogenesis of novel AAV serotypes in NHP and other animal models.

To achieve this goal, the genome walker system is employed to obtain 5' and 3' terminal sequences (ITRs) and complete construction of clones containing intact novel AAV serotype genomes.

Briefly, utilizing a commercially available Universal Genome Walker Kit [Clontech], genomic DNAs from monkey tissues or cell lines that are identified as positive for the presence of AAV7 sequence are digested with Dra I, EcoR V, Pvu II and Stu I endonucleases and ligated to Genome Walker Adaptor to generate 4 individual Genome Walker Libraries (GWLs). Using DNAs from GWLs as templates, AAV7 and adjacent genomic sequences will be PCR-amplified by the adaptor primer 1 (AP1, provided in the kit) and an AAV7 specific primer 1, followed by a nested PCR using the adaptor primer 2 (AP2) and another AAV7 specific primer 2, both of which are internal to the first set of primers. The major PCR products from the nested PCR are cloned and characterized by sequencing analysis.

In this experiment, the primers covering the 257 bp or other signature fragment of a generic AAV genome are used for PCR amplification of cellular DNAs extracted from Human and NHP derived cell lines to identify and characterize latent AAV sequences. The identified latent AAV genomes are rescued from the positive cell lines using adenovirus helpers of different species and strains.

To isolate infectious AAV clones from NHP derived cell lines, a desired cell line is obtained from ATCC and screened by PCR to identify the 257 bp amplicon, i.e., signature region of the invention. The 257 bp PCR product is cloned and serotyped by sequencing analysis. For these cell lines containing the AAV7 sequence, the cells are infected with SV-15, a simian adenovirus purchased from ATCC, human Ad5 or transfected with plasmid construct housing the human Ad genes that are responsible for AAV helper functions. At 48 hour post infection or transfection, the cells are harvested and Hirt DNA is prepared for cloning of AAV7 genome following Xiao et al., 1999, J. Virol, 73:3994-4003.

Example 5 - Production of AAV Vectors

A pseudotyping strategy similar to that of Example 3 for AAV1/7 was employed to produce AAV2 vectors packaged with AAV1, AAV5 and AAV8 capsid proteins. Briefly,

recombinant AAV genomes equipped with AAV2 ITRs were packaged by triple transfection of 293 cells with cis-plasmid, adenovirus helper plasmid and a chimeric packaging construct where the AAV2 rep gene is fused with cap genes of novel AAV serotypes. To create the chimeric packaging constructs, the Xho I site of p5E18 plasmid at 3169 bp was ablated and the modified plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene and replace it with a 2267 bp Spe I/Xho I fragment containing the AAV8 cap gene [Xiao, W., et al., (1999) *J Virol* **73**, 3994-4003]. A similar cloning strategy was used for creation of chimeric packaging plasmids of AAV2/1 and AAV2/5. All recombinant vectors were purified by the standard $CsCl_2$ sedimentation method except for AAV2/2, which was purified by single step heparin chromatography.

Genome copy (GC) titers of AAV vectors were determined by TaqMan analysis using probes and primers targeting SV40 poly A region as described previously [Gao, G., et al., (2000) *Hum Gene Ther* **11**, 2079-91].

Vectors were constructed for each serotype for a number of *in vitro* and *in vivo* studies. Eight different transgene cassettes were incorporated into the vectors and recombinant virions were produced for each serotype. The recovery of virus, based on genome copies, is summarized in Table 4 below. The yields of vector were high for each serotype with no consistent differences between serotypes. Data presented in the table are average genome copy yields with standard deviation x 10^{13} of multiple production lots of 50 plate (150 mm) transfections.

Table 4. Production of Recombinant Vectors

	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8
CMV LacZ	7.30 ± 4.33 (n=9)	4.49 ± 2.89 (n=6)	5.19 ± 5.19 (n=8)	3.42 (n=1)	0.87 (n=1)
CMV EGFP	6.43 ± 2.42 (n=2)	3.39 ± 2.42 (n=2)	5.55 ± 6.49 (n=4)	2.98 ± 2.66 (n=2)	3.74 ± 3.88 (n=2)
TBG LacZ	4.18 (n=1)	0.23 (n=1)	0.704 ± 0.43 (n=2)	2.16 (n=1)	0.532 (n=1)
Alb A1AT	4.67 ± 0.75 (n=2)	4.77 (n=1)	4.09 (n=1)	5.04 (n=1)	2.02 (n=1)
CB A1AT	0.567 (n=1)	0.438 (n=1)	2.82 (n=1)	2.78 (n=1)	0.816 ± 0.679 (n=2)

Table 4 (cont'd).

	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8
TBG rhCG	8.51 ± 6.65 (n=6)	3.47 ± 2.09 (n=5)	5.26 ± 3.85 (n=4)	6.52 ± 3.08 (n=4)	1.83 ± 0.98 (n=5)
TBG cFIX	1.24 ± 1.29 (n=3)	0.63 ± 0.394 (n=6)	3.74 ± 2.48 (n=7)	4.05 (n=1)	15.8 ± 15.0 (n=5)

Example 6 - Serologic Analysis of Pseudotyped Vectors

C57BL/6 mice were injected with vectors of different serotypes of AAVCBA1AT vectors intramuscularly (5×10^{11} GC) and serum samples were collected 34 days later. To test neutralizing and cross-neutralizing activity of sera to each serotype of AAV, sera was analyzed in a transduction based neutralizing antibody assay [Gao, G. P., et al., (1996) *J Virol* 70, 8934-43]. More specifically, the presence of neutralizing antibodies was determined by assessing the ability of serum to inhibit transduction of 84-31 cells by reporter viruses (AAVCMVEGFP) of different serotypes. Specifically, the reporter virus AAVCMVEGFP of each serotype [at multiplicity of infection (MOI) that led to a transduction of 90% of indicator cells] was pre-incubated with heat-inactivated serum from animals that received different serotypes of AAV or from naïve mice. After 1-hour incubation at 37° C, viruses were added to 84-31 cells in 96 well plates for 48 or 72- hour, depending on the virus serotype. Expression of GFP was measured by FluoroImagin (Molecular Dynamics) and quantified by Image Quant Software. Neutralizing antibody titers were reported as the highest serum dilution that inhibited transduction to less than 50%.

The availability of GFP expressing vectors simplified the development of an assay for neutralizing antibodies that was based on inhibition of transduction in a permissive cell line (i.e., 293 cells stably expressing E4 from Ad5). Sera to selected AAV serotypes were generated by intramuscular injection of the recombinant viruses. Neutralization of AAV transduction by 1:20 and 1:80 dilutions of the antisera was evaluated (See Table 5 below). Antisera to AAV1, AAV2, AAV5 and AAV8 neutralized transduction of the serotype to which the antiserum was generated (AAV5 and AAV8 to a lesser extent than AAV1 and AAV2) but not to the other serotype (i.e., there was no evidence of cross neutralization suggesting that AAV 8 is a truly unique serotype).

Table 5. Serological Analysis of New AAV Serotypes.

		% Infection on 84-31 cells with AAVCMVEGFP virus:									
		AAV2/1		AAV2/2		AAV2/5		AAV2/7		AAV2/8	
		Serum dilution:		Serum dilution:		Serum dilution:		Serum dilution:		Serum dilution:	
Sera:	Immunization Vector	*1/20*	*1/80*	*1/20*	*1/80*	*1/20*	*1/80*	*1/20*	*1/80*	*1/20*	*1/80*
Group 1	**AAV2/1**	**0**	**0**	100	100	100	100	100	100	100	100
Group 2	**AAV2/2**	100	100	**0**	**0**	100	100	100	100	100	100
Group 3	**AAV2/5**	100	100	100	100	**16.5**	**16.5**	100	100	100	100
Group 4	**AAV2/7**	100	100	100	100	100	100	**61.5**	100	100	100
Group 5	**AAV2/8**	100	100	100	100	100	100	100	100	**26.3**	**60**

Human sera from 52 normal subjects were screened for neutralization against selected serotypes. No serum sample was found to neutralize AAV2/7 and AAV2/8 while AAV2/2 and AAV2/1 vectors were neutralized in 20% and 10% of sera, respectively. A fraction of human pooled IgG representing a collection of 60,000 individual samples did not neutralize AAV2/7 and AAV2/8, whereas AAV2/2 and AAV2/1 vectors were neutralized at titers of serum equal to 1/1280 and 1/640, respectively.

Example 7 - *In vivo* Evaluation of Different Serotypes of AAV Vectors

In this study, 7 recombinant AAV genomes, AAV2CBhA1AT, AAV2AlbhA1AT, AAV2CMVrhCG, AAV2TBGrhCG, AAV2TBGcFIX, AAV2CMVLacZ and AAV2TBGLacZ were packaged with capsid proteins of different serotypes. In all 7 constructs, minigene cassettes were flanked with AAV2 ITRs. cDNAs of human α-antitrypsin (A1AT) [Xiao, W., et al., (1999) J Virol 73, 3994-4003] β-subunit of rhesus monkey choriogonadotropic hormone (CG) [Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* 2, 657-9] canine factor IX [Wang, L., et al., (1997) *Proc Natl Acad Sci U S A* 94, 11563-6] and bacterial β-glactosidase (i.e., Lac Z) genes were used as reporter genes. For liver-directed gene transfer, either mouse albumin gene promoter (Alb) [Xiao, W. (1999), cited above] or human thyroid hormone binding globulin gene promoter (TBG) [Wang (1997), cited above] was used to drive liver specific expression of reporter genes. In muscle-directed gene transfer experiments, either cytomegalovirus early promoter (CMV) or chicken β-actin promoter with CMV enhancer (CB) was employed to direct expression of reporters.

For muscle-directed gene transfer, vectors were injected into the right tibialis anterior of 4-6 week old NCR nude or C57BL/6 mice (Taconic, Germantown, NY). In liver-directed gene transfer studies, vectors were infused intraportally into 7-9 week old NCR nude or C57BL/6 mice (Taconic, Germantown, NY). Serum samples were collected intraorbitally at

different time points after vector administration. Muscle and liver tissues were harvested at different time points for cryosectioning and Xgal histochemical staining from animals that received the lacZ vectors. For the re-administration experiment, C56BL/6 mice initially received AAV2/1, 2/2, 2/5, 2/7 and 2/8CBA1AT vectors intramuscularly and followed for A1AT gene expression for 7 weeks. Animals were then treated with AAV2/8TBGcFIX intraportally and studied for cFIX gene expression.

ELISA based assays were performed to quantify serum levels of hA1AT, rhCG and cFIX proteins as described previously [Gao, G. P., et al., (1996) *J Virol* 70, 8934-43; Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* 2, 657-9; Wang, L., et al., *Proc Natl Acad Sci U S A* 94, 11563-6]. The experiments were completed when animals were sacrificed for harvest of muscle and liver tissues for DNA extraction and quantitative analysis of genome copies of vectors present in target tissues by TaqMan using the same set of primers and probe as in titration of vector preparations [Zhang, Y., et al., (2001) *Mol Ther* 3, 697-707].

The performance of vectors base on the new serotypes were evaluated in murine models of muscle and liver-directed gene transfer and compared to vectors based on the known serotypes AAV1, AAV2 and AAV5. Vectors expressing secreted proteins (alpha-antitrypsin (A1AT) and chorionic gonadotropin (CG)) were used to quantitate relative transduction efficiencies between different serotypes through ELISA analysis of sera. The cellular distribution of transduction within the target organ was evaluated using lacZ expressing vectors and X-gal histochemistry .

The performance of AAV vectors in skeletal muscle was analyzed following direct injection into the tibialis anterior muscles. Vectors contained the same AAV2 based genome with the immediate early gene of CMV or a CMV enhanced β-actin promoter driving expression of the transgene. Previous studies indicated that immune competent C57BL/6 mice elicit limited humoral responses to the human A1AT protein when expressed from AAV vectors [Xiao, W., et al., (1999) *J Virol* 73, 3994-4003].

In each strain, AAV2/1 vector produced the highest levels of A1AT and AAV2/2 vector the lowest, with AAV2/7 and AAV2/8 vectors showing intermediate levels of expression. Peak levels of CG at 28 days following injection of nu/nu NCR mice showed the highest levels from AAV2/7 and the lowest from AAV2/2 with AAV2/8 and AAV2/1 in between. Injection of AAV2/1 and AAV2/7 lacZ vectors yielded gene expression at the injection sites in all muscle fibers with substantially fewer lacZ positive fibers observed with AAV2/2 and AAV 2/8 vectors. These data indicate that the efficiency of transduction with

AAV2/7 vectors in skeletal muscle is similar to that obtained with AAV2/1, which is the most efficient in skeletal muscle of the previously described serotypes [Xiao, W. (1999), cited above; Chao, H., et al., (2001) *Mol Ther* 4, 217-22; Chao, H., et al., (2000) *Mol Ther* 2, 619-23].

Similar murine models were used to evaluate liver-directed gene transfer. Identical doses of vector based on genome copies were infused into the portal veins of mice that were analyzed subsequently for expression of the transgene. Each vector contained an AAV2 based genome using previously described liver-specific promoters (i.e., albumin or thyroid hormone binding globulin) to drive expression of the transgene. More particularly, CMVCG and TBGCG minigene cassettes were used for muscle and liver-directed gene transfer, respectively. Levels of rhCG were defined as relative units (RUs x 10^3). The data were from assaying serum samples collected at day 28, post vector administration (4 animals per group). As shown in Table 3, the impact of capsid proteins on the efficiency of transduction of A1AT vectors in nu/nu and C57BL/6 mice and CG vectors in C57BL/6 mice was consistent (See Table 6).

Table 6. Expression of β-unit of Rhesus Monkey Chorionic Gonadotropin (rhCG)

Vector	Muscle	Liver
AAV2/1	4.5 ± 2.1	1.6 ± 1.0
AAV2	0.5 ± 0.1	0.7 ± 0.3
AAV2/5	ND*	4.8 ± 0.8
AAV2/7	14.2 ± 2.4	8.2 ± 4.3
AAV2/8	4.0 ± 0.7	76.0 ± 22.8

* Not determined in this experiment.

In all cases, AAV2/8 vectors yielded the highest levels of transgene expression that ranged from 16 to 110 greater than what was obtained with AAV2/2 vectors; expression from AAV2/5 and AAV2/7 vectors was intermediate with AAV2/7 higher than AAV2/5. Analysis of X-Gal stained liver sections of animals that received the corresponding lacZ vectors showed a correlation between the number of transduced cells and overall levels of transgene expression. DNAs extracted from livers of C57BL/6 mice who received the A1AT vectors were analyzed for abundance of vector DNA using real time PCR technology.

The amount of vector DNA found in liver 56 days after injection correlated with the levels of transgene expression (See Table 7). For this experiment, a set of probe and primers targeting the SV40 polyA region of the vector genome was used for TaqMan PCR. Values shown are means of three individual animals with standard deviations. The animals were sacrificed at day 56 to harvest liver tissues for DNA extraction. These studies indicate that AAV8 is the most efficient vector for liver-directed gene transfer due to increased numbers of transduced hepatocytes.

Table 7 - Real Time PCR Analysis for Abundance of AAV Vectors in nu/nu Mouse Liver Following Injection of $1x10^{11}$ Genome Copies of Vector.

AAV vectors/Dose	Genome Copies per Cell
AAV2/1AlbA1AT	0.6 ± 0.36
AAV2AlbA1AT	0.003 ± 0.001
AAV2/5AlbA1AT	0.83 ± 0.64
AAV2/7AlbA1AT	2.2 ± 1.7
AAV2/8AlbA1AT	18 ± 11

The serologic data described above suggest that AAV2/8 vector should not be neutralized *in vivo* following immunization with the other serotypes. C57BL/6 mice received intraportal injections of AAV2/8 vector expressing canine factor IX (10^{11} genome copies) 56 days after they received intramuscular injections of A1AT vectors of different serotypes. High levels of factor IX expression were obtained 14 days following infusion of AAV2/8 into naïve animals (17±2 μg/ml, n=4) which were not significantly different that what was observed in animals immunized with AAV2/1 (31±23 μg/ml, n=4), AAV2/2 (16 μg/ml, n=2), and AAV2/7 (12 μg/ml, n=2). This contrasts to what was observed in AAV2/8 immunized animals that were infused with the AAV2/8 factor IX vector in which no detectable factor IX was observed (< 0.1 μg/ml, n=4).

Oligonucleotides to conserved regions of the cap gene did amplify sequences from rhesus monkeys that represented unique AAVs. Identical cap signature sequences were found in multiple tissues from rhesus monkeys derived from at least two different colonies. Full-length rep and cap open reading frames were isolated and sequenced from single

sources. Only the cap open reading frames of the novel AAVs were necessary to evaluate their potential as vectors because vectors with the AAV7 or AAV8 capsids were generated using the ITRs and rep from AAV2. This also simplified the comparison of different vectors since the actual vector genome is identical between different vector serotypes. In fact, the yields of recombinant vectors generated using this approach did not differ between serotypes.

Vectors based on AAV7 and AAV8 appear to be immunologically distinct (i.e., they are not neutralized by antibodies generated against other serotypes). Furthermore, sera from humans do not neutralize transduction by AAV7 and AAV8 vectors, which is a substantial advantage over the human derived AAVs currently under development for which a significant proportion of the human population has pre-existing immunity that is neutralizing [Chirmule, N., et al., (1999) *Gene Ther* **6**, 1574-83].

The tropism of each new vector is favorable for *in vivo* applications. AAV2/7 vectors appear to transduce skeletal muscle as efficiently as AAV2/1, which is the serotype that confers the highest level of transduction in skeletal muscle of the primate AAVs tested to date [Xiao, W., cited above; Chou (2001), cited above, and Chou (2000), cited above]. Importantly, AAV2/8 provides a substantial advantage over the other serotypes in terms of efficiency of gene transfer to liver that until now has been relatively disappointing in terms of the numbers of hepatocytes stably transduced. AAV2/8 consistently achieved a 10 to 100-fold improvement in gene transfer efficiency as compared to the other vectors. The basis for the improved efficiency of AAV2/8 is unclear, although it presumably is due to uptake via a different receptor that is more active on the basolateral surface of hepatocytes. This improved efficiency will be quite useful in the development of liver-directed gene transfer where the number of transduced cells is critical, such as in urea cycle disorders and familial hypercholesterolemia.

Thus, the present invention provides a novel approach for isolating new AAVs based on PCR retrieval of genomic sequences. The amplified sequences were easily incorporated into vectors and tested in animals. The lack of pre-existing immunity to AAV7 and the favorable tropism of the vectors for muscle indicates that AAV7 is suitable for use as a vector in human gene therapy and other *in vivo* applications. Similarly, the lack of pre-existing immunity to the AAV serotypes of the invention, and their tropisms, renders them useful in delivery of therapeutic molecules and other useful molecules.

Example 9 – Tissue Tropism Studies

In the design of a high throughput functional screening scheme for novel AAV constructs, a non-tissue specific and highly active promoter, CB promoter (CMV enhanced chicken β actin promoter) was selected to drive an easily detectable and quantifiable reporter gene, human α anti-trypsin gene. Thus only one vector for each new AAV clone needs to be made for gene transfer studies targeting 3 different tissues, liver, lung and muscle to screen for tissue tropism of a particular AAV construct. The following table summarizes data generated from 4 novel AAV vectors in the tissue tropism studies (AAVCBA1AT), from which a novel AAV capsid clone, 44.2, was found to be a very potent gene transfer vehicle in all 3 tissues with a big lead in the lung tissue particularly. Table 8 reports data obtained (in μg A1AT/mL serum) at day 14 of the study.

Table 8

Vector	Target Tissue		
	Lung	Liver	Muscle
AAV2/1	ND	ND	45±11
AAV2/5	0.6±0.2	ND	ND
AAV2/8	ND	84±30	ND
AAV2/rh.2 (43.1)	14±7	25±7.4	35±14
AAV2/rh.10 (44.2)	23±6	53±19	46±11
AAV2/rh.13 (42.2)	3.5±2	2±0.8	3.5±1.7
AAV2/rh.21 (42.10)	3.1±2	2±1.4	4.3±2

A couple of other experiments were then performed to confirm the superior tropism of AAV 44.2 in lung tissue. First, AAV vector carried CC10hA1AT minigene for lung specific expression were pseudotyped with capsids of novel AAVs were given to Immune deficient animals (NCR nude) in equal volume (50 μl each of the original preps without dilution) via intratracheal injections as provided in the following table. In Table 9, 50 μl of each original prep per mouse, NCR Nude, detection limit ≥0.033 μg/ml, Day 28

Table 9

Vector	Total GC in 50 µl vector	µg of A1AT/ml with 50µl vector	µg of A1AT/ml with $1x10^{11}$ vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	$3x10^{12}$	2.6±0.5	0.09±0.02	2.2
2/2	$5.5x10^{11}$	<0.03	<0.005	<0.1
2/5	$3.6x10^{12}$	0.65±0.16	0.02±0.004	0.5
2/7	$4.2x10^{12}$	1±0.53	0.02±0.01	0.5
2/8	$7.5x10^{11}$	0.9±0.7	0.12±0.09	2.9
2/ch.5 (A.3.1)	$9x10^{12}$	1±0.7	0.01±0.008	0.24
2/rh.8 (43.25)	$4.6x10^{12}$	26±21	0.56±0.46	13.7
2/rh.10 (44.2)	$2.8x10^{12}$	115±38	4.1±1.4	100
2/rh.13 (42.2)	$6x10^{12}$	7.3±0.8	0.12±0.01	2.9
2/rh.21 (42.10)	$2.4x10^{12}$	9±0.9	0.38±0.04	9.3
2/rh.22 (42.11)	$2.6x10^{12}$	6±0.4	0.23±0.02	5.6
2/rh.24 (42.13)	$1.1x10^{11}$	0.4±0.3	0.4±0.3	1

The vectors were also administered to immune competent animals (C57BL/6) in equal genome copies ($1x10^{11}$ GC) as shown in the Table 10. ($1x10^{11}$ GC per animal, C57BL/6, day 14, detection limit ≥0.033 µg/ml)

Table 10

AAV Vector	µg of A1AT/ml with $1x10^{11}$ vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	0.076±0.031	2.6
2/2	0.1±0.09	3.4
2/5	0.0840.033	2.9
2/7	0.33±0.01	11
2/8	1.92±1.3	2.9
2/ch.5 (A.3.1)	0.048±0.004	1.6
2/rh.8 (43.25)	1.7±0.7	58
2/rh.10 (44.2)	2.93±1.7	100
2/rh.13 (42.2)	0.45±0.15	15
2/rh.21 (42.10)	0.86±0.32	29
2/rh.22 (42.11)	0.38±0.18	13
2/rh.24 (42.13)	0.3±0.19	10

The data from both experiments confirmed the superb tropism of clone 44.2 in lung-directed gene transfer.

Interestingly, performance of clone 44.2 in liver and muscle directed gene transfer was also outstanding, close to that of the best liver transducer, AAV8 and the best muscle transducer AAV1, suggesting that this novel AAV has some intriguing biological significance.

To study serological properties of those novel AAVs, pseudotyped AAVGFP vectors were created for immunization of rabbits and in vitro transduction of 84-31 cells in the presence and absence of antisera against different capsids. The data are summarized below:

Table 11a. Cross-NAB assay in 8431 cells and adenovirus (Adv) coinfection
Infection in 8431 cells (coinfected with Adv) with:

Serum from rabbit immunized with:	10^9 GC ***rh.13*** AAV2/42.2	10^9 GC ***rh.21*** AAV2/42.10	10^9 GC ***rh.22*** AAV2/42.11	10^{10} GC ***rh.24*** AAV2/42.13
AAV2/1	1/20	1/20	1/20	No NAB
AAV2/2	1/640	1/1280	1/5120	No NAB
AAV2/5	No NAB	1/40	1/160	No NAB
AAV2/7	1/81920	1/81920	1/40960	1/640
AAV2/8	1/640	1/640	1/320	1/5120
Ch.5 AAV2/A3	1/20	1/160	1/640	1/640
rh.8 AAV2/43.25	1/20	1/20	1/20	1/320
rh.10 AAV2/44.2	No NAB	No NAB	No NAB	1/5120
rh.13 AAV2/42.2	1/5120	1/5120	1/5120	No NAB
rh.21 AAV2/42.10	1/5120	1/10240	1/5120	1/20
rh.22 AAV2/42.11	1/20480	1/20480	1/40960	No NAB
rh.24 AAV2/42.13	No NAB	1/20	1/20	1/5120

Table 11b. Cross-NAB assay in 8431 cells and Adv coinfection

Infection in 8431 cells (coinfected with Adv) with:

Serum from rabbit immunized with:	10^9 GC	10^{10} GC	10^{10}GC	10^9 GC	10^9 GC
	rh.12	***ch.5***	***rh.8***	***rh.10***	***rh.20***
	AAV2/42.1B	AAV2/A3	AAV2/43.25	AAV2/44.2	AAV2/42.8.2
AAV2/1	No NAB	1/20480	No NAB	1/80	ND
AAV2/2	1/20	No NAB	No NAB	No NAB	ND
AAV2/5	No NAB	1/320	No NAB	No NAB	ND
AAV2/7	1/2560	1/640	1/160	1/81920	ND
AAV2/8	1/10240	1/2560	1/2560	1/81920	ND
ch.5 AAV2/A3	1/1280	1/10240	ND	1/5120	1/320
rh.8 AAV2/43.25	1/1280	ND	1/20400	1/5120	1/2560
rh.10 AAV2/44.2	1/5120	ND	ND	1/5120	1/5120
rh.13 AAV2/42.2	1/20	ND	ND	No NAB	1/320
rh.21 AAV2/42.10	1/20	ND	ND	1/40	1/80
rh.22 AAV2/42.11	No NAB	ND	ND	ND	No NAB
rh.24 AAV2/42.13	1/5120	ND	ND	ND	1/2560

Table 12

Titer of rabbit sera			Titer after Boosting
Vector		Titer d21	
ch.5	AAV2/A3	1/10,240	1/40,960
rh.8	AAV2/43.25	1/20,400	1/163,840
rh.10	AAV2/44.2	1/10,240	1/527,680
rh.13	AAV2/42.2	1/5,120	1/20,960
rh.21	AAV2/42.10	1/20,400	1/81,920
rh.22	AAV2/42.11	1/40,960	ND
rh.24	AAV2/42.13	1/5,120	ND

Table 13 a. Infection in 8431 cells (coinfected with Adv) with GFP

	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well
						ch.5
	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8	AAV2/A3
# GFU/field	128	>200	95	56	13	1
	83	>200	65	54	11	1

Table 13b. Infection in 8431 cells (coinfected with Adv) with GFP

	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well	10^9 GC/well
	rh.8	*rh.10*	*rh.13*	*rh.21*	*rh.22*	*rh.24*	*rh.12*
	AAV2/43.25	AAV2/44.2	AAV2/42.2	AAV2/42.10	AAV2/42.11	AAV2/42.13	AAV2/42.1B
# GFU/field	3	13	54	62	10	3	18
	2	12	71	60	14	2	20
			48	47	16	3	12

Example 10 – Mouse Model of Familial Hypercholesterolemia

The following experiment demonstrates that the AAV2/7 construct of the invention delivers the LDL receptor and express LDL receptor in an amount sufficient to reduce the levels of plasma cholesterol and triglycerides in animal models of familial hypercholesterolemia.

A. *Vector Construction*

AAV vectors packaged with AAV7 or AAV8 capsid proteins were constructed using a pseudotyping strategy [Hildinger M, *et al., J. Virol* 2001; 75:6199-6203]. Recombinant AAV genomes with AAV2 inverted terminal repeats (ITR) were packaged by triple transfection of 293 cells with the *cis*-plasmid, the adenovirus helper plasmid and a chimeric packaging construct, a fusion of the capsids of the novel AAV serotypes with the rep gene of AAV2. The chimeric packaging plasmid was constructed as previously described [Hildinger et al, cited above]. The recombinant vectors were purified by the standard $CsCl_2$ sedimentation method. To determine the yield TaqMan (Applied Biosystems) analysis was performed using probes and primers targeting the SV40 poly(A) region of the vectors [Gao GP, *et al., Hum Gene Ther.* 2000 Oct 10;**11**(15):2079-91]. The resulting vectors express the transgene under the control of the human thyroid hormone binding globulin gene promoter (TBG).

B. *Animals*

LDL receptor deficient mice on the C57Bl/6 background were purchased from the Jackson Laboratory (Bar Harbor, ME, USA) and maintained as a breeding colony. Mice were given unrestricted access to water and obtained a high fat Western Diet (high % cholesterol) starting three weeks prior vector injection. At day –7 as well at day 0, blood was obtained via retroorbital bleeds and the lipid profile evaluated. The mice were randomly divided into seven groups. The vector was injected via an intraportal injection as previously

described ([Chen SJ *et al.*, *Mol Therapy* 2000; 2(3), 256-261]. Briefly, the mice were anaesthetized with ketamine and xylazine. A laparotomy was performed and the portal vein exposed. Using a 30g needle the appropriate dose of vector diluted in 100ul PBS was directly injected into the portal vein. Pressure was applied to the injection site to ensure a stop of the bleeding. The skin wound was closed and draped and the mice carefully monitored for the following day. Weekly bleeds were performed starting at day 14 after liver directed gene transfer to measure blood lipids. Two animals of each group were sacrificed at the time points week 6 and week 12 after vector injection to examine atherosclerotic plaque size as well as receptor expression. The remaining mice were sacrificed at week 20 for plaque measurement and determination of transgene expression.

Table 14

	Vector	*dose*	*n*
Group 1	AAV2/7-TBG-hLDLr	1x 10^{12} gc	12
Group 2	AAV2/7-TBG-hLDLr	3x 10^{11} gc	12
Group 3	AAV2/7-TBG-hLDLr	1x 10^{11} gc	12
Group 4	AAV2/8-TBG-hLDLr	1x 10^{12} gc	12
Group 5	AAV2/8-TBG-hLDLr	3x 10^{11} gc	12
Group 6	AAV2/8-TBG-hLDLr	1x 10^{11} gc	12
Group 7	AAV2/7-TBG- LacZ	1x 10^{11} gc	16

C. *Serum lipoprotein and liver function analysis*

Blood samples were obtained from the retroorbital plexus after a 6 hour fasting period. The serum was separated from the plasma by centrifugation. The amount of plasma lipoproteins and liver transaminases in the serum were detected using an automatized clinical chemistry analyzer (ACE, Schiapparelli Biosystems, Alpha Wassermann)

D. *Detection of transgene expression*

LDL receptor expression was evaluated by immuno-fluorescence staining and Western blotting. For Western Blot frozen liver tissue was homogenized with lysis buffer (20 mM Tris, pH7.4, 130mM NaCl, 1% Triton X 100, proteinase inhibitor (complete, EDTA-free, Roche, Mannheim, Germany). Protein concentration was determined using the Micro BCA Protein Assay Reagent Kit (Pierce, Rockford, IL). 40 µg of protein was resolved on 4- 15% Tris-HCl Ready Gels (Biorad, Hercules, CA) and transferred to a nitrocellulose

membrane (Invitrogen,). To generate Anti-hLDL receptor antibodies a rabbit was injected intravenously with an AdhLDLr prep ($1x10^{13}$ GC). Four weeks later the rabbit serum was obtained and used for Western Blot. A 1:100 dilution of the serum was used as a primary antibody followed by a HRP-conjugated anti-rabbit IgG and ECL chemiluminescent detection (ECL Western Blot Detection Kit, Amersham, Arlington Heights, IL).

E. *Immunocytochemistry*

For determination of LDL receptor expression in frozen liver sections immunohistochemistry analyses were performed. 10um cryostat sections were either fixed in acetone for 5 minutes, or unfixed. Blocking was obtained *via a* 1 hour incubation period with 10% of goat serum. Sections were then incubated for one hour with the primary antibody at room temperature. A rabbit polyclonal antibody anti-human LDL (Biomedical Technologies Inc., Stoughton, MA) was used diluted accordingly to the instructions of the manufacturer. The sections were washed with PBS, and incubated with 1:100 diluted fluorescein goat anti-rabbit IgG (Sigma, St Louis, MO). Specimens were finally examined under fluorescence microscope Nikon Microphot-FXA. In all cases, each incubation was followed by extensive washing with PBS. Negative controls consisted of preincubation with PBS, omission of the primary antibody, and substitution of the primary antibody by an isotype-matched non-immune control antibody. The three types of controls mentioned above were performed for each experiment on the same day.

F. Gene transfer efficiency

Liver tissue was obtained after sacrificing the mice at the designated time points. The tissue was shock frozen in liquid nitrogen and stored at -80°C until further processing. DNA was extracted from the liver tissue using a QIAamp DNA Mini Kit (QIAGEN GmbH, Germany) according to the manufacturers protocol. Genome copies of AAV vectors in the liver tissue were evaluated using Taqman analysis using probes and primers against the SV40 poly(A) tail as described above.

G. *Atherosclerotic plaque measurement*

For the quantification of the atherosclerotic plaques in the mouse aorta the mice were anaesthetized (10% ketamine and xylazine, ip), the chest opened and the arterial system perfused with ice-cold phosphate buffered saline through the left ventricle. The aorta was then carefully harvested, slit down along the ventral midline from the aortic arch down to the femoral arteries and fixed in formalin. The lipid-rich atherosclerotic plaques were stained with Sudan IV (Sigma, Germany) and the aorta pinned out flat on a

black wax surface. The image was captured with a Sony DXC-960 MD color video camera. The area of the plaque as well as of the complete aortic surface was determined using Phase 3 Imaging Systems (Media Cybernetics).

H. *Clearance of I^{125} LDL*

Two animals per experimental group were tested. A bolus of I^{125}–labeled LDL (generously provided by Dan Rader, U Penn) was infused slowly through the tail vein over a period of 30 sec (1,000,000 counts of [I^{125}]-LDL diluted in 100µl sterile PBS/ animal). At time points 3min, 30 min, 1.5hr, 3hr, 6hr after injection a blood sample was obtained *via* the retro-orbital plexus. The plasma was separated off from the whole blood and 10µl plasma counted in the gamma counter. Finally the fractional catabolic rate was calculated from the lipoprotein clearance data.

I. *Evaluation of Liver Lipid accumulation*

Oil Red Staining of frozen liver sections was performed to determine lipid accumulation. The frozen liver sections were briefly rinsed in distilled water followed by a 2 minute incubation in absolute propylene glycol. The sections were then stained in oil red solution (0.5% in propylene glycol) for 16 hours followed by counterstaining with Mayer's hematoxylin solution for 30 seconds and mounting in warmed glycerin jelly solution.

For quantification of the liver cholesterol and triglyceride content liver sections were homogenized and incubated in chloroform/methanol (2:1) overnight. After adding of 0.05% H_2SO_4 and centrifugation for 10 minutes, the lower layer of each sample was collected, divided in two aliquots and dried under nitrogen. For the cholesterol measurement the dried lipids of the first aliquot were dissolved in 1% Triton X-100 in chloroform. Once dissolved, the solution was dried under nitrogen. After dissolving the lipids in ddH_20 and incubation for 30 minutes at 37°C the total cholesterol concentration was measured using a Total Cholesterol Kit (Wako Diagnostics). For the second aliquot the dried lipids were dissolved in alcoholic KOH and incubated at 60°C for 30 minutes. Then 1M MgCl2 was added, followed by incubation on ice for 10 minutes and centrifugation at 14,000 rpm for 30 minutes. The supernatant was finally evaluated for triglycerides (Wako Diagnostics).

All of the vectors pseudotyped in an AAV2/8 or AAV2/7 capsid lowered total cholesterol, LDL and triglycerides as compared to the control. These test vectors also corrected phenotype of hypercholesterolemia in a dose-dependent manner. A reduction in

plaque area for the AAV2/8 and AAV2/7 mice was observed in treated mice at the first test (2 months), and the effect was observed to persist over the length of the experiment (6 months).

Example 10 – Functional Factor IX Expression and Correction of Hemophilia

A. *Knock-Out Mice*

Functional canine factor IX (FIX) expression was assessed in hemophilia B mice. Vectors with capsids of AAV1, AAV2, AAV5, AAV7 or AAV8 were constructed to deliver AAV2 5' ITR – liver-specific promoter [LSP] - canine FIX – woodchuck hepatitis post-regulatory element (WPRE) - AAV2 3' ITR . The vectors were constructed as described in Wang et al, 2000, *Molecular Therapy* 2: 154-158), using the appropriate capsids.

Knock-out mice were generated as described in Wang et al, 1997. *Proc. Natl. Acad. Sci. USA* 94: 11563-11566. This model closely mimic the phenotypes of hemophilia B in human.

Vectors of different serotypes (AAV1, AAV2, AAV5, AAV7 and AAV8) were delivered as a single intraportal injection into the liver of adult hemophiliac C57Bl/6 mice in a dose of $1x10^{11}$ GC/mouse for the five different serotypes and one group received an AAV8 vector at a lower dose, $1x10^{10}$ GC/mouse. Control group was injected with $1x10^{11}$ GC of AAV2/8 TBG LacZ3. Each group contains 5-10 male and female mice. Mice were bled bi-weekly after vector administration.

1. *ELISA*

The canine FIX concentration in the mouse plasma was determined by an ELISA assay specific for canine factor IX, performed essentially as described by Axelrod et al, 1990, *Proc.Natl.Acad.Sci.USA, 87:5173-5177* with modifications. Sheep anti-canine factor IX (Enzyme Research Laboratories) was used as primary antibody and rabbit anti-canine factor IX ((Enzyme Research Laboratories) was used as secondary antibody. Beginning at two weeks following injection, increased plasma levels of cFIX were detected for all test vectors. The increased levels were sustained at therapeutic levels throughout the length of the experiment, i.e., to 12 weeks. Therapeutic levels are considered to be 5% of normal levels, i.e., at about 250 ng/mL.

The highest levels of expression were observed for the AAV2/8 (at 10^{11}) and AAV2/7 constructs, with sustained superphysiology levels cFIX levels (ten-fold higher than the normal level). Expression levels for AAV2/8 (10^{11}) were approximately **10** fold higher

than those observed for AAV2/2 and AAV2/8 (10^{10}). The lowest expression levels, although still above the therapeutic range, were observed for AAV2/5.

2. *In Vitro Activated Partial Thromboplastin time (aPTT) Assay*

Functional factor IX activity in plasma of the FIX knock-out mice was determined by an *in vitro* activated partial thromboplastin time (aPTT) assay–Mouse blood samples were collected from the retro-orbital plexus into 1/10 volume of citrate buffer. The aPTT assay was performed as described by Wang et al, 1997, *Proc. Natl. Acad. Sci. USA* 94: 11563-11566.

Clotting times by aPTT on plasma samples of all vector injected mice were within the normal range (approximately 60 sec) when measured at two weeks post-injection, and sustained clotting times in the normal or shorter than normal range throughout the study period (12 weeks).

Lowest sustained clotting times were observed in the animals receiving AAV2/8 (10^{11}) and AAV2/7. By week 12, AAV2/2 also induced clotting times similar to those for AAV2/8 and AAV2/7. However, this lowered clotting time was not observed for AAV2/2 until week 12, whereas lowered clotting times (in the 25 – 40 sec range) were observed for AAV2/8 and AAV2/7 beginning at week two.

Immuno-histochemistry staining on the liver tissues harvested from some of the treated mice is currently being performed. About 70-80% of hepatocytes are stained positive for canine FIX in the mouse injected with AAV2/8.cFIX vector.

B. *Hemophilia B Dogs*

Dogs that have a point mutation in the catalytic domain of the F.IX gene, which, based on modeling studies, appears to render the protein unstable, suffer from hemophilia B [Evans et al, 1989, Proc. Natl. Acad. Sci. USA, 86:10095-10099). A colony of such dogs has been maintained for more than two decades at the University of North Carolina, Chapel Hill. The homeostatic parameters of these dogs are well described and include the absence of plasma F.IX antigen, whole blood clotting times in excess of 60 minutes, whereas normal dogs are 6-8 minutes, and prolonged activated partial thromboplastin time of 50-80 seconds, whereas normal dogs are 13-28 seconds. These dogs experience recurrent spontaneous hemorrhages. Typically, significant bleeding episodes are successfully managed by the single intravenous infusion of 10 ml/kg of normal canine plasma; occasionally, repeat infusions are required to control bleeding.

Four dogs are injected intraportally with AAV.cFIX according to the schedule below. A first dog receives a single injection with AAV2/2.cFIX at a dose of $3.7x10^{11}$ genome copies (GC)/kg. A second dog receives a first injection of AAV2/2.cFIX ($2.8x10^{11}$ GC/kg), followed by a second injection with AAV2/7.cFIX ($2.3x10^{13}$ GC/kg) at day 1180. A third dog receives a single injection with AAV2/2.cFIX at a dose of $4.6x10^{12}$ GC/kg. The fourth dog receives an injection with AAV2/2.cFIX ($2.8x10^{12}$ GC/kg) and an injection at day 995 with AAV2/7.cFIX ($5x10^{12}$ GC/kg).

The abdomen of hemophilia dogs are aseptically and surgically opened under general anesthesia and a single infusion of vector is administered into the portal vein. The animals are protected from hemorrhage in the peri-operative period by intravenous administration of normal canine plasma. The dog is sedated, intubated to induce general anesthesia, and the abdomen shaved and prepped. After the abdomen is opened, the spleen is moved into the operative field. The splenic vein is located and a suture is loosely placed proximal to a small distal incision in the vein. A needle is rapidly inserted into the vein, then the suture loosened and a 5 F cannula is threaded to an intravenous location near the portal vein threaded to an intravenous location near the portal vein bifurcation. After hemostasis is secured and the catheter balloon inflated, approximately 5.0 ml of vector diluted in PBS is infused into the portal vein over a 5 minute interval. The vector infusion is followed by a 5.0 ml infusion of saline. The balloon is then deflated, the callula removed and venous hemostasis is secured. The spleen is then replaced, bleeding vessels are cauterized and the operative wound is closed. The animal is extubated having tolerated the surgical procedure well. Blood samples are analyzed as described. [Wang et al, 2000, *Molecular Therapy* 2: 154-158]

Results showing correction or partial correction are anticipated for AAV2/7.

All publications cited in this specification are incorporated herein by reference. While the invention has been described with reference to a particularly preferred embodiments, it will be appreciated that modifications can be made without departing from the spirit of the invention. Such modifications are intended to fall within the scope of the claims.

CLAIMS

1. A kit for detecting the presence of an unknown adeno-associated virus (AAV) in a sample from cellular DNA suspected of containing a latent AAV infection, said kit comprising:

(a) a first set of primers which specifically amplify a first region comprising at least 250 bp of AAV capsid nucleic acid sequences, said first region having at least 18 base pairs of highly conserved sequence at its 5' end, a variable sequence, and at least 18 base pairs of highly conserved sequence at its 3' end, said base pairs being highly conserved relative to an alignment of at least *AAV 1, AAV2, AAV3, AAV4, AAV5 and AAV6*;

(b) optionally a second set of primers specific for a second region of the AAV nucleic acid sequences which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;

(c) optionally a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained,

each of said second and third regions being predetermined based upon the alignment of the nucleic acid sequences of at least *AAV 1, AAV2, AAV3, AAV4, AAV5 and AAV6* and each of said regions comprising nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of the at least *AAV 1, AAV2, AAV3, AAV4, AAV5 and AAV6*;

each of the sets of primers consisting of a 5' primer and a 3' primer, each of said primers comprising 15 nucleotides complementary to its respective highly conserved sequence and having exact identity with its respective highly conserved sequence over at least 5 base pairs in its 3' end.

2. A kit according to claim 1, wherein the 5' primer and/or the 3' primer comprises at least 18 nucleotides.

3. A kit according to claim 1, wherein the 5' primer and/or the 3' primer comprises 25 nucleotides.

4. A kit according to claim 1, wherein the 5' primer and/or the 3' primer comprises at least 9 base pairs of exact identity at its 3' end.

5. A kit according to claim 1, wherein the 5' primer and/or the 3' primer comprises at least 18 base pairs of exact identity at its 3' end.

6. The kit according to claim 1, wherein the first set of primers allows isolation of full-length adeno-associated virus capsid sequences from a sample,

the first set of primers comprising a 5' primer directed to a region located in the middle of an AAV rep gene, based on a predetermined conserved region of AAV, and a 3' primer directed to a region downstream of an AAV cap gene, based on a predetermined conserved region of AAV.

7. A kit according to claim 1, wherein the 5' primer has a sequence comprising GCTGCGTCAACTGGACCAATGAGAAC, which corresponds to nt 1398 to 1423 of SEQ ID NO:6.

8. A kit according to claim 1, wherein the 3' primer has a sequence comprising CGCAGAGACCAAAGTTCAACTGAAACGA, which corresponds to the nucleotides complementary to 4462- 4435 of SEQ ID NO:7.

9. A kit according to claim 1, wherein the sample comprises AAV integrated into the chromosome.

10. An isolated adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence selected from the group consisting of:

AAV7, amino acids 1 to 737 of SEQ ID NO:2; C1, SEQ ID NO:60; C2, SEQ ID NO:61; C5, SEQ ID NO:62; A3-3, SEQ ID NO:66; A3-7, SEQ ID NO:67; A3-4, SEQ ID NO:68; A3-5, SEQ ID NO: 69; 3.3b, SEQ ID NO: 62; 223.4, SEQ ID NO: 73; 223-5,

SEQ ID NO:74; 223-10, SEQ ID NO:75; 223-2, SEQ ID NO:76; 223-7, SEQ ID NO: 77; 223-6, SEQ ID NO: 78; 44-1, SEQ ID NO: 79; 44-5, SEQ ID NO:80; 44-2, SEQ ID NO:81; 42-15, SEQ ID NO: 84; 42-8, SEQ ID NO: 85; 42-13, SEQ ID NO:86; 42-3A, SEQ ID NO:87; 42-4, SEQ ID NO:88; 42-5A, SEQ ID NO:89; 42-1B, SEQ ID NO:90; 42-5B, SEQ ID NO:91; 43-1, SEQ ID NO: 92; 43-12, SEQ ID NO: 93; 43-5, SEQ ID NO:94; 43-21, SEQ ID NO:96; 43-25, SEQ ID NO: 97; 43-20, SEQ ID NO:99; 24.1, SEQ ID NO: 101; 42.2, SEQ ID NO:102; 7.2, SEQ ID NO: 103; 27.3, SEQ ID NO: 104; 16.3, SEQ ID NO: 105; 42.10, SEQ ID NO: 106; 42-3B, SEQ ID NO: 107; 42-11, SEQ ID NO: 108; F1, SEQ ID NO: 109; F5, SEQ ID NO: 110; F3, SEQ ID NO:111; 42-6B, SEQ ID NO: 112; and 42-12, SEQ ID NO: 113.

11. A protein comprising a fragment of an AAV capsid protein, said fragment selected from the group consisting of:

vp2 capsid protein, amino acids (aa) 138 to 737;

vp3 capsid protein, aa 203 to 737;

hypervariable region (HVR)1 through 12: aa 146 to 152; aa 182 to 187; aa 262 to 264; aa 263 to 266; aa 263 to 266; aa 381 to 383; aa 383 to 385; aa 450 to 474; aa 451 to 475; aa 490 to 495; aa 491 to 496; aa500 to 504; aa 501 to 505; aa 514 to 522; aa 533 to 554; aa 534 to 555; aa 581 to 594; aa 583 to 596; aa 658 to 667; aa 660 to 669; and aa 705 to 719; aa 707 to 772;

aa 24 – 42, aa 25 – 28; aa 81 – 85; aa133 to 165; aa 134 – 165; aa 137 to 143; aa 154 to 156; aa 194 to 208; aa 261 to 274; aa 262 to 274; aa 171 to 173; aa 413 to 417; aa 449 to 478; aa 494 to 525; aa 534 to 571; aa 581 to 601; aa 660 to 671; aa 709 to 723; and

aa 1 to 184, aa 199 to 259; aa 274 to 446; aa 603 to 659; aa 670 to 706; aa 724 to 736; aa 185 to 198; aa 260 to 273; aa 447 to 477; aa 495 to 602; aa 660 to 669; and aa 707 to 723,

wherein the amino acid numbers are those of the AAV7 capsid, SEQ ID NO:2, and corresponding regions in the capsid of C1, SEQ ID NO:60; C2, SEQ ID NO:61; C5, SEQ ID NO:62; A3-3, SEQ ID NO:66; A3-7, SEQ ID NO:67; A3-4, SEQ ID NO:68; A3-5, SEQ ID NO: 69; 3.3b, SEQ ID NO: 62; 223.4, SEQ ID NO: 73; 223-5, SEQ ID NO:74; 223-10, SEQ ID NO:75; 223-2, SEQ ID NO:76; 223-7, SEQ ID NO: 77; 223-6, SEQ ID NO: 78; 44-1, SEQ ID NO: 79; 44-5, SEQ ID NO:80; 44-2, SEQ ID NO:81; 42-15, SEQ

ID NO: 84; 42-8, SEQ ID NO: 85; 42-13, SEQ ID NO:86; 42-3A, SEQ ID NO:87; 42-4, SEQ ID NO:88; 42-5A, SEQ ID NO:89; 42-1B, SEQ ID NO:90; 42-5B, SEQ ID NO:91; 43-1, SEQ ID NO: 92; 43-12, SEQ ID NO: 93; 43-5, SEQ ID NO:94; 43-21, SEQ ID NO:96; 43-25, SEQ ID NO: 97; 43-20, SEQ ID NO:99; 24.1, SEQ ID NO: 101; 42.2, SEQ ID NO:102; 7.2, SEQ ID NO: 103; 27.3, SEQ ID NO: 104; 16.3, SEQ ID NO: 105; 42.10, SEQ ID NO: 106; 42-3B, SEQ ID NO: 107; 42-11, SEQ ID NO: 108; F1, SEQ ID NO: 109; F5, SEQ ID NO: 110; F3, SEQ ID NO:111; 42-6B, SEQ ID NO: 112; and 42-12, SEQ ID NO: 113.

12. An artificial adeno-associated virus (AAV) capsid protein comprising one or more of the protein fragments according to claim 11.

13. A recombinant adeno-associated virus (AAV) comprising an artificial capsid according to claim 12.

14. A molecule comprising a nucleic acid sequence encoding a protein according to claim 11 to 12.

15. A molecule comprising a nucleic acid sequence encoding a novel adeno-associated virus (AAV) serotype capsid protein having an amino acid sequence selected from the group consisting of: AAV7, amino acids 1 to 737 of SEQ ID NO:2; C1, SEQ ID NO:60; C2, SEQ ID NO:61; C5, SEQ ID NO:62; A3-3, SEQ ID NO:66; A3-7, SEQ ID NO:67; A3-4, SEQ ID NO:68; A3-5, SEQ ID NO: 69; 3.3b, SEQ ID NO: 62; 223.4, SEQ ID NO: 73; 223-5, SEQ ID NO:74; 223-10, SEQ ID NO:75; 223-2, SEQ ID NO:76; 223-7, SEQ ID NO: 77; 223-6, SEQ ID NO: 78; 44-1, SEQ ID NO: 79; 44-5, SEQ ID NO:80; 44-2, SEQ ID NO:81; 42-15, SEQ ID NO: 84; 42-8, SEQ ID NO: 85; 42-13, SEQ ID NO:86; 42-3A, SEQ ID NO:87; 42-4, SEQ ID NO:88; 42-5A, SEQ ID NO:89; 42-1B, SEQ ID NO:90; 42-5B, SEQ ID NO:91; 43-1, SEQ ID NO: 92; 43-12, SEQ ID NO: 93; 43-5, SEQ ID NO:94; 43-21, SEQ ID NO:96; 43-25, SEQ ID NO: 97; 43-20, SEQ ID NO:99; 24.1, SEQ ID NO: 101; 42.2, SEQ ID NO:102; 7.2, SEQ ID NO: 103; 27.3, SEQ ID NO: 104; 16.3, SEQ ID NO: 105; 42.10, SEQ ID NO: 106; 42-3B, SEQ ID NO: 107; 42-11, SEQ ID NO: 108; F1, SEQ

ID NO: 109; F5, SEQ ID NO: 110; F3, SEQ ID NO:111; 42-6B, SEQ ID NO: 112; and 42-12, SEQ ID NO: 113.

16. A molecule comprising a nucleic acid sequence encoding a novel adeno-associated virus (AAV) serotype capsid protein, said nucleic acid sequence selected from the group consisting of: AAV5, SEQ ID NO:2; 42-2 , SEQ ID NO:9; 42-8 ,SEQ ID NO:27; 42-15 , SEQ ID NO:28; 42-5b ,SEQ ID NO: 29; 42-1b ,SEQ ID NO:30; 42-13, SEQ ID NO: 31; 42-3a , SEQ ID NO: 32; 42-4 ,SEQ ID NO:33; 42-5a , SEQ ID NO: 34; 42-10, SEQ ID NO:35; 42-3b, SEQ ID NO: 36; 42-11, SEQ ID NO: 37; 42-6b, SEQ ID NO:38; 43-1, SEQ ID NO: 39; 43-5, SEQ ID NO: 40; 43-12 ,SEQ ID NO:41; 43-20, SEQ ID NO:42; 43-21, SEQ ID NO: 43; 43-23, SEQ ID NO:44; 43-25 ,SEQ ID NO: 45; 44.1, SEQ ID NO:47; 44.5, SEQ ID NO:47; 223.10, SEQ ID NO:48; 223.2 , SEQ ID NO:49; 223.4, SEQ ID NO:50; 223.5, SEQ ID NO: 51; 223.6, SEQ ID NO: 52; 223.7, SEQ ID NO: 53; A3.4, SEQ ID NO: 54; A3.5, SEQ ID NO:55; A3.7 , SEQ ID NO: 56; A3.3 ,SEQ ID NO:57; 42.12, SEQ ID NO: 58; 44.2, SEQ ID NO: 59; AAV10 , SEQ ID NO: 117; AAV11, SEQ ID NO: 118; AAV12 ,SEQ ID NO:119; A3.1, SEQ ID NO:120; and H6, SEQ ID NO: 25.

17. A molecule comprising a nucleic acid sequence encoding a fragment of an adeno-associated virus capsid protein, said nucleic acid sequence selected from the group consisting of:

vp1, nt 825 to 3049;

vp2, nt 1234 to 3049;

vp 3, nt 1434 to 3049;

nt 468 to 3090; and

nt 725 to 3090,

wherein the nucleotides numbers are of AAV7, SEQ ID NO:1 and correspond to sequences in 42-2 , SEQ ID NO:9; 42-8 ,SEQ ID NO:27; 42-15 , SEQ ID NO:28; 42-5b ,SEQ ID NO: 29; 42-1b ,SEQ ID NO:30; 42-13, SEQ ID NO: 31; 42-3a , SEQ ID NO: 32; 42-4 ,SEQ ID NO:33; 42-5a , SEQ ID NO: 34; 42-10, SEQ ID NO:35; 42-3b, SEQ ID NO: 36; 42-11, SEQ ID NO: 37; 42-6b, SEQ ID NO:38; 43-1, SEQ ID NO: 39; 43-5, SEQ ID NO: 40; 43-12 ,SEQ ID NO:41; 43-20, SEQ ID NO:42; 43-21, SEQ ID NO: 43; 43-23, SEQ ID NO:44; 43-25 ,SEQ ID NO: 45; 44.1, SEQ ID NO:47; 44.5, SEQ ID NO:47; 223.10,

SEQ ID NO:48; 223.2 , SEQ ID NO:49; 223.4, SEQ ID NO:50; 223.5, SEQ ID NO: 51; 223.6, SEQ ID NO: 52; 223.7, SEQ ID NO: 53; A3.4, SEQ ID NO: 54; A3.5, SEQ ID NO:55; A3.7 , SEQ ID NO: 56; A3.3 ,SEQ ID NO:57; 42.12, SEQ ID NO: 58; 44.2, SEQ ID NO: 59; AAV10 , SEQ ID NO: 117; AAV11, SEQ ID NO: 118; AAV12 ,SEQ ID NO:119; A3.1, SEQ ID NO:120; and H6, SEQ ID NO: 25.

18. The molecule according to claim 12 or claim 14 to 17, wherein said molecule is a plasmid.

19. The molecule according to claim 12 or claim 14 to 17, wherein said molecule further comprises a functional AAV *rep* gene.

20. The molecule according to claim 16, wherein said nucleic acid sequence is the AAV7 sequence, SEQ ID NO:1.

21. A method of generating a recombinant adeno-associated virus (AAV) comprising an AAV serotype capsid comprising the steps of culturing a host cell containing: (a) a molecule according to any of claims 12 or claim 14 to 17 which encodes an adeno-associated virus capsid; (b) a functional rep gene; (c) a minigene comprising AAV inverted terminal repeats (ITRs) and a transgene; and (d) sufficient helper functions to permit packaging of the minigene into the AAV capsid protein.

22. A host cell transfected with an adeno-associated virus according to claim 10 or a molecule according to any of claims 12, or claims 14 to 17.

23. A composition comprising an AAV according to claim 10 or claim 13, and a physiologically compatible carrier.

24. A composition comprising a molecule according to any of claims 12, or claims 14 to 17 and a physiologically compatible carrier.

25. A method of delivering a transgene to a cell, said method comprising the step of contacting the cell with an AAV according to claim 10 or claim 13, wherein said rAAV comprises the transgene.

26. A molecule comprising a heterologous adeno-associated virus (AAV) serotype 7 nucleic acid sequence, said sequence comprising:

nucleotides (nt) 1 to 107 of SEQ ID NO: 1;
nt 107 to 2215 of SEQ ID NO:1;
nt 334 to 2215 of SEQ ID NO:1;
nt 2222 to 4435 of SEQ ID NO:1.
nt 2633 to 4435 of SEQ ID NO:1;
nt 2831 to 4435 of SEQ ID NO:1; and
nt 4704 to 4721 of SEQ ID NO: 1.

27. A molecule encoding an adeno-associated virus (AAV) serotype 7 rep protein or a fragment thereof, said protein or fragment selected from the group consisting of:

amino acid (aa) 1 to 623, aa 1 to 171; aa 172 to 372, aa 373 to 444, and aa 445 to 623 of SEQ ID NO:3.

28. A host cell containing a molecule according to claim 26 or 27.

29. An adeno-associated virus (AAV) comprising a capsid protein of AAV serotype 7, wherein the capsid protein is serologically cross-reactive with antibodies to a capsid protein having the sequence of SEQ ID NO:2.

30. The AAV according to claim 29, wherein the antibodies are polyclonal antibodies generated using SEQ ID NO: 2.

31. The AAV according to claim 29, wherein said capsid protein is not neutralized by antibodies generated against AAV serotypes 1 – 6.

32. The AAV according to claim 29, which is produced recombinantly.

33. The AAV according to claim 32, wherein said AAV has a capsid protein that is 95% to 99% identical to aa 1 to 737 of SEQ ID NO:2 as determined by alignment and a Fasta program in GCG Version 6.1.

34. The AAV according to any of claims 30 to 33, wherein the recombinant AAV comprises inverted terminal repeats (ITRs) from a serotype heterologous to the capsid protein.

35. The recombinant AAV according to claim 34, wherein the ITRs are from AAV serotype 2.

36. The recombinant AAV according to any of claims 30 to 35, wherein the capsid protein is encoded by a molecule having the sequence of nt 825 to 3049 of SEQ ID NO: 1.

37. The recombinant AAV according to any of claims 30 to 36, wherein the capsid protein comprises a sequence of amino acids having the sequence of aa 138 to 737 of SEQ ID NO:2.

38. The recombinant AAV according to claim 35, wherein the capsid protein comprises a sequence of amino acids having the sequence of aa 203 to 737 of SEQ ID NO:2.

39. The recombinant AAV according to claim 35, wherein the capsid protein comprises a sequence of amino acids having the sequence of aa 1 to 737 of SEQ ID NO:2.

40. A composition comprising an AAV according to any of claims 30 to 39.

41. Use of a recombinant AAV according to any of claims 30 to 39 in preparing a medicament for delivering a heterologous molecule to a target cell.