(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
24 January 2019 (24.01.2019)

WIPO | PCT

(10) International Publication Number
WO 2019/016756 A1

(51) International Patent Classification:
C12N 15/861 (2006.01) *C07K 14/18* (2006.01)
A61K 39/12 (2006.01)

(21) International Application Number:
PCT/IB2018/055389

(22) International Filing Date:
19 July 2018 (19.07.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/535,371 21 July 2017 (21.07.2017) US
62/589,729 22 November 2017 (22.11.2017) US

(71) Applicant: **GLAXOSMITHKLINE BIOLOGICALS SA** [BE/BE]; rue de l'Institut 89, B-1330 Rixensart (BE).

(72) Inventors: **WIZEL, Benjamin**; 14200 Shady Grove Road, Rockville, Maryland 20850 (US). **HARVEY, Martine**; 525 Cartier Quest, Laval, Québec H7V358 (CA). **WARTER, Lucile**; rue de l'Institut 89, B-1330 Rixensart (BE). **LUISI, Kate**; 14200 Shady Grove Road, Rockville, Maryland 20850 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:
— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

Published:
— *with international search report (Art. 21(3))*
— *with sequence listing part of description (Rule 5.2(a))*
— *in black and white; the international application as filed contained color or greyscale and is available for download from PATENTSCOPE*

(54) Title: CHIKUNGUNYA VIRUS ANTIGEN CONSTRUCTS

(57) Abstract: The invention provides adenoviral vectors comprising transgenes encoding Chikungunya virus antigens. The vectors can be used to produce vaccines for the prophylaxis, amelioration and treatment of diseases caused by Chikungunya virus infections.

WO 2019/016756 A1

CHIKUNGUNYA VIRUS ANTIGEN CONSTRUCTS

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been filed electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on July 17, 2018, is named VU66387 WO SeqLstg.txt and is 374,654 bytes in size.

FIELD OF THE INVENTION

This invention is in the field of treating and preventing viral infections. In particular, the present invention relates to chimpanzee adenoviral vectors encoding a *Chikungunya virus* antigen. It includes the use of *Chikungunya virus* antigens for treating and preventing *Chikungunya virus* infections.

BACKGROUND

Chikungunya virus (CHIKV) is a single-stranded, positive-sense RNA virus in the family *Togaviridae*, within the *Alphavirus* genus. The virus is transmitted by infected female mosquitoes of the genus *Aedes*. About 2.5 billion people live in CHIKV-transmitting *Aedes* mosquito vector areas, and outbreaks can involve millions of people. Local transmission of CHIKV has been reported in over 100 countries or territories, and its range is expanding. Infections can cause myalgia, arthritis/arthralgia, fever, rash, headache, nausea and vomiting which typically last weeks to months. Approximately 35-50% of infected patients develop chronic symptoms that include sever joint pain that can persist for years.

The CHIKV genome encodes four non-structural proteins (nsP1-4) and five structural proteins, including a capsid (C), envelope proteins E1-E3, and membrane-associated peptide 6K. Three genotypes (lineages) of CHIKV have been identified: West African, Asian and East/Central/South African (ECSA). The three genotypes share 95.2-99.8% amino acid sequence identity.

Several vaccine approaches are currently under evaluation for the prevention of CHIKV infection, including live-attenuated or inactivated whole virus, virus-like particles (VLPs), recombinant subunit vaccines, DNA vaccines and recombinant vector vaccines. Wang *et al*., *Vaccine*. 29(15): 2803–2809 (2011). However, to date no licensed vaccine is available.

Adenovirus has been widely used for gene transfer applications due to its ability to achieve highly efficient gene transfer in a variety of target tissues and large transgene capacity. Conventionally, adenovirus E1 genes are deleted and replaced with a transgene cassette

consisting of a promoter of choice, cDNA sequence of the gene of interest and a poly A signal, resulting in a replication defective recombinant virus.

Recombinant adenoviruses are useful in both gene therapy and as vaccines. However, the use of human-derived adenoviral vectors is complicated by pre-existing immunity to human adenoviruses, which may neutralize the vaccine vector. Viral vectors based on non-human simian adenovirus represent an alternative to the use of human derived vectors for the development of genetic vaccines. Certain adenoviruses isolated from non-human simians are closely related to adenoviruses isolated from humans, as demonstrated by their efficient propagation in cells of human origin.

There is a need for a CHIKV vaccine with a simplified dosing schedule, increased safety and an enhanced manufacturing profile. Accordingly, there is an unmet need to develop non-human simian adenoviral vectors for use in a CHIKV vaccine.

SUMMARY OF THE INVENTION

The present inventors provide constructs useful as components of immunogenic compositions for the induction of an immune response in a subject against *Chikungunya virus* (CHIKV) infection, methods for their use in treatment and prevention of EBV infection and EBV-associated diseases, and processes for their manufacture.

There is provided an isolated polynucleotide, wherein the polynucleotide encodes a polypeptide selected from the group consisting of:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;

wherein the isolated polynucleotide comprises a nucleic acid sequence encoding a *Chikungunya virus* antigen.

Also provided is a recombinant polynucleotide comprising a polynucleotide selected from the group consisting of:

(a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1, and

(c) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3;

wherein the recombinant polynucleotide comprises a nucleic acid sequence encoding a *Chikungunya virus* antigen.

Also provided is a recombinant vector comprising a polynucleotide selected from the group consisting of:

(a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1, and

(c) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3;

wherein the recombinant vector comprises a nucleic acid sequence encoding a *Chikungunya virus* antigen.

Also provided is a recombinant adenovirus comprising at least one polynucleotide or polypeptide selected from the group consisting of:

(a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,

(c) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3,

(d) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(e) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence

which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1, and

(f) a polypeptide having the amino acid sequence according to SEQ ID NO: 3;

wherein the recombinant adenovirus comprises a nucleic acid sequence encoding a *Chikungunya virus* antigen; and wherein the nucleic acid sequence is operatively linked to one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell.

Also provided is a recombinant adenovirus comprising a polynucleotide encoding at least one polypeptide selected from the group consisting of:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1 or a functional derivative thereof,

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 3 or a functional derivative thereof, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 5 or a functional derivative thereof,

wherein the adenovirus further comprises at least one nucleic acid sequence encoding a *Chikungunya virus* antigen, wherein the nucleic acid sequence is operatively linked to one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell.

Also provided is a composition comprising the recombinant adenovirus as described above, and a pharmaceutically acceptable excipient.

Also provided is a composition comprising at least one of the following:

(a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,

(c) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3,

(d) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(e) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence

which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,

(f) a polypeptide having the amino acid sequence according to SEQ ID NO: 3,

(g) a vector comprising a polynucleotide as described in (a), (b) or (c) above, and

(h) a recombinant adenovirus comprising a polynucleotide as described in (a), (b) or (c) above and a pharmaceutically acceptable excipient.

wherein the composition comprises a nucleic acid sequence encoding a *Chikungunya virus* antigen or a *Chikungunya virus* antigen polypeptide sequence; and, optionally, the nucleic acid sequence is operatively linked to one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell.

Also provided is a cell comprising at least one of the following:

(a) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,

(c) a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3,

(d) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(e) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1,

(f) a polypeptide having the amino acid sequence according to SEQ ID NO: 3,

(g) a vector comprising a polynucleotide as described in (a), (b) or (c) above, and

(h) a recombinant adenovirus comprising a polynucleotide as described in (a), (b) or (c) above;

wherein the cell comprises an adenovirus comprising a nucleic acid sequence encoding a *Chikungunya virus* antigen; and wherein the nucleic acid sequence is operatively linked to one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell.

Also provided is an isolated adenoviral polypeptide selected from the group consisting of:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1,

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 3; and

further comprising a *Chikungunya virus* antigen polypeptide sequence.

Also provided is an isolated polynucleotide, vector, recombinant adenovirus, composition or cell comprising the sequence according to SEQ ID NO: 6 and further comprising a *Chikungunya virus* antigen.

The recombinant adenoviruses and compositions may be used as medicaments, in particular for the stimulation of an immune response against *Chikungunya virus* infection.

Typically, the aim of the methods of the invention is to induce a protective immune response, *i.e.* to immunize or vaccinate the subject against a related pathogen. The invention may therefore be applied for the prophylaxis, treatment or amelioration of diseases due to infection by *Chikungunya virus*.

The invention may be provided for the purpose of both pre-exposure prophylaxis and post-exposure prophylaxis to diseases caused by *Chikungunya virus* infections. In some embodiments, the subject has previously been vaccinated with a *Chikungunya virus* vaccine. The approaches of the present invention may, for example, be used for a subject at least one year after *Chikungunya virus* vaccination, at least two years after *Chikungunya virus* vaccination, at least at least five years after *Chikungunya virus* vaccination or at least ten years after *Chikungunya virus* vaccination.

The *Chikungunya virus* antigen is an antigenic sequence, *i.e.* a sequence from a *Chikungunya virus* protein which comprises at least one B or T cell epitope. Suitably the *Chikungunya virus* antigen comprises at least one T cell epitope. In an embodiment of the invention the adenovirus comprises a nucleic acid sequence encoding a *Chikungunya virus* structural polyprotein antigen. In a specific embodiment of the invention, the adenovirus comprises a nucleic acid derived from SEQ ID NO: 21 or SEQ ID NO: 22. In another specific embodiment of the invention, the adenovirus comprises a nucleic acid encoding a polypeptide derived from SEQ ID NO: 23. Suitably, the nucleic acid sequence encoding a

Chikungunya virus antigen comprises or consists of a polynucleotide at least 80%, at least 90%, at least 95% or at least 99% identical to SEQ ID NOs: 21 or 22.

The elicited immune response may be an antigen specific B cell response, which produces neutralizing antibodies. The elicited immune response may be an antigen specific T cell response, which may be a systemic and/or a local response. The antigen specific T cell response may comprise a CD4+ T cell response, such as a response involving CD4+ T cells expressing a plurality of cytokines, *e.g.* IFNgamma, TNFalpha and/or IL2. Alternatively, or additionally, the antigen specific T cell response comprises a CD8+ T cell response, such as a response involving CD8+ T cells expressing a plurality of cytokines, e.g., IFNgamma, TNFalpha and/or IL2.

DESCRIPTION OF THE DRAWINGS

Figure 1 Diagram of the *Chikungunya virus* genome encoding four non-structural proteins (nsP1-4) and five structural proteins: the capsid (C), and the envelope glycoproteins (E3, E2, 6k and E1).

Figure 2A-C: Alignment of fiber protein sequences from the indicated simian adenoviruses.
ChAd3 (SEQ ID NO:11)
PanAd3 (SEQ ID NO:12)
ChAd17 (SEQ ID NO:13)
ChAd19 (SEQ ID NO:14)
ChAd24 (SEQ ID NO:15)
ChAd155 (SEQ ID NO:1)
ChAd11 (SEQ ID NO:16)
ChAd20 (SEQ ID NO:17)
ChAd31 (SEQ ID NO:18)
PanAd1 (SEQ ID NO:19)
PanAd2 (SEQ ID NO:20)

Figure 3: Flow diagram for the production of ChAd155 plasmids and vectors. The final step involves insertion of an expression construct encoding the CHIKV structural proteins into the pChAd155#1434 vector, to produce the vector pChAd155 ΔE1, ΔE4_Ad5 orf6 hCMV-CHIKV.

Figure 4: Diagram of plasmid pvjTetOhCMV CHIKV bghpolyA.

Figure 5: Diagram of vector pChAd155 ΔE1, ΔE4_Ad5 orf6 hCMV-CHIKV.

Figure 6: Diagram of pMax-CHIKV VLP expression vector.

Figure 7: Characterization of ChAd155-CHIKV expressed in HeLa cells. Two different lots of ChAd155-CHIKV were evaluated (CHIKV-1 and CHIKV-2). CHIKV capsid protein was detected in both the soluble cell lysate fraction (left panel) and the supernatant (right panel) of infected Hela cells. Lane1: Molecular weight markers (Ladder precision plus); Lane 2: ChAd155-CHIKV-1 (MOI 250); Lane 3: ChAd155-CHIKV-1 (MOI 500); Lane 4: ChAd155-CHIKV-1 (MOI 1250); Lane 5: ChAd155-CHIKV-2 (MOI 250); Lane 6: ChAd155-CHIKV-2 (MOI 500); and Lane 7: ChAd155-CHIKV-2 (MOI 1250).

Figure 8: Electron micrograph of CHIKV VLPs showing intact VLPs of the expected diameter.

Figure 9: Immunogenicity of CHIKV VLPs in mice. CHIKV VLPs induced high neutralizing antibody (nAb) titers in a dose-dependent fashion. nAbs elicited to VLPs based on the West-African CHIKV strain (#37997) exhibited activity against La Reunion and Caribbean strains. Adjuvants enhanced immunogenicity at the 1 and 0.1 μg doses.

Figure 10: Immunogenicity of CHAd155-CHIKV in mice. ChAd155-CHIKV induced high nAb titers after a single immunization with doses of 10^8 or 10^9 viral particles (vp).

Figure 11: Durability of ChAd155-CHIKV immunogenicity in mice. A single dose of ChAd155-CHIKV ($5x10^8$ viral particles, i.m.) elicited high and durable neutralizing antibody (nAb) titers, expressed as 50% Tissue culture Infective Dose (TCID50). nAb titers above the detection threshold (dotted line) were observed at 3, 6 and 9 weeks post-immunization. In addition, antibodies elicited by the West-African CHIKV-based ChAd construct were capable of neutralizing both the La Reunion and Caribbean CHIKV strains. No difference was observed between the unadjuvanted and AS01E-adjuvanted groups.

Figure 12: Durability of CHIKV VLP immunogenicity in mice. CHIKV VLPs induced high nAb titers following 2 immunizations. The West-African CHIKV VLPs were capable of eliciting nAbs against the La Reunion (LR) and Caribbean (CRBN) CHIKV strains. Elevated nAb titers were observed 3, 6 and 9 weeks after the second immunization. A single immunization with CHIKV VLPs alone did not produce a robust nAb response, but an adjuvanting effect was observed for the single immunization combined with AS01E.

Figure 13: Efficacy of ChAd155-CHIKV and CHIKV VLP in mice. (A) All immunized groups showed complete protection against CHIKV (LR strain) challenge, except the group receiving a single dose of CHIKV VLPs, which showed low levels of viremia at d2 and d3 post-challenge. Control animals exhibited CHIKV viremia peaking at d2. (B) All immunized groups showed complete protection from disease as measured by foot pad swelling. A small but not significant trend in foot pad swelling was noted at d2 post challenge in the group immunized with a single dose of CHIKV VLPs. Control animals exhibited foot pad swelling peaking at d6.

DESCRIPTION OF THE SEQUENCES

SEQ ID NO: 1 - Amino acid sequence of ChAd155 fiber
SEQ ID NO: 2 - Nucleotide sequence encoding ChAd155 fiber
SEQ ID NO: 3 - Amino acid sequence of ChAd155 penton
SEQ ID NO: 4 - Nucleotide sequence encoding ChAd155 penton
SEQ ID NO: 5 - Amino acid sequence of ChAd155 hexon
SEQ ID NO: 6 - Nucleotide sequence encoding ChAd155 hexon
SEQ ID NO: 7 - Nucleotide sequence encoding ChAd155#1434
SEQ ID NO: 8 - Nucleotide sequence encoding ChAd155#1390
SEQ ID NO: 9 - Nucleotide sequence encoding ChAd155#1375
SEQ ID NO: 10 - Nucleotide sequence encoding wild type ChAd155
SEQ ID NO: 11 - Amino acid sequence for the fiber protein of ChAd3
SEQ ID NO: 12 - Amino acid sequence for the fiber protein of PanAd3
SEQ ID NO: 13 - Amino acid sequence for the fiber protein of ChAd17
SEQ ID NO: 14 - Amino acid sequence for the fiber protein of ChAd19
SEQ ID NO: 15 - Amino acid sequence for the fiber protein of ChAd24
SEQ ID NO: 16 - Amino acid sequence for the fiber protein of ChAd11

SEQ ID NO: 17 - Amino acid sequence for the fiber protein of ChAd20
SEQ ID NO: 18 - Amino acid sequence for the fiber protein of ChAd31
SEQ ID NO: 19 - Amino acid sequence for the fiber protein of PanAd1
SEQ ID NO: 20 - Amino acid sequence for the fiber protein of PanAd2
SEQ ID NO: 21 - Nucleotide sequence for CHIKV structural polypeptide, strain #37997 (wild type)
SEQ ID NO: 22 - Nucleotide sequence for CHIKV structural polypeptide, strain #37997 (codon optimized)
SEQ ID NO: 23 - Amino acid sequence for CHIKV structural polypeptide, strain #37997
SEQ ID NO: 24 - Nucleotide sequence of plasmid pvjTetOhCMV CHIKV bghpolyA
SEQ ID NO: 25 - Nucleotide sequence of expression vector the pChAd155 ΔE1, ΔE4_Ad5 orf6 hCMV-CHIKV

DETAILED DESCRIPTION OF THE INVENTION

Adenoviral vectors

Adenovirus has been widely used for gene transfer applications due to its proven safety, ability to achieve highly efficient gene transfer in a variety of target tissues and large transgene capacity. Adenoviral vectors of use in the present invention may be derived from a range of mammalian hosts. Over 100 distinct serotypes of adenovirus have been isolated which infect various mammalian species. These adenoviral serotypes have been categorized into six subgenera (A–F; B is subdivided into B1 and B2) according to sequence homology and on their ability to agglutinate red blood cells.

In one embodiment, the adenoviral vector or recombinant adenovirus of the present invention is derived from a nonhuman simian adenovirus, also referred to simply as a simian adenovirus. Numerous adenoviruses have been isolated from nonhuman simians such as chimpanzees, bonobos, rhesus macaques and gorillas, and vectors derived from these adenoviruses induce strong immune responses to transgenes encoded by these vectors (Colloca *et al.* (2012) Sci. Transl. Med. 4:1-9; Roy *et al.* (2004) Virol.324: 361-372; Roy *et al.* (2010) J. of Gene Med. 13:17-25). Some advantages of vectors based on nonhuman simian adenoviruses include the relative lack of cross-neutralizing antibodies to these adenoviruses in the target population, thus their use overcomes the pre-existing immunity to human adenoviruses. For example, cross-reaction of certain chimpanzee adenoviruses with pre-existing neutralizing antibody responses is only present in 2% of the target population compared with 35% in the case of certain candidate human adenovirus vectors.

Specifically, the adenoviral vector may be derived from a non-human adenovirus, such as a simian adenovirus and in particular a chimpanzee adenovirus such as ChAd3, ChAd63, ChAd83, ChAd155, Pan 5, Pan 6, Pan 7 (also referred to as C7) or Pan 9 and may include, in whole or in part, a nucleotide encoding the fiber, penton or hexon of a non-human adenovirus. Examples of such strains are described in WO03/000283, WO2010/086189 and GB1510357.5 and are also available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, and other sources. Alternatively, adenoviral vectors may be derived from nonhuman simian adenoviruses isolated from bonobos, such as PanAd1, PanAd2 or PanAd3. Examples of such vectors described herein can be found for example in WO2005/071093 and WO2010/086189. Adenoviral vectors may also be derived from adenoviruses isolated from gorillas as described in WO2013/52799, WO2013/52811 and WO2013/52832.

Adenoviral vector structure

Adenoviruses have a characteristic morphology with an icosahedral capsid comprising three major proteins, hexon (II), penton base (III) and a knobbed fiber (IV), along with a number of other minor proteins, VI, VIII, IX, IIIa and IVa2. The hexon accounts for the majority of the structural components of the capsid, which consists of 240 trimeric hexon capsomeres and 12 penton bases. The hexon has three conserved double barrels, while the top has three towers, each tower containing a loop from each subunit that forms most of the capsid. The base of the hexon is highly conserved between adenoviral serotypes, while the surface loops are variable. The penton is another adenoviral capsid protein that forms a pentameric base to which the fiber attaches. The trimeric fiber protein protrudes from the penton base at each of the 12 vertices of the capsid and is a knobbed rod-like structure. The primary role of the fiber protein is the tethering of the viral capsid to the cell surface via the interaction of the knob region with a cellular receptor, and variations in the flexible shaft as well as knob regions of fiber are characteristic of the different serotypes.

The adenoviral genome has been well characterized. The linear, double-stranded DNA is associated with the highly basic protein VII and a small peptide pX (also termed mu). Another protein, V, is packaged with this DNA-protein complex and provides a structural link to the capsid via protein VI. There is general conservation in the overall organization of the adenoviral genome with respect to specific open reading frames being similarly positioned, *e.g.* the location of the E1A, E1B, E2A, E2B, E3, E4, L1, L2, L3, L4 and L5 genes of each virus. Each extremity of the adenoviral genome comprises a sequence known as an inverted terminal repeat (ITR), which is necessary for viral replication. The 5' end of the

adenoviral genome contains the 5' cis-elements necessary for packaging and replication; i.e., the 5' ITR sequences (which function as origins of replication) and the native 5' packaging enhancer domains (that contain sequences necessary for packaging linear adenoviral genomes and enhancer elements for the E1 promoter). The 3' end of the adenoviral genome includes the 3' cis-elements (including the ITRs) necessary for packaging and encapsidation. The virus also comprises a virus-encoded protease, which is necessary for processing some of the structural proteins required to produce infectious virions.

The structure of the adenoviral genome is described on the basis of the order in which the viral genes are expressed following host cell transduction. More specifically, the viral genes are referred to as early (E) or late (L) genes according to whether transcription occurs prior to or after onset of DNA replication. In the early phase of transduction, the E1A, E1B, E2A, E2B, E3 and E4 genes of adenovirus are expressed to prepare the host cell for viral replication. During the late phase of infection, expression of the late genes L1-L5, which encode the structural components of the virus particles, is activated.

Adenovirus capsid proteins and their encoding polynucleotides

As outlined above, the adenoviral capsid comprises three major proteins, hexon, penton and fiber. The hexon accounts for the majority of the structural components of the capsid, which consists of 240 trimeric hexon capsomeres and 12 penton bases. The hexon has three conserved double barrels, while the top has three towers, each tower containing a loop from each subunit that forms most of the capsid. The base of hexon is highly conserved between adenoviral serotypes, while the surface loops are variable.

The penton is another adenoviral capsid protein that forms a pentameric base to which fiber attaches. The trimeric fiber protein protrudes from the penton base at each of the 12 vertices of the capsid and is a knobbed rod-like structure. A remarkable difference in the surface of adenovirus capsids compared to that of most other icosahedral viruses is the presence of the long, thin fiber protein. The primary role of the fiber protein is the tethering of the viral capsid to the cell surface via its interaction with a cellular receptor.

The fiber proteins of many adenovirus serotypes share a common architecture: an N-terminal tail, a central shaft made of repeating sequences, and a C-terminal globular knob domain (or “head”). The central shaft domain consists of a variable number of beta-repeats. The beta-repeats connect to form an elongated structure of three intertwined spiralling

strands that is highly rigid and stable. The shaft connects the N-terminal tail with the globular knob structure, which is responsible for interaction with the target cellular receptor. The globular nature of the adenovirus knob domain presents large surfaces for binding the receptor laterally and apically. The effect of this architecture is to project the receptor-binding site far from the virus capsid, thus freeing the virus from steric constraints presented by the relatively flat capsid surface.

Although fibers of many adenovirus serotypes have the same overall architecture, they have variable amino acid sequences that influence their function as well as structure. For example, a number of exposed regions on the surface of the fiber knob present an easily adaptable receptor binding site. The globular shape of the fiber knob allows receptors to bind at the sides of the knob or on top of the fiber knob. These binding sites typically lie on surface-exposed loops connecting beta-strands that are poorly conserved among human adenoviruses. The exposed side chains on these loops give the knob a variety of surface features while preserving the tertiary and quaternary structure. For example, the electrostatic potential and charge distributions at the knob surfaces can vary due to the wide range of isoelectric points in the fiber knob sequences, varying from a pI of approximately 9 for adenovirus “Ad” 8, Ad 19, and Ad 37 to approximately 5 for subgroup B adenoviruses. As a structurally complex virus ligand, the fiber protein allows the presentation of a variety of binding surfaces (knob) in a number of orientations and distances (shaft) from the viral capsid.

One of the most obvious variations between some serotypes is fiber length. Studies have shown that the length of the fiber shaft strongly influences the interaction of the knob and the virus with its target receptors. Further, fiber proteins between serotypes can also vary in their ability to bend. Although beta-repeats in the shaft form a highly stable and regular structure, electron microscopy (EM) studies have shown distinct hinges in the fiber. Analysis of the protein sequence from several adenovirus serotype fibers pinpoints a disruption in the repeating sequences of the shaft at the third beta-repeat from the N-terminal tail, which correlates strongly with one of the hinges in the shaft, as seen by EM. The hinges in the fiber allow the knob to adopt a variety of orientations relative to the virus capsid, which may circumvent steric hindrances to receptor engagement requiring the correct presentation of the receptor binding site on the knob. For example, the rigid fibers of subgroup D Ads thus require a flexible receptor or one prepositioned for virus attachment, as they are unable to bend themselves.

The identification of specific cell receptors for different Ad serotypes and the knowledge of how they contribute to tissue tropism have been achieved through the use of fiber pseudotyping technology. Although Ads of some subgroups use *Coxsackievirus* and adenovirus receptor ("CAR") as a primary receptor, it is becoming clear that many Ads use alternate primary receptors, leading to vastly different tropism *in vitro* and *in vivo*. The fibers of these serotypes show clear differences in their primary and tertiary structures, such as fiber shaft rigidity, the length of the fiber shaft, and the lack of a CAR binding site and/or the putative HSPG binding motif, together with the differences in net charge within the fiber knob. Pseudotyping Ad 5 particles with an alternate fiber shaft and knob therefore provides an opportunity to remove important cell binding domains and, in addition, may allow more efficient (and potentially more cell-selective) transgene delivery to defined cell types compared to that achieved with Ad 5. Neutralization of fiber-pseudotyped Ad particles may also be reduced if the fibers used are from Ads with lower seroprevalence in humans or experimental models, a situation that favours successful administration of the vector. Furthermore, full length fiber as well as isolated fiber knob regions, but not hexon or penton alone, are capable of inducing dendritic cell maturation and are associated with induction of a potent CD8+ T cell response. Taken together, adenoviral fiber plays an important role in at least receptor-binding and immunogenicity of adenoviral vectors.

"Low seroprevalence" may mean having a reduced pre-existing neutralizing antibody level as compared to human adenovirus 5 (Ad5). Similarly or alternatively, "low seroprevalence" may mean less than about 20% seroprevalence, less than about 15% seroprevalence, less than about 10% seroprevalence, less than about 5% seroprevalence, less than about 4% seroprevalence, less than about 3% seroprevalence, less than about 2% seroprevalence, less than about 1% seroprevalence or no detectable seroprevalence. Seroprevalence can be measured as the percentage of individuals having a clinically relevant neutralizing titer (defined as a 50% neutralisation titer >200) using methods as described in Aste-Amézaga *et al.*, *Hum. Gene Ther.* (2004) 15(3):293-304.

Illustrating the differences between the fiber proteins of Group C simian adenoviruses is the alignment provided in Figure 2. A striking feature is that the fiber sequences of these adenoviruses can be broadly grouped into having a long fiber, such as ChAd155, or a short fiber, such as ChAd3. This length differential is due to a 36 amino acid deletion at approximately position 321 in the short fiber relative to the long fiber. In addition, there are a number of amino acid substitutions that differ between the short versus long fiber subgroup yet are consistent within each subgroup. While the exact function of these differences have

not yet been elucidated, given the function and immunogenicity of fiber, they are likely to be significant. It has been shown that one of the determinants of viral tropism is the length of the fiber shaft. It has been demonstrated that an Ad5 vector with a shorter shaft has a lower efficiency of binding to CAR receptor and a lower infectivity. It has been speculated that this impairment is the result of an increased rigidity of the shorter fiber leading to a less efficient attachment to the cell receptor. These studies may explain the improved properties of ChAd155 carrying a longer and more flexible fiber in comparison with the previously described ChAd3 and PanAd3 carrying a fiber with a shorter shaft.

In one aspect of the invention there is provided isolated polynucleotides encoding the fiber, penton and hexon capsid polypeptides of chimp adenovirus ChAd155, and a *Chikungunya virus* antigen. An "isolated" polynucleotide is one that is removed from its original environment. For example, a naturally-occurring polynucleotide is isolated if it is separated from some or all of the coexisting materials in the natural system. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of its natural environment or if it is comprised within cDNA.

All three capsid proteins are expected to contribute to low seroprevalence and can, thus, be used independently from each other or in combination to suppress the affinity of an adenovirus to pre-existing neutralizing antibodies, e.g. to manufacture a recombinant adenovirus with a reduced seroprevalence. Such a recombinant adenovirus may be a chimeric adenovirus with capsid proteins from different serotypes with at least a fiber protein from ChAd155.

In one embodiment of the adenovirus according to the invention, the polynucleotide encodes at least two polypeptides selected from the group consisting of:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1 or a functional derivative thereof,

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 3 or a functional derivative thereof, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 5 or a functional derivative thereof.

In one embodiment of the adenovirus according to the invention, the polynucleotide encodes:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1 or a functional derivative thereof,

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 3 or a functional derivative thereof, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 5 or a functional derivative thereof.

In one embodiment, the adenovirus according to the invention comprises at least one polynucleotide selected from the group consisting of:

(a) a polynucleotide having the sequence of SEQ ID NO: 2;

(b) a polynucleotide having the sequence of SEQ ID NO: 4; and

(c) a polynucleotide having the sequence of SEQ ID NO: 6.

Transgenes

Adenoviral vectors may be used to deliver desired RNA or protein sequences, for example heterologous sequences, for *in vivo* expression. A vector may include any genetic element including naked DNA, a phage, transposon, cosmid, episome, plasmid, or virus. Such vectors contain DNA of ChAd155 as disclosed herein and an expression cassette. By "expression cassette" (or "minigene") is meant the combination of a selected heterologous gene (“transgene”) and the other regulatory elements necessary to drive translation, transcription and/or expression of the gene product in a host cell.

Typically, "heterologous" means derived from a genotypically distinct entity from that of the rest of the entity to which it is being compared. A heterologous nucleic acid sequence refers to any nucleic acid sequence that is not isolated from, derived from, or based upon a naturally occurring nucleic acid sequence of the adenoviral vector. "Naturally occurring" means a sequence found in nature and not synthetically prepared or modified. A sequence is "derived" from a source when it is isolated from a source but modified (e.g., by deletion, substitution (mutation), insertion, or other modification), suitably so as not to disrupt the normal function of the source gene.

Typically, an adenoviral vector is designed such that the expression cassette is located in a nucleic acid molecule which contains other adenoviral sequences in the region native to a selected adenoviral gene. The expression cassette may be inserted into an existing gene region to disrupt the function of that region, if desired. Alternatively, the expression cassette

may be inserted into the site of a partially or fully deleted adenoviral gene. For example, the expression cassette may be located in the site of a mutation, insertion or deletion which renders non-functional at least one gene of a genomic region selected from the group consisting of E1A, E1B, E2A, E2B, E3 and E4. The term "renders non-functional" means that a sufficient amount of the gene region is removed or otherwise disrupted, so that the gene region is no longer capable of producing functional products of gene expression. If desired, the entire gene region may be removed (and suitably replaced with the expression cassette). Suitably, E1 genes of adenovirus are deleted and replaced with an expression cassette consisting of a promoter of choice, a cDNA sequence of the gene of interest and a poly A signal, resulting in a replication defective recombinant virus.

As used herein, induction of an immune response refers to the ability of a protein, also known as an "antigen" or "immunogen," to induce a T cell and/or a humoral immune response to the protein. For example, an immunogenic composition may induce a memory T and/or B cell population relative to an untreated subject following CHIKV infection, particularly in those embodiments where the composition comprises a nucleic acid comprising a sequence which encodes a CHIKV antigen or comprises a CHIKV antigen. In some embodiments, the subject is a vertebrate, such as a mammal e.g. a human or a veterinary mammal.

In an embodiment, the transgene is a nucleic acid sequence, heterologous to the vector sequences flanking the transgene, which encodes a CHIKV protein capable of inducing an immune response in a subject. The nucleic acid coding sequence of the transgene is operatively linked to regulatory components in a manner which permits transgene transcription, translation, and/or expression in a host cell.

In an embodiment the transgene encodes an immunogen derived from at least one *Chikungunya virus*, for example from a CHIKV West African genotype, from a CHIKV East/Central/South African (ECSA) genotype, and/or from a CHIKV Asian genotype.

Representative CHIKV antigen sequences can be derived from known CHIKV variants, including those described in Genbank Accession Nos. KX702402.1, KY055011.1, KY435486.1 and DQ443544.2. In a specific embodiment, the immunogen is from the West African genotype strain 37997, corresponding to Genbank Accession No. ABX40011.

Suitably, the *Chikungunya virus* antigen is derived from *Chikungunya virus* strain #37997.

Suitably, the *Chikungunya virus* antigen comprises a sequence which is an immunogenic fragment of at least 20 amino acid residues .

Such immunogens may be derived from one or more CHIKV structural proteins. In an embodiment, the antigen consists of, or alternatively comprises, a CHIKV capsid protein (C) or a fragment thereof (suitably a fragment of at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200 or at least 250 amino acids). As used herein, a "CHIKV capsid protein" is intended to mean a protein having a polypeptide sequence corresponding to amino acids 1 to 261 of SEQ ID NO: 23, or a protein having at least 90% sequence identity to amino acids 1 to 261 of SEQ ID NO: 23 such as at least 91.0%, at least 93.0%, at least 95.0%, at least 97.0%, at least 98.0%, at least 99.0%, at least 99.2%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.8% or at least 99.9% identity over its entire length to amino acids 1 to 261 of SEQ ID NO: 23.

In an embodiment, the antigen consists of, or alternatively comprises, a CHIKV E3 protein or a fragment thereof (suitably a fragment of at least 20, at least 30, at least 40 or at least 50 amino acids). As used herein, a "CHIKV E3 protein" is intended to mean a protein having a polypeptide sequence corresponding to amino acids 262 to 325 of SEQ ID NO:23, or a protein having at least 90% sequence identity to amino acids 262 to 325 of SEQ ID NO: 23, such as at least 91.0%, at least 93.0%, at least 95.0%, at least 97.0%, at least 98.0%, at least 99.0%, at least 99.2%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.8% or at least 99.9% identity over its entire length to amino acids 262 to 325 of SEQ ID NO: 23.

In an embodiment, the antigen consists of, or alternatively comprises, a CHIKV E2 protein or a fragment thereof (suitably a fragment of at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350 or at least 400 amino acids). As used herein, a "CHIKV E2 protein" is intended to mean a protein having a polypeptide sequence corresponding to amino acids 326 to 748 of SEQ ID NO: 23, or a protein having at least 90% sequence identity to amino acids 326 to 748 of SEQ ID NO: 23, such as at least 91.0%, at least 93.0%, at least 95.0%, at least 97.0%, at least 98.0%, at least 99.0%, at least 99.2%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.8% or at least 99.9% identity over its entire length to amino acids 326 to 748 of SEQ ID NO: 23.

In an embodiment, the antigen consists of, or alternatively comprises, a CHIKV 6k protein or a fragment thereof (suitably a fragment of at least 20, at least 30, at least 40 or at least 50 amino acids). As used herein, a "CHIKV 6k protein" is intended to mean a protein having a polypeptide sequence corresponding to amino acids 749 to 809 of SEQ ID NO: 23, or a protein having at least 90% sequence identity to amino acids 749 to 809 of SEQ ID NO: 23, such as at least 91.0%, at least 93.0%, at least 95.0%, at least 97.0%, at least 98.0%, at least 99.0%, at least 99.2%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.8% or at least 99.9% identity over its entire length to amino acids 749 to 809 of SEQ ID NO: 23.

In an embodiment, the antigen consists of, or alternatively comprises, a CHIKV E1 protein or a fragment thereof (suitably a fragment of at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350 or at least 400 amino acids). As used herein, a "CHIKV E1 protein" is intended to mean a protein having a polypeptide sequence corresponding to amino acids 810 to 1248 of SEQ ID NO: 23, or a protein having at least 90% sequence identity to amino acids 810 to 1248 of SEQ ID NO: 23, such as at least 91.0%, at least 93.0%, at least 95.0%, at least 97.0%, at least 98.0%, at least 99.0%, at least 99.2%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.8% or at least 99.9% identity over its entire length to amino acids 810 to 1248 of SEQ ID NO: 23.

In an embodiment, the immunogen(s) expressed by the vectors of the invention comprise, or alternatively consist of, a CHIKV structural polyprotein, or a fragment thereof (suitably a fragment of at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350 or at least 400, at least 450, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1100 or at least 1200 amino acids). As used herein, a "CHIKV structural polyprotein" is intended to mean a protein having a polypeptide sequence corresponding to amino acids 1 to 1248 of SEQ ID NO: 23, or a protein having at least 90% sequence identity to amino acids 1 to 1248 of SEQ ID NO: 23, such as at least 91.0%, at least 93.0%, at least 95.0%, at least 97.0%, at least 98.0%, at least 99.0%, at least 99.2%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.8% or at least 99.9% identity over its entire length to amino acids 1 to 1248 of SEQ ID NO: 23.

Alternatively or in addition, a transgene sequence may include 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.

In addition to the transgene, the expression cassette also may include conventional control elements which are operably linked to the transgene in a manner that permits its transcription, translation and/or expression in a cell transfected with the adenoviral vector. 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 (poly A) signals including rabbit beta-globin polyA; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (*e.g.*, Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. Among other sequences, chimeric introns may be used.

A "promoter" is a nucleotide sequence that permits binding of RNA polymerase and directs the transcription of a gene. Typically, a promoter is located in the 5' non-coding region of a gene, proximal to the transcriptional start site of the gene. Sequence elements within promoters that function in the initiation of transcription are often characterized by consensus nucleotide sequences. Examples of promoters include, but are not limited to, promoters from bacteria, yeast, plants, viruses, and mammals (including humans). A great number of expression control sequences, including promoters which are internal, native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

Examples of constitutive promoters include, without limitation, the TBG promoter, the retroviral Rous sarcoma virus LTR promoter (optionally with the enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer, see, *e.g.*, Boshart et al, Cell, 41:521-530 (1985)), the CASI promoter (WO2012/115980), the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1a 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. For example, inducible promoters include the zinc-inducible sheep metallothionine (MT) promoter and the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter. Other inducible systems include the T7 polymerase promoter system; the ecdysone insect promoter, the tetracycline-repressible system and the tetracycline-inducible system. Other systems include the FK506 dimer, VP16 or p65 using castradiol, diphenol murislerone, the RU486-inducible system and the rapamycin-inducible system. The effectiveness of some inducible promoters increases over time. In such cases one can enhance the effectiveness of such systems by inserting multiple repressors in tandem, *e.g.*, TetR linked to a TetR by an IRES.

In another embodiment, the native promoter for the transgene may 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.

The transgene may be 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. Examples of promoters that are tissue-specific

are known for liver; hepatitis B virus core; alpha-fetoprotein, bone osteocalcin; bone sialoprotein, lymphocytes, immunoglobulin heavy chain; T cell receptor chain), neuronal such as neuron-specific enolase (NSE) promoter, neurofilament light-chain gene, and the neuron-specific vgf gene, among others.

In some embodiments, the Woodchuck Hepatitis Virus Posttranscriptional Regulatory Element (WPRE) (Zuffrey *et al.* (1999) J. Virol.; 73(4):2886-9) may be operably linked to the transgene.

Suitably, the adenovirus according to the invention has a seroprevalence of less than 10% in human subjects and preferably no seroprevalence in human subjects.

Suitably, the adenovirus according to the invention is capable of infecting a mammalian cell.

The transgene may be used for treatment, e.g., as a vaccine, for induction of an immune response, and/or for prophylactic vaccine purposes. As used herein, induction of an immune response refers to the ability of a protein to induce a T cell and/or a humoral immune response to the protein.

Immune responses can be measured by methods known in the art, including assays of the induction of proliferation or effector function of the particular lymphocyte type of interest, e.g., B cells, T cells, T cell lines, and T cell clones. For example, spleen cells from immunized mice can be isolated and the capacity of cytotoxic T lymphocytes to lyse autologous target cells that contain a self-replicating RNA molecule that encodes a CHIKV antigen. In addition, T helper cell differentiation can be analyzed by measuring proliferation or production of TH1 (IL-2 and IFN-γ) and /or TH2 (IL-4 and IL-5) cytokines by ELISA or directly in CD4+ T cells by cytoplasmic cytokine staining and flow cytometry.

Adenoviral vector construction

Adenoviral vectors are generated by modifying wild type adenovirus to express heterologous genes and/or delete or inactivate undesirable adenoviral sequences. Adenoviral vectors may also have altered replication competency. For example the vector may be replication defective or have limited replication such that it has a reduced ability to replicate in non-complementing cells, compared to the wild type virus. This may be brought about by mutating the virus *e.g.*, by deleting a gene involved in replication, for example deleting the adenoviral E1A, E1B, E3 or E4 gene.

The adenoviral vectors in accordance with the present invention may comprise a functional E1 deletion. Thus the adenoviral vectors according to the invention may be replication defective due to the absence of the ability to express adenoviral E1A and/or E1B. The recombinant adenoviruses may also bear functional deletions in other genes for example, deletions in E3 or E4 genes. The adenovirus delayed early gene E3 may be eliminated from the adenovirus sequence which forms part of the recombinant virus. The function of E3 is not necessary to the production of the recombinant adenovirus particle. Thus, it is unnecessary to replace the function of this gene product in order to package a recombinant adenovirus useful in the invention. In one particular embodiment the recombinant adenoviruses have functionally deleted E1 and E3 genes. The construction of such vectors is described in Roy *et al.*, Human Gene Therapy 15:519-530, 2004.

Recombinant adenoviruses may also be constructed having a functional deletion of the E4 gene. In a particular embodiment, the recombinant adenoviruses have functionally deleted E1 and E4 genes as described in Colloca *et al.* (2012) Sci. Transl. Med. 4:1-9; Roy *et al.* (2004) Virol.324: 361-372. In some embodiments, it may be desirable to retain the E4 ORF6 function. In one embodiment, the E4 ORF6 region may be replaced by a heterologous E4 ORF6, such as from human adenovirus 5 (Ad5). Thus, in one particular embodiment, the adenoviral vector may be functionally deleted in E1 and have the E4 ORF6 region from Ad5. Adenovirus vectors according to the invention may also contain a functional deletion in the delayed early gene E2a. Deletions may also be made in any of the late genes L1 through to L5 of the adenovirus genome. Similarly, deletions in the intermediate genes IX and IVa may be useful.

Other deletions may be made in the other structural or non-structural adenovirus genes. The above deletions may be used individually, *e.g.* an adenovirus sequence for use in the present invention may contain deletions of E1 only. Alternatively, deletions of entire genes or portions thereof effective to destroy their biological activity may be used in any combination. For example in one exemplary vector, the adenovirus sequences may have deletions of the E1 genes and the E4 gene, or of the E1, E2a and E3 genes, or of the E1 and E3 genes (such as functional deletions in E1a and E1b, and a deletion of at least part of E3), or of the E1, E2a and E4 genes, with or without deletion of E3 and so on. Such deletions may be partial or full deletions of these genes and may be used in combination with other mutations, such as temperature sensitive mutations to achieve a desired result.

These vectors are generated using techniques known to those of skill in the art. Such techniques include conventional cDNA cloning techniques such as those described in texts, the use of overlapping oligonucleotide sequences of the adenovirus genomes, polymerase chain reaction, and any suitable method which provides the desired nucleotide sequence. Particularly suitable methods include standard homologous recombination methods such as those provided in Colloca *et al.* (2012) Sci. Transl. Med. 4:1-9; Roy *et al.* (2004) Virol.324: 361-372; Roy *et al.* (2010) J. of Gene Med. 13:17-25; and WO2010/085984 or recombineering methods as described in Warming *et al.* Nuc. Acids Res. (2005) 33:e36.

In one embodiment of the adenovirus according to the invention, the polynucleotide comprises at least one of the following:

(a) an adenoviral 5'-end, preferably an adenoviral 5' inverted terminal repeat;

(b) an adenoviral E1A region, or a fragment thereof selected from among the E1A_280R and E1A_243R regions;

(c) an adenoviral E1B or IX region, or a fragment thereof selected from among the group consisting of the E1B_19K, E1B_55K or IX regions;

(d) an adenoviral E2b region; or a fragment thereof selected from among the group consisting of the E2B_pTP, E2B_Polymerase and E2B_IVa2 regions;

(e) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1_13.6k protein, L1_52k and L1_IIIa protein;

(f) an adenoviral L2 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2_penton protein, L2_pVII, L2_V, and L2_pX protein;

(g) an adenoviral L3 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L3_pVI protein, L3_hexon protein and L3_protease;

(h) an adenoviral E2A region;

(i) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4_100k protein, the L4_33k protein and protein L4_VIII;

(j) an adenoviral E3 region, or a fragment thereof selected from the group consisting of E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, and E3 ORF9;

(k) an adenoviral L5 region, or a fragment thereof said fragment encoding the L5_fiber fiber protein;

(l) an adenoviral E4 region, or a fragment thereof selected from the group consisting of E4 ORF7, E4 ORF6, E4 ORF4, E4 ORF3, E4 ORF2, and E4 ORF1;

(m) an adenoviral 3'-end, preferably an adenoviral 3' inverted terminal repeat; and

(n) an adenoviral VAI or VAII RNA region, preferably an adenoviral VAI or VAII RNA region from an adenovirus other than ChAd155, more preferably from Ad5.

Suitably, the polynucleotide comprises at least one of the following:

(a) an adenoviral 5'-end, preferably an adenoviral 5' inverted terminal repeat;

(b) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1_13.6k protein, L1_52k and L1_IIIa protein;

(c) an adenoviral L2 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2_penton protein, L2_pVII, L2_V, and L2_pX protein;

(d) an adenoviral L3 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L3_pVI protein, L3_hexon hexon protein and L3_protease;

(e) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4_100k protein, the L4_33k protein and protein L4_VIII;

(f) an adenoviral L5 region, or a fragment thereof said fragment encoding the L5_fiber fiber protein; and

(g) an adenoviral 3'-end, preferably an adenoviral 3' inverted terminal repeat.

Alternatively, the polynucleotide comprises an adenoviral VAI or VAII RNA region. Suitably the VAI or VAII RNA region is from an adenovirus other than ChAd155. Alternatively, the VAI or VAII RNA region is from Ad5.

Adenoviral vector production

The adenoviral vectors can be produced in any suitable cell line in which the virus is capable of replication. In particular, complementing cell lines which provide the factors missing from the viral vector that result in its impaired replication characteristics (such as E1) can be used.

Without limitation, such a cell line may be HeLa (ATCC Accession No. CCL 2), A549 (ATCC Accession No. CCL 185), HEK 293, KB (CCL 17), Detroit (*e.g.*, Detroit 510, CCL 72) and WI-38 (CCL 75) cells, among others. These cell lines are all available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. Other suitable parent cell lines may be obtained from other sources, such as PGK-E1 retinoblasts, e.g., PER.C6™ cells, as represented by the cells deposited under ECACC no. 96022940 at the European Collection of Animal Cell Cultures (ECACC) at the Centre for Applied Microbiology and Research (CAMR, UK) or Her 96 cells (Crucell).

In many circumstances, a cell line expressing the one or more missing genes which are essential to the replication and infectivity of the virus, such as human E1, can be used to transcomplement a chimp adenoviral vector. This is particularly advantageous because, due to the diversity between the chimp adenovirus sequences of the invention and the human adenovirus sequences found in currently available packaging cells, the use of the current human E1-containing cells prevents the generation of replication-competent adenoviruses during the replication and production process.

Alternatively, if desired, one may utilize the sequences provided herein to generate a packaging cell or cell line that expresses, at a minimum, the E1 gene from ChAd155 under the transcriptional control of a promoter for expression in a selected parent cell line. Inducible or constitutive promoters may be employed for this purpose. Examples of such promoters are described in detail elsewhere in this document. A parent cell is selected for the generation of a novel cell line expressing any desired ChAd155 gene. Without limitation, such a parent cell line may be HeLa [ATCC Accession No. CCL 2], A549 [ATCC Accession No. CCL 185], HEK 293, KB [CCL 17], Detroit [e.g., Detroit 510, CCL 72] and WI-38 [CCL 75] cells, among others. These cell lines are all available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, USA.

Such E1-expressing cell lines are useful in the generation of recombinant adenovirus E1 deleted vectors. Additionally, or alternatively, cell lines that express one or more adenoviral gene products, e.g., E1A, E1B, E2A, E3 and/or E4, can be constructed using essentially the same procedures as used in the generation of recombinant viral vectors. Such cell lines can be utilised to transcomplement adenovirus vectors deleted in the essential genes that encode those products, or to provide helper functions necessary for packaging of a helper-dependent virus (e.g., adeno-associated virus). The preparation of a host cell involves techniques such as the assembly of selected DNA sequences.

In an embodiment, the essential adenoviral gene products are provided in *trans* by the adenoviral vector and/or helper virus. In such an instance, a suitable host cell can be selected from any biological organism, including prokaryotic (e.g., bacterial) cells, and eukaryotic cells, including insect cells, yeast cells and mammalian cells.

Host cells may be selected from among any mammalian species, including, without limitation, cells such as A549, WEHI, 3T3, 10T1/2, HEK 293 cells or Per.C6 (the latter two of 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.

A particularly suitable complementation cell line is the Procell92 cell line. The Procell92 cell line is based on HEK 293 cells which express adenoviral E1 genes, transfected with the Tet repressor under control of the human phosphoglycerate kinase-1 (PGK) promoter, and the G418-resistance gene (Vitelli *et al.* PLOS One (2013) 8(e55435):1-9). Procell92.S is adapted for growth in suspension conditions and is also useful for producing adenoviral vectors expressing toxic proteins (www.okairos.com/e/inners.php?m=00084, last accessed 29 June 2017).

Adenoviral delivery methods and dosage

The adenoviral vectors may be as administered in immunogenic compositions. An immunogenic composition as described herein is a composition comprising one or more recombinant vectors capable of inducing an immune response, for example a humoral (*e.g.*, antibody) and/or cell-mediated (*e.g.*, a cytotoxic T cell) response, against a transgene product delivered by the vector following delivery to a mammal, suitably a human. A recombinant adenovirus may comprise (suitably in any of its gene deletions) a gene encoding a desired immunogen and may therefore be used in a vaccine. The recombinant adenoviruses can be used as prophylactic or therapeutic vaccines against any pathogen for which the antigen(s) crucial for induction of an immune response, is able to limit the spread of the pathogen and for which cDNA is available.

Such vaccine or other immunogenic compositions may be formulated in a suitable delivery vehicle. The levels of immunity of the selected gene can be monitored to determine the need, if any, for boosters. Following an assessment of antibody titers in the serum, optional booster immunizations may be desired.

Optionally, a vaccine or immunogenic composition of the invention may be formulated to contain other components, including, *e.g.*, adjuvants, stabilizers, pH adjusters, preservatives and the like. Examples of suitable adjuvants are provided below under "Adjuvants." Such an adjuvant can be administered with a priming DNA vaccine encoding an antigen to enhance the antigen-specific immune response compared with the immune response generated upon priming with a DNA vaccine encoding the antigen only. Alternatively, such an adjuvant can be administered with a polypeptide antigen which is administered in an administration regimen involving the vectors of the invention.

The adenoviral vector may be prepared for administration by being suspended or dissolved in a pharmaceutically or physiologically acceptable carrier such as isotonic saline, isotonic salt, solution or other formulations that will be apparent to those skilled in the art. 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 described herein may be administered to a mammal in a sustained release formulation using a biodegradable biocompatible polymer, or by on-site delivery using micelles, gels and liposomes.

In some embodiments, the recombinant adenovirus of the invention is administered to a subject by intramuscular injection, intravenous injection, intraperitoneal injection, subcutaneous injection, epicutaneous administration, intradermal administration, transdermal administration, intravaginal administration nasal administration, rectal administration or oral administration.

If the therapeutic regimen involves co-administration of one or more adenoviral vectors and a further component, each formulated in different compositions, they are favorably administered co-locationally at or near the same site. For example, the components can be administered (*e.g.* via an administration route selected from intramuscular, transdermal, intradermal, sub-cutaneous) to the same side or extremity ("co-lateral" administration) or to opposite sides or extremities ("contra-lateral" administration).

Dosages of the viral vector will depend primarily on factors such as the condition being treated, the severity of the condition being treated and the age, weight and health of the patient, thus may vary among patients. For example, a therapeutically effective adult human dosage of the viral vector generally contains $1x10^5$ to $1x10^{15}$ viral particles, such as from $1x10^8$ to $1x10^{12}$ (*e.g.*, $1x10^8$, $5x10^8$, $1x10^9$, $5x10^9$, $1x10^{10}$, $2.5x10^{10}$, $5x10^{10}$, $1x10^{11}$ $5x10^{11}$ or

$1x10^{12}$ particles). Alternatively, a viral vector can be administered at a dose that is typically from $1x10^5$ to $1x10^{10}$ plaque forming units (PFU), such as $1x10^5$ PFU, $5x10^5$ PFU, $1x10^6$ PFU, $5x10^6$ PFU, $1x10^7$ PFU, $5x10^7$ PFU, $1x10^8$ PFU, $5x10^8$ PFU, $1x10^9$ PFU, $5x10^9$ PFU, or $1x10^{10}$ PFU. Dosages will vary depending upon the size of the subject and the route of administration. For example, a suitable human dosage (for about an 80 kg subject) for intramuscular injection is in the range of about $1x10^5$ to about $5x10^{12}$ particles per ml, for a single site. Optionally, multiple sites of administration may be used. In another example, a suitable human or veterinary dosage may be in the range of about $1x10^7$ to about $1x10^{15}$ particles for an oral formulation.

The adenoviral vector can be quantified by Quantitative PCR Analysis (Q-PCR), for example with primers and probes designed based on the CMV promoter region, using as the standard curve serial dilutions of plasmid DNA containing the vector genome with the expression cassette, including the human CMV (hCMV) promoter. The copy number in the test sample is determined by the parallel line analysis method. Alternative methods for vector particle quantification include analytical HPLC or spectrophotometric methods based on A_{260} nm.

An immunologically effective amount of a nucleic acid may suitably be between 1 ng and 100 mg. For example, a suitable amount can be from 1 µg to 100 mg. An appropriate amount of the particular nucleic acid (*e.g.*, vector) can readily be determined by those of skill in the art.

Exemplary effective amounts of a nucleic acid component can be between 1 ng and 100 µg, such as between 1 ng and 1 µg (*e.g.*, 100 ng-1 µg), or between1 µg and 100 µg, such as 10 ng, 50 ng, 100 ng, 150 ng, 200 ng, 250 ng, 500 ng, 750 ng, or 1 µg. Effective amounts of a nucleic acid can also include from 1 µg to 500 µg, such as between 1 µg and 200 µg, such as between 10 and 100 µg, for example 1 µg, 2 µg, 5 µg, 10 µg, 20 µg, 50 µg, 75 µg, 100 µg, 150 µg, or 200 µg. Alternatively, an exemplary effective amount of a nucleic acid can be between 100 µg and 1 mg, such as from 100 µg to 500 µg, for example, 100 µg, 150 µg, 200 µg, 250 µg, 300 µg, 400 µg, 500 µg, 600 µg, 700 µg, 800 µg, 900 µg or 1 mg.

Generally a human dose will be in a volume of between 0.1 ml and 2ml, such as 0.5 ml and 2 ml. Thus the composition described herein can be formulated in a volume of, for example 0.1, 0.25, 0.5, 1.0, 1.5 or 2.0 ml human dose per individual or combined immunogenic components.

One of skill in the art may adjust these doses, depending on the route of administration and the therapeutic or vaccine application for which the recombinant vector is employed. The levels of expression of the transgene, or for an adjuvant, the level of circulating antibody, can be monitored to determine the frequency of dosage administration.

If one or more priming and/or boosting steps are used, this step may include a single dose that is administered hourly, daily, weekly or monthly, or yearly. As an example, mammals may receive one or two doses containing between about 10 µg to about 50 µg of plasmid in carrier. The amount or site of delivery is desirably selected based upon the identity and condition of the mammal.

The therapeutic level of, or the level of immune response against, the protein encoded by the selected transgene can be monitored to determine the need, if any, for boosters. Following an assessment of CD8+ T cell response, or optionally, antibody titers, in the serum, optional booster immunizations may be desired. Optionally, the adenoviral vector may be delivered in a single administration or in various combination regimens, *e.g.*, in combination with a regimen or course of treatment involving other active ingredients or in a prime-boost regimen.

Recombinant adenoviruses or compositions comprising polypeptide sequences

Suitably the polynucleotides of the invention are recombinant. Recombinant means that the polynucleotide is the product of at least one of cloning, restriction or ligation steps, or other procedures that result in a polynucleotide that is distinct from a polynucleotide found in nature. A recombinant adenovirus is an adenovirus comprising a recombinant polynucleotide. A recombinant vector is a vector comprising a recombinant polynucleotide. A “recombinant virus” includes progeny of the original recombinant virus. A “recombinant vector” includes replicates of the original recombinant vector. A “recombinant polynucleotide” includes replicates of the original recombinant polynucleotide.

A "functional derivative" of a polypeptide suitably refers to a modified version of a polypeptide, e.g. wherein one or more amino acids of the polypeptide may be deleted, inserted, modified and/or substituted. A derivative of an unmodified adenoviral capsid protein is considered functional if, for example:

(a) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a lower seroprevalence compared to an adenovirus comprising the unmodified capsid protein and/or

(b) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a higher host cell infectivity compared to an adenovirus comprising the unmodified capsid protein and/or

(c) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a higher immunogenicity compared to an adenovirus comprising the unmodified capsid protein and/or

(d) an adenovirus comprising the derivative capsid protein within its capsid retains substantially the same or a higher level of transgene productivity compared to an adenovirus comprising the unmodified capsid protein.

Suitably the recombinant adenovirus or composition of the invention comprises a polypeptide having the amino acid sequence according to SEQ ID NO: 1. Suitably the recombinant adenovirus or composition of the invention comprises a polypeptide which is a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1. Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1 has an amino acid sequence which is at least 80% identical, such as at least 85.0% identical, such as at least 90% identical, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0% identical, such as at least 99.2% identical, such as at least 99.4% identical, such as 99.5% identical, such as at least 99.6% identical, such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 1. Alternatively the functional derivative has no more than 130, more suitably no more than 120, more suitably no more than 110, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 1.

Suitably the recombinant adenovirus or composition according to the invention further comprises:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3; or
(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 50.0% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,

and/or

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5; or
(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 50% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3 has an amino acid sequence which is at least 60.0%, such as at least 70.0%, such as at least 80.0%, such as at least 85.0%, such as at least 90.0%, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0%, such as at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as 99.7% identical such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 3. Alternatively the functional derivative has no more than 300, more suitably no more than 250, more suitably no more than 200, more suitably no more than 150, more suitably no more than 125, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 3.

Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5 has an amino acid sequence which is at least 60.0%, such as at least 70.0%, such as at least 80.0%, such as at least 85.0%, such as at least 90.0%, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0%, such as

at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as 99.7% identical such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 5. Alternatively the functional derivative has no more than 500, more suitably no more than 400, more suitably no more than 450, more suitably no more than 300, more suitably no more than 250, more suitably no more than 200, more suitably no more than 150, more suitably no more than 125, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 5.

Suitably the recombinant adenovirus or composition of the invention comprises a polypeptide having the amino acid sequence according to SEQ ID NO: 3.

Suitably the recombinant adenovirus or composition of the invention further comprises:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1; or

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1

and/or

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5; or

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 60% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1 has an amino acid sequence which is at least 60.0% identical, such as at least 70.0% identical, such as at least 80.0% identical, such as at least 85.0% identical, such as at least 87.0% identical, such as at least 89.0% identical, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0% identical, such as at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as at

least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 1. Alternatively the functional derivative has no more than 130, more suitably no more than 120, more suitably no more than 110, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 1.

Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5 has an amino acid sequence which is at least 60.0%, such as at least 70.0%, such as at least 80.0%, such as at least 85.0%, such as at least 90.0%, such as at least 95.0%, such as at least 97.0%, such as at least 99.0%, such as at least 99.0%, such as at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO:5. Alternatively the functional derivative has no more than 500, more suitably no more than 400, more suitably no more than 450, more suitably no more than 300, more suitably no more than 250, more suitably no more than 200, more suitably no more than 150, more suitably no more than 125, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 5.

Suitably the recombinant adenovirus or composition of the invention comprises a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1. Suitably the polynucleotide has a sequence according to SEQ ID NO: 2.

Alternatively, the recombinant adenovirus or composition of the invention comprises a polynucleotide which encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80% identical over its entire length to the amino acid sequence of SEQ ID NO: 1. Suitably the functional derivative of a polypeptide having the amino acid

sequence according to SEQ ID NO: 1 has an amino acid sequence which is at least 80% identical, such as at least 85.0% identical, such as at least 90% identical, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0% identical, such as at least 99% identical, such as at least 99.4% identical, such as at least 99.6% identical or such as at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 1. Alternatively the functional derivative has no more than 130, more suitably no more than 120, more suitably no more than 110, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 1.

Suitably the recombinant adenovirus or composition of the invention further comprises a polynucleotide encoding:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 3; or
(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 50.0% identical over its entire length to the amino acid sequence of SEQ ID NO: 3,

and/or

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5; or
(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 50% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

Suitably the functional derivative of the polypeptide having the amino acid sequence according to SEQ ID NO: 3 has an amino acid sequence which is at least 60.0%, such as at least 70.0%, such as at least 80.0%, such as at least 85.0%, such as at least 90.0%, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0%, such as at least 99%, such as at least 99.4%, such as at least 99.6%, such as at least 99.8% identical over its entire length to the amino acid sequence of SEQ ID NO: 3.

Alternatively the functional derivative has no more than 300, more suitably no more than 250, more suitably no more than 200, more suitably no more than 150, more suitably no more than 125, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 3.

Suitably the functional derivative of the polypeptide having the amino acid sequence according to SEQ ID NO: 5 has an amino acid sequence which is at least 60.0%, such as at least 70.0%, such as at least 80.0%, such as at least 85.0%, such as at least 90.0%, such as at least 95.0%, such as at least 97.0%, such as at least 98.0%, such as at least 99.0%, such as at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as 99.7% identical such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 5. Alternatively the functional derivative has no more than 500, more suitably no more than 400, more suitably no more than 450, more suitably no more than 300, more suitably no more than 250, more suitably no more than 200, more suitably no more than 150, more suitably no more than 125, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 5.

Suitably the recombinant adenovirus or composition of the invention comprises a polynucleotide which encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3. Suitably the polynucleotide has a sequence according to SEQ ID NO: 4.

Suitably the recombinant adenovirus or composition of the invention further comprises a polynucleotide encoding:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1; or

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 50% identical over its entire length to the amino acid sequence of SEQ ID NO: 1

and/or

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 5; or

(b) a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 50% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1 has an amino acid sequence which is at least 60.0% identical, such as at least 70.0% identical, such as at least 80.0% identical, such as at least 85.0% identical, such as at least 87.0% identical, such as at least 89.0% identical, such as at least 91.0% identical, such as at least 93.0% identical, such as at least 95.0% identical, such as at least 97.0% identical, such as at least 98.0% identical, such as at least 99.0%, such as at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as 99.7% identical such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 1. Alternatively the functional derivative has no more than 130, more suitably no more than 120, more suitably no more than 110, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 1.

Suitably the functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5 has an amino acid sequence which is at least 60.0%, such as at least 70.0%, such as at least 80.0%, such as at least 85.0%, such as at least 90.0%, such as at least 95.0%, such as at least 97.0%, such as at least 98.0%, such as at least 99.0%, such as at least 99.2%, such as at least 99.4%, such as 99.5% identical, such as at least 99.6%, such as 99.7% identical such as at least 99.8% identical, such as 99.9% identical over its entire length to the amino acid sequence of SEQ ID NO: 5. Alternatively the functional derivative has no more than 500, more suitably no more than 400, more suitably no more

than 450, more suitably no more than 300, more suitably no more than 250, more suitably no more than 200, more suitably no more than 150, more suitably no more than 125, more suitably no more than 100, more suitably no more than 90, more suitably no more than 80, more suitably no more than 70, more suitably no more than 60, more suitably no more than 50, more suitably no more than 40, more suitably no more than 30, more suitably no more than 20, more suitably no more than 10, more suitably no more than 5, more suitably no more than 4, more suitably no more than 3, more suitably no more than 2 and more suitably no more than 1 addition(s), deletion(s) and/or substitutions(s) compared to SEQ ID NO: 5.

There is also provided a non-human simian adenovirus comprising the penton of SEQ ID NO: 3, the hexon of SEQ ID NO: 5 and/or the fiber of SEQ ID NO: 1 and also comprising a transgene encoding a *Chikungunya virus* antigen. Suitably, the non-human simian adenovirus comprises the penton (SEQ ID NO: 3), hexon (SEQ ID NO: 5) and fiber (SEQ ID NO: 1) protein from ChAd155 and also comprising a transgene encoding a *Chikungunya virus* antigen. Suitably, the encoded antigen comprises a sequence having at least 90% identity to SEQ ID NO: 23. Suitably, the non-human simian adenovirus is a replication deficient adenovirus. For example, the non-human simian adenovirus comprises a functional inactivation (such as deletion) of the E1 gene, a functional inactivation (such as deletion) of the E4 gene, a functional inactivation (such as deletion) of the E3 gene, and or an Ad5E4orf6 gene substitution.

There is also provided an adenovirus comprising a polynucleotide having a sequence at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length identical to SEQ ID NO: 24.

There is also provided an adenovirus comprising a polynucleotide having a sequence at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length identical to SEQ ID NO: 25.

ChAd155 Backbones

The present application describes isolated polynucleotide sequences of chimpanzee adenovirus ChAd155, including that of wild type, unmodified ChAd155 (SEQ ID NO: 10) and modified backbone constructs of ChAd155. These modified backbone constructs include ChAd155#1434 (SEQ ID NO: 7), ChAd155#1390 (SEQ ID NO: 8) and ChAd155#1375 (SEQ

ID NO: 9). ChAd155 backbones may be used in the construction of recombinant replication-competent or replication-incompetent adenoviruses for the delivery of transgenes.

The term “construct” refers to a nucleic acid that encodes polypeptide sequences described herein and may comprise DNA or non-naturally occurring nucleic acid monomers.

The term "replication-competent" adenovirus refers to an adenovirus which can replicate in a host cell in the absence of any recombinant helper proteins comprised in the cell. Suitably, a "replication-competent" adenovirus comprises the following intact or functional essential early genes: E1A, E1B, E2A, E2B, E3 and E4. Wild type adenoviruses isolated from a particular animal will be replication competent in that animal.

The sequences of the invention are useful as therapeutic and/or prophylactic agents and in construction of a variety of vector systems, recombinant adenovirus and host cells. Suitably the term “vector” refers to a nucleic acid that has been substantially altered (*e.g.*, a gene or functional region that has been deleted and/or inactivated) relative to a wild type sequence and/or incorporates a heterologous sequence, *i.e.*, nucleic acid obtained from a different source (also called an “insert”), and replicating and/or expressing the inserted polynucleotide sequence, when introduced into a cell (e.g., a host cell). For example, the insert may be all or part of the ChAd155 sequences described herein. In addition or alternatively, a ChAd155 vector may be a ChAd155 adenovirus comprising one or more deletions or inactivations of viral genes, such as E1 or other viral gene or functional region described herein. Such a ChAd155, which may or may not comprise a heterologous sequence, is often called a "backbone" and may be used as is or as a starting point for additional modifications to the vector.

The term "replication-incompetent" or “replication-defective” adenovirus refers to an adenovirus which is incapable of replication because it has been engineered to comprise at least a functional deletion (or “loss-of-function” mutation), i.e. a deletion or mutation which impairs the function of a gene without removing it entirely, e.g. introduction of artificial stop codons, deletion or mutation of active sites or interaction domains, mutation or deletion of a regulatory sequence of a gene etc., or a complete removal of a gene encoding a gene product that is essential for viral replication, such as one or more of the adenoviral genes selected from E1A, E1B, E2A, E2B, E3 and E4 (such as E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, E3 ORF9, E4 ORF7, E4 ORF6, E4 ORF4, E4 ORF3, E4 ORF2 and/or E4 ORF1). Particularly suitably E1, and optionally E3 and/or E4,

are deleted. If deleted, the aforementioned deleted gene region will suitably not be considered in the alignment when determining % identity with respect to another sequence.

Annotation of the ChAd155 wild type sequence (SEQ ID NO: 10) sequence is provided below.

```
     LOCUS       ChAd155                37830 bp    DNA     linear
10-JUN-2015
     DEFINITION  Chimp adenovirus 155, complete genome.
     COMMENT     Annotation according to alignment of ChAd155 against
the human
                 Adenovirus 2 reference strain NC_001405
                 Two putative ORFs in the E3 region added manually
     FEATURES             Location/Qualifiers
          source          1..37830
                          /organism="Chimpanzee adenovirus 155"
                          /mol_type="genomic DNA"
                          /acronym="ChAd155"
          repeat_region   1..101
                          /standard_name="ITR"
                          /rpt_type=inverted
          gene            466..1622
                          /gene="E1A"
          TATA_signal     466..471
                          /gene="E1A"
          prim_transcript 497..1622
                          /gene="E1A"
          CDS             join(577..1117,1231..1532)
                          /gene="E1A"
                          /product="E1A_280R"
          CDS             join(577..979,1231..1532)
                          /gene="E1A"
                          /product="E1A_243R"
          polyA_signal    1600..1605
                          /gene="E1A"
          gene            1662..4131
                          /gene="E1B"
          TATA_signal     1662..1667
```

```
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     prim_transcript 1692..4131
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     CDS            1704..2267
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                    /product="E1B_19K"
     CDS            2009..3532
                    /gene="E1B"
                    /product="E1B_55K"
     gene           3571..4131
                    /gene="IX"
     TATA_signal    3571..3576
                    /gene="IX"
     prim_transcript 3601..4131
                    /gene="IX"
     CDS            3628..4092
                    /gene="IX"
                    /product="IX"
     polyA_signal   4097..4102
                    /note="E1B, IX"
     gene           complement(4117..27523)
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     prim_transcript complement(4117..27494)
                    /gene="E2B"
     gene           complement(4117..5896)
                    /gene="IVa2"
     prim_transcript complement(4117..5896)
                    /gene="IVa2"
     CDS            complement(join(4151..5487,5766..5778))
                    /gene="IVa2"
                    /product="E2B_IVa2"
     polyA_signal   complement(4150..4155)
                    /note="IVa2, E2B"
     CDS            complement(join(5257..8838,14209..14217))
                    /gene="E2B"
                    /product="E2B_polymerase"
     gene           6078..34605
                    /gene="L5"
```

```
gene            6078..28612
                /gene="L4"
gene            6078..22658
                /gene="L3"
gene            6078..18164
                /gene="L2"
gene            6078..14216
                /gene="L1"
TATA_signal     6078..6083
                /note="L"
prim_transcript 6109..34605
                /gene="L5"
prim_transcript 6109..28612
                /gene="L4"
prim_transcript 6109..22658
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prim_transcript 6109..18164
                /gene="L2"
prim_transcript 6109..14216
                /gene="L1"
CDS             join(8038..8457,9722..9742)
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                /product="L1_13.6K"
CDS             complement(join(8637..10640,14209..14217))
                /gene="E2B"
                /product="E2B_pTP"
gene            10671..10832
                /gene="VAI"
misc_RNA        10671..10832
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gene            10902..11072
                /gene="VAII"
misc_RNA        10902..11072
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CDS             11093..12352
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     CDS            12376..14157
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                    /product="L1_pIIIa"
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     CDS            14254..16035
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     CDS            16050..16646
                    /gene="L2"
                    /product="L2_pVII"
     CDS            16719..17834
                    /gene="L2"
                    /product="L2_V"
     CDS            17859..18104
                    /gene="L2"
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     polyA_signal   18143..18148
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     CDS            18196..18951
                    /gene="L3"
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     CDS            19063..21945
                    /gene="L3"
                    /product="L3_hexon"
     CDS            21975..22604
                    /gene="L3"
                    /product="L3_protease"
     polyA_signal   22630..22635
                    /gene="L3"
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     prim_transcript complement(22632..27494)
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     gene           complement(22632..26357)
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     prim_transcript complement(22632..26328)
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polyA_signal        complement(22649..22654)
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CDS                 complement(22715..24367)
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                    /note="DBP; genus-common; DBP family"
                    /codon_start=1
                    /product="E2A"
CDS                 24405..26915
                    /gene="L4"
                    /product="L4_100k"
TATA_signal         complement(26352..26357)
                    /gene="E2A-L"
CDS                 join(26602..26941,27147..27529)
                    /gene="L4"
                    /product="L4_33K"
CDS                 26602..27207
                    /gene="L4"
                    /product="L4_22K"
TATA_signal         complement(27518..27523)
                    /note="E2A, E2B; nominal"
CDS                 27604..28287
                    /gene="L4"
                    /product="L4_pVIII"
gene                27969..32686
                    /gene="E3B"
gene                27969..31611
                    /gene="E3A"
TATA_signal         27969..27974
                    /note="E3A, E3B"
prim_transcript     27998..32686
                    /gene="E3B"
prim_transcript     27998..31611
                    /gene="E3A"
CDS                 28288..28605
                    /gene="E3A"
                    /product="E3 ORF1"
polyA_signal        28594..28599
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                        /gene="E3A"
                        /product="E3 ORF2"
             CDS        29300..29797
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                        /product="E3 ORF3"
             CDS        29826..30731
                        /gene="E3A"
                        /product="E3 ORF4"
             CDS        30728..31579
                        /gene="E3A"
                        /product="E3 ORF5"
             CDS        31283..31579
                        /gene="E3A"
                        /product="E3 ORF6"
             polyA_signal 31578..31584
                        /gene="E3A"
             CDS        31591..31863
                        /gene="E3B"
                        /product="E3 ORF7"
             CDS        31866..32264
                        /gene="E3B"
                        /product="E3 ORF8"
             CDS        32257..32643
                        /gene="E3B"
                        /product="E3 ORF9"
             polyA_signal 32659..32664
                        /gene="E3B"
             gene       complement(<32678..32838)
                        /gene="U"
             CDS        complement(<32678..32838)
                        /gene="U"
                        /note="exon    encoding    C    terminus
unidentified;
                        genus-common"
                        /product="protein U"
             CDS        32849..34585
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```
                    /gene="L5"
                    /product="L5_fiber"
     polyA_signal   34581..34586
                    /gene="L5"
     gene           complement(34611..37520)
                    /gene="E4"
     prim_transcript complement(34611..37490)
                    /gene="E4"
     polyA_signal   complement(34625..34630)
                    /gene="E4"
     CDS            complement(join(34794..35069,35781..35954))
                    /gene="E4"
                    /product="E4 ORF7"
     CDS            complement(35070..35954)
                    /gene="E4"
                    /product="E4 ORF6"
     CDS            complement(35875..36219)
                    /gene="E4"
                    /product="E4 ORF4"
     CDS            complement(36235..36582)
                    /gene="E4"
                    /product="E4 ORF3"
     CDS            complement(36579..36971)
                    /gene="E4"
                    /product="E4 ORF2"
     CDS            complement(37029..37415)
                    /gene="E4"
                    /product="E4 ORF1"
     TATA_signal    complement(37515..37520)
                    /gene="E4"
     repeat_region  37740..37830
                    /standard_name="ITR"
                    /rpt_type=inverted
```

Sequence identity

Identity with respect to a sequence is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the reference amino acid sequence after aligning the sequences and introducing gaps, if necessary, to achieve the

maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity.

Sequence identity can be determined by standard methods that are commonly used to compare the similarity in position of the amino acids of two polypeptides. Using a computer program such as BLAST or FASTA, two polypeptides are aligned for optimal matching of their respective amino acids (either along the full length of one or both sequences or along a pre-determined portion of one or both sequences). The programs provide a default opening penalty and a default gap penalty, and a scoring matrix such as PAM 250 (a standard scoring matrix can be used in conjunction with the computer program. For example, the percent identity can then be calculated as the total number of identical matches multiplied by 100 and then divided by the sum of the length of the longer sequence within the matched span and the number of gaps introduced into the shorter sequences in order to align the two sequences.

Where the present disclosure refers to a sequence by reference to a UniProt or Genbank accession code, the sequence referred to is the current version as of the filing date of the present application.

The skilled person will recognise that individual substitutions, deletions or additions to a protein which alters, adds or deletes a single amino acid or a small percentage of amino acids is an “immunogenic derivative” where the alteration(s) results in the substitution of an amino acid with a functionally similar amino acid or the substitution/deletion/addition of residues which do not substantially impact the immunogenic function.

Conservative substitution tables providing functionally similar amino acids are well known in the art. In general, such conservative substitutions will fall within one of the amino-acid groupings specified below, though in some circumstances other substitutions may be possible without substantially affecting the immunogenic properties of the antigen. The following eight groups each contain amino acids that are typically conservative substitutions for one another:

1) Alanine (A), Glycine (G);
2) Aspartic acid (D), Glutamic acid (E);
3) Asparagine (N), Glutamine (Q);
4) Arginine (R), Lysine (K);
5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V);
6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W);

7) Serine (S), Threonine (T); and
8) Cysteine (C), Methionine (M).

Suitably such substitutions do not occur in the region of an epitope, and do not therefore have a significant impact on the immunogenic properties of the antigen.

Immunogenic derivatives may also include those wherein additional amino acids are inserted compared to the reference sequence. Suitably such insertions do not occur in the region of an epitope, and do not therefore have a significant impact on the immunogenic properties of the antigen. One example of insertions includes a short stretch of histidine residues (e.g. 2-6 residues) to aid expression and/or purification of the antigen in question.

Immunogenic derivatives include those wherein amino acids have been deleted compared to the reference sequence. Suitably such deletions do not occur in the region of an epitope, and do not therefore have a significant impact on the immunogenic properties of the antigen. The skilled person will recognise that a particular immunogenic derivative may comprise substitutions, deletions and additions (or any combination thereof).

Adjuvants

An “adjuvant” as used herein refers to a composition that enhances the immune response to an immunogen. A composition according to the invention that comprises an adjuvant can be used as a vaccine, e.g. for human subjects. The adjuvant accelerates, prolongs and/or enhances the quality and/or strength of an immune response to an antigen/immunogen in comparison to the administration of the antigen alone, thus, reduces the quantity of antigen/immunogen necessary in any given vaccine, and/or the frequency of injection necessary in order to generate an adequate immune response to the antigen/immunogen of interest.

Examples of adjuvants that may be used in the context of the compositions of the invention include inorganic adjuvants (e.g. inorganic metal salts such as aluminum phosphate or aluminum hydroxide), gel-like precipitates of aluminum hydroxide (alum); $AlPO_4$; alhydrogel; bacterial products from the outer membrane of Gram-negative bacteria, in particular monophosphoryl lipid A (MPLA), lipopolysaccharides (LPS), muramyl dipeptides and derivatives thereof; Freund’s incomplete adjuvant; liposomes, in particular neutral liposomes, liposomes containing the composition and optionally cytokines; AS01B, AS01E, AS02; non-ionic block copolymers; ISCOMATRIX adjuvant; unmethylated DNA comprising CpG

dinucleotides (CpG motif), in particular CpG ODN with a phosphorothioate (PTO) backbone (CpG PTO ODN) or phosphodiester (PO) backbone (CpG PO ODN); synthetic lipopeptide derivatives, in particular Pam_3Cys; lipoarabinomannan; peptidoglycan; zymosan; heat shock proteins (HSP), in particular HSP 70; dsRNA and synthetic derivatives thereof, in particular Poly I:poly C; polycationic peptides, in particular poly-L-arginine; taxol; fibronectin; flagellin; imidazoquinoline; cytokines with adjuvant activity, in particular GM-CSF, interleukin- (IL-)2, IL-6, IL-7, IL-18, type I and II interferons, in particular interferon-gamma, TNF-alpha; 25-dihydroxyvitamin D3 (calcitriol); and synthetic oligopeptides, in particular MHCII-presented peptides. Non-ionic block polymers containing polyoxyethylene (POE) and polyoxypropylene (POP), such as POE-POP-POE block copolymers may be used as an adjuvant.

Additional examples of adjuvants include inorganic adjuvants (e.g. inorganic metal salts such as aluminium phosphate or aluminium hydroxide), organic adjuvants (e.g. saponins, such as QS21, or squalene), oil-based adjuvants (e.g. Freund's complete adjuvant and Freund's incomplete adjuvant), cytokines (e.g. IL-1β, IL-2, IL-7, IL-12, IL-18, GM-CFS, and INF-γ) particulate adjuvants (e.g. immuno-stimulatory complexes (ISCOMS), liposomes, biodegradable microspheres, virosomes, bacterial adjuvants (e.g. monophosphoryl lipid A, such as 3-de-O-acylated monophosphoryl lipid A (3D-MPL), or muramyl peptides), synthetic adjuvants (e.g. monophosphoryl lipid A (MPL), in particular 3-de-O-acylated monophosphoryl lipid A (3D-MPL and muramyl peptide analogues, or synthetic lipid A, and synthetic polynucleotides adjuvants, e.g., polyarginine or polylysine.

Saponins are also suitable adjuvants, for example, the saponin Quil A, derived from the bark of the South American tree Quillaja Saponaria Molina, and fractions thereof. Purified fractions of Quil A are also known as immunostimulants, such as squalene, QS21, QS17 and QS7, a non-haemolytic fraction of Quil-A. Combinations of QS21 and polysorbate or cyclodextrin are also suitable.

Another example of an adjuvant is an immunostimulatory oligonucleotide containing unmethylated cytosine-guanosine dinucleotide motifs present in DNA ("CpG"). CpG is known as an adjuvant when administered by both systemic and mucosal routes. When formulated into vaccines, it may be administered in free solution together with free antigen or covalently conjugated to an antigen or formulated with a carrier such as aluminium hydroxide.

Activation of specific receptors can stimulate an immune response. Such receptors are known to the skilled artisan and comprise, for example, cytokine receptors, in particular type I cytokine receptors, type II cytokine receptors, TNF receptors; and a vitamin D receptor acting as transcription factor; and the Toll-like receptors 1 (TLR1), TLR-2, TLR 3, TLR4, TLR5, TLR-6, TLR7, and TLR9. Agonists to such receptors have adjuvant activity, i.e., are immunostimulatory. Other suitable adjuvants include alkyl glucosaminide phosphates (AGPs) or pharmaceutically acceptable salts of AGPs. Some AGPs are TLR4 agonists, and some are TLR4 antagonists. An adjuvant of the composition of the present invention may be one or more Toll-like receptor agonists. In a more preferred embodiment, the adjuvant is a Toll-like receptor 4 agonist. In a particular preferred embodiment, the adjuvant is a Toll-like receptor 9 agonist.

Adjuvants such as those described above may be formulated together with carriers, such as liposomes, oil in water emulsions, and/or metallic salts (including aluminum salts such as aluminum hydroxide). For example, 3D-MPL may be formulated with aluminum hydroxide or oil in water emulsions; QS21 may be formulated with cholesterol containing liposomes, oil in water emulsions or alum; CpG may be formulated with alum or with other cationic carriers.

Combinations of adjuvants may be utilized in the present invention, in particular a combination of a monophosphoryl lipid A and a saponin derivative, more particularly the combination of QS21 and 3D-MPL or a composition where the QS21 is quenched in cholesterol-containing liposomes (DQ). Alternatively, a combination of CpG plus a saponin such as QS21 is an adjuvant suitable for use in the present invention, as is a potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil in water emulsion. Saponin adjuvants may be formulated in a liposome and combined with an immunostimulatory oligonucleotide. Thus, suitable adjuvant systems include, for example, a combination of monophosphoryl lipid A, preferably 3D-MPL, together with an aluminium salt. A further exemplary adjuvant comprises QS21 and/or MPL and/or CpG. QS21 may be quenched in cholesterol-containing liposomes.

The fusion of the invariant chain to an antigen which is comprised by an expression system used for vaccination increases the immune response against said antigen, if it is administered with an adenovirus. Accordingly, in one embodiment of the invention, the immunogenic transgene may be co-expressed with invariant chain in a recombinant ChAd155 viral vector.

In another embodiment, the invention provides the use of the capsid of ChAd155 (optionally an intact or recombinant viral particle or an empty capsid is used) to induce an immunomodulatory response, or to enhance or adjuvant a cytotoxic T cell response to another active agent by delivering a ChAd155 capsid to a subject. The ChAd155 capsid can be delivered alone or in a combination regimen with an active agent to enhance the immune response thereto. Advantageously, the desired effect can be accomplished without infecting the host with an adenovirus.

DESCRIPTION OF THE SEQUENCES

SEQ ID NO: 1 - Polypeptide sequence of ChAd155 fiber

SEQ ID NO: 2 - Polynucleotide sequence encoding ChAd155 fiber

SEQ ID NO: 3 - Polypeptide sequence of ChAd155 penton

SEQ ID NO: 4 - Polynucleotide sequence encoding ChAd155 penton

SEQ ID NO: 5 - Polypeptide sequence of ChAd155 hexon

SEQ ID NO: 6 - Polynucleotide sequence encoding ChAd155 hexon

SEQ ID NO: 7 - Polynucleotide sequence encoding ChAd155#1434 backbone construct

SEQ ID NO: 8 - Polynucleotide sequence encoding ChAd155#1390 backbone construct

SEQ ID NO: 9 - Polynucleotide sequence encoding ChAd155#1375 backbone construct

SEQ ID NO: 10 -Polynucleotide sequence encoding wild type ChAd155

SEQ ID NO: 11 - ChAd3 fiber amino acid sequence

SEQ ID NO: 12- PanAd3 fiber amino acid sequence

SEQ ID NO: 13 - ChAd17 fiber amino acid sequence

SEQ ID NO: 14 - ChAd19 fiber amino acid sequence

SEQ ID NO: 15 - ChAd24 fiber amino acid sequence

SEQ ID NO: 16 - ChAd11 fiber amino acid sequence

SEQ ID NO: 17 - ChAd20 fiber amino acid sequence

SEQ ID NO: 18 - ChAd31 fiber amino acid sequence

SEQ ID NO: 19 - PanAd1 fiber amino acid sequence

SEQ ID NO: 20 - PanAd2 fiber amino acid sequence

SEQ ID NO: 21 - Nucleotide sequence for CHIKV structural polypeptide, strain #37997 (wild type, nts 7569-11315 of Genbank Accession No. EU224270)

SEQ ID NO: 22 - Nucleotide sequence for CHIKV structural polypeptide, strain #37997 (codon optimized)

SEQ ID NO: 23 - Amino acid sequence for CHIKV structural polypeptide, strain #37997

SEQ ID NO: 24 - Nucleotide sequence of plasmid pvjTetOhCMV CHIKV bghpolyA

SEQ ID NO: 25 - Nucleotide sequence of expression vector the pChAd155 ΔE1, ΔE4_Ad5 orf6 hCMV-CHIKV

General

Unless otherwise explained, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. The singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. The term "plurality" refers to two or more. Additionally, numerical limitations given with respect to concentrations or levels of a substance, such as solution component concentrations or ratios thereof, and reaction conditions such as temperatures, pressures and cycle times are intended to be approximate. The term “about” used herein is intended to mean the amount ±10%.

The invention will be further described by reference to the following, non-limiting, examples and figures.

EXAMPLES

Example 1: ChAd155-CHIKV Vector Construction

Wild type chimpanzee adenovirus type 155 (ChAd155) was isolated from a healthy young chimpanzee housed at the New Iberia Research Center facility (New Iberia Research Center, The University of Louisiana at Lafayette) using standard procedures as described in Colloca *et al.* (2012) Sci. Transl. Med. 4:1-9 and WO2010086189, the latter of which is hereby incorporated by reference for the purpose of describing adenoviral isolation and characterization techniques.

The ChAd155 viral genome was then cloned in a plasmid and subsequently modified as described in WO2016/198621 (which is hereby incorporated by reference for the purpose of describing adenoviral vector construction) and as shown in Figure 3:

a) deletion of the E1 region (from bp 449 to bp 3529) of the viral genome;

b) deletion of the E4 region (from bp 34731 to bp 37449) of the viral genome;

c) insertion of the E4orf6 derived from human Ad5; and

d) insertion of hCMV-CHIKV expression cassette.

The expression cassette encoding CHIKV antigens was inserted into the ChAd155#1434 expression vector (SEQ ID NO: 7) using methods described in WO2016/198621. Briefly, the wild type DNA encoding the CHIKV strain #37997 structural polyprotein (C-E3-E2-6K-E1, SEQ ID NO: 21) was codon optimized by GENEWIZ (Plainfield, NJ) to produce a coding sequence appropriate for expression in human cells. The codon optimized CHIKV coding sequence (SEQ ID NO: 22) was synthesized and cloned into plasmid pvjTetOhCMV-bghpolyA (Figure 4). Plasmid pvjTetOhCMV-bghpolyA contains the tetOhCMV promoter and bovine growth hormone poly-adenylation signal (BGH pA). The nucleic acid sequence of the resulting plasmid (pvjTetOhCMV CHIKV bghpolyA) is shown in SEQ ID NO: 24. The CHIKV expression cassette was then transferred into the ChAd155#1434 modified vector backbone (SEQ ID NO: 7) by homologous recombination in *E. coli* BJ5183 competent cells to produce the pChAd155 ΔE1, ΔE4_Ad5 orf6 hCMV-CHIKV vector. A diagram of the pChAd155 ΔE1, ΔE4_Ad5 orf6 hCMV-CHIKV vector is shown in Figure 5, and the nucleic acid sequence of the vector is shown in SEQ ID NO: 25. ChAd155-CHIKV vector construction was confirmed by transgene sequencing and restriction analysis.

Position 15,997 of SEQ ID NO: 25 can be any nucleotide (A, T, C, G). In a preferred embodiment, position 15,997 of SEQ ID NO: 25 is A.

Using these methods, CHIKV adenoviral vectors can be prepared using alternative modified ChAd155 backbones, including ChAd155#1390 (SEQ ID NO: 8) and ChAd#1375 (SEQ ID NO: 9).

Example 2: ChAd155-CHIKV Viral Particle Production

Recombinant chimp adenoviruses were generated by linearizing pChAd155 ΔE1-E4_Ad5 orf6 hCMV-CHIKV with the restriction endonuclease PmeI and transfecting the linear vectors into a HEK293-derived cell line (Procell92.S), as described in Vitelli et al., PLOS One (2013)

8(e55435):1-9. These cells are genetically modified to constitutively express the TetO repressor in order to repress transgene expression during virus generation. Two lots of the same CHAd155-CHIKV adenovirus construct were tested: CHIKV-1 and CHIKV-2. Viral amplification was performed at small scale (shake flask) and viruses were purified on double CsCl gradient from 1 liter scale suspension culture.

Purified viral particles were used to infect HeLa cells at Multiplicities of Infection (MOI) of 250, 500 and 1250 to determine the expression of the encoded transgene. Cell lysates and supernatants of infected cells were collected and analyzed by Western blot.

For Western analysis, a polyclonal antibody against the CHIKV structural polyprotein was generated by immunizing mice with DNA encoding CHIKV C-E3-E2-6K-E1 using DNA Electro Gene Transfer (EGT) (Takis Biotech, Roma, Italy). The immunodominant response was against the capsid protein. Expected protein sizes were observed, as shown in Figure 7. Specifically, CHIKV capsid protein was detected in both the soluble cell lysate fraction (left panel) and the supernatant (right panel) of infected HeLa cells. Lane 1: Molecular weight markers (Ladder precision plus); Lane 2: ChAd155-CHIKV-1 (MOI 250); Lane 3: ChAd155-CHIKV-1 (MOI 500); Lane 4: ChAd155-CHIKV-1 (MOI 1250); Lane 5: ChAd155-CHIKV-2 (MOI 250); Lane 6: ChAd155-CHIKV-2 (MOI 500); and Lane 7: ChAd155-CHIKV-2 (MOI 1250).

ChAd155-CHIKV viral particle titers were determined by QPCR targeting the tetOhCMV promoter and expressed as genome equivalents (gE)/mL, and by CCID50 (Cell Culture Infectious Dose, 50%) for infectivity and expressed as CCID50/mL. Data are summarized in Table 1:

Table 1.

ChAd155-CHIKV seed	QPCR (gE/ml)	CCID50/ml or ifu/ml	Ratio gE/CCID50 (< 300)
ChAd155- CHIKV	$7.46x10^{10}$	$4.5x10^{8}$	166

Example 3: CHIKV VLP Production

Molecular Cloning

To generate CHIKV VLP expression plasmids, the codon-optimized nucleic acid encoding CHIKV C-E3-E2-6k-E1 (SEQ ID NO: 22) was inserted into the pMAX eukaryotic expression vector (Lonza, Basel Switzerland) using routine molecular biology techniques. See, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2000; and Ausubel et al. Short Protocols in Molecular Biology, 4th ed., John Wiley & Sons, Inc., 15 1999. A diagram of the resulting pMAX-CHIKV plasmid is shown in Figure 6.

Production

HEK293 cells (EXPI293-F cells; Thermo Fisher Scientific, Waltham, MA) were grown in EXPI293 expression medium (Thermo Fisher Scientific). The cells were transfected with the pMAX-CHIKV plasmid prepared above (Figure 6), and EXPIFECTAMINE transfection reagent (Thermo Fischer Scientific). One day after transfection, EXPIFECTAMINE 293 Transfection Enhancer was added. Production proceeded for 4 days post-transfection at 37°C, and cell culture supernatants were collected for purification.

Purification

Cell culture supernatants were centrifuged and filtered on 0.22µm filters. Samples were diluted 1:2 (v:v) in 50mM Hepes buffer (pH 8.5) and EDTA-free protease inhibitor cocktail (COMPLETE; Roche, Basel, Switzerland). Anion Exchange Chromatography Hicap Chromotography was used as the first purification step, followed by concentration steps (ViVaspin 70-30,000; Sigma Aldrich, St. Louis, MO). A second purification step was carried out, using a sucrose discontinuous gradient (20-60%) followed by a polishing step (SUPERDEX 200 size exclusion chromatography; GE Healthcare Life Sciences; Little Chalfont, United Kingdom) in buffer (50mM Tris, 100mM NaCl, 1mM EDTA pH7.5).

Fractions containing CHIKV VLP antigen were selected on the basis of purity by SDS-PAGE. Protein concentration was determined using Lowry RC/DC Protein Assay of BioRad. The purified bulk was sterile-filtered on 0.22 µm filters and stored at -80°C.

Characterization

Purified CHIKV VLPs were analyzed for expression of CHIKV structural proteins by Western blot. The results confirmed expected protein sizes for CHIKV structural proteins (data not shown).

Purified CHIKV VLP antigen was also examined by electron microscopy (EM) using standard techniques. Briefly, samples were prepared for EM negative staining analysis according to a standard two-step negative staining method using phosphotungstic acid as contrasting agent (Hayat M.A. & Miller S.E., 1990, Negative Staining, McGraw-Hill ed., 253 pp.) A glow discharge was applied to the grids to improve the adsorption of the particles on the grids. A nickel grid (400 mesh) with carbon-coated formvar film was floated on a drop of the sample for 10 min at room temperature to allow adsorption of the material. Excess solution was blotted. To remove most of the sample salts, the grid was briefly floated on a drop of distilled water. The grid was then transferred on a drop of stain prepared according to Harris (Harris, J.R., 1994, Proc. ICEM XIII, Les Editions de Physique, ed., p.557): 2% (w/v) Na phosphotungstate in water supplemented with 1% trehalose (w/v). The grid was blotted dry after 30 s. The material was left to dry completely and examined under the LIBRA 120 transmission electron microscope (Carl Zeiss AG, Oberkochen, Germany) at 100 kV.

An example of an electron micrograph of CHIKV VLPs is shown in Figure 8. The results show intact VLPs of the expected diameter.

Example 4: Immunogenicity of ChAd155-CHIKV and VLP-CHIKV

Mouse study design

Immunogenicity of the ChAd155-CHIKV vector expressing the structural polyprotein C-E3-E2-6K-E1 was evaluated in C57BL/6 (B6) mice (10/group), immunized intramuscularly (IM) with a single dose of ChAd155-CHIKV at 10^7, 10^8 or 10^9 viral particles. Sera were collected before immunization and at day 21 (d21).

A separate study was conducted to evaluate the immunogenicity of CHIKV viral like particles (VLPs) expressing the same CHIKV structural polyproteins. C57BL/6 (B6) mice (10/group) were immunized intramuscularly at days 0 and 28 (d0, d28) with 10, 1 or 0.1 µg VLP. In addition, to evaluate the effect of adjuvant on CHIKV VLP immunogenicity, immunizations were performed with either no adjuvant, or with an adjuvant selected from aluminum hydroxide (alum), AS01E or AS04. AS01E is an Adjuvant System containing MPL, QS-21 and liposome (25 g MPL and 25 µg QS-21). See, e.g., Fochesato et al., Human Vaccines &

Immunotherapeutics, 2016, Vol. 12, No. 8, 2092–2095. AS04 is an Adjuvant System containing MPL (50 µg MPL) adsorbed on Al salt (500 µg Al3+). *Id.*

Neutralization assay

Micro-neutralisation assays were performed essentially as previously described using Vero cells (ATCC® CCL81™) and CHIKV prepared using C6/36 cells (ATCC ® CRL-1660™). See Gardner et al. (2010) J Virol 84:8021-8032; and Wang et al. (2011) Vaccine 29:2803-2809.

All cells and viruses were tested for mycoplasma and shown to be negative. Cell line identification was confirmed by Short Tandem Repeats profiling (Promega Geneprint 10). A single fetal calf serum batch (Gibco) was used throughout and confirmed to be endotoxin free by bioassay (Johnson et al. (2005) J Biol Chem 280:4037-4047).

Two viruses were used in the neutralization assay: (i) a La Reunion Island isolate (LR2006-OPY1) sequence representing the ECSA genotype (Indian Ocean Lineage) (Poo et al. (2014) PLoS Negl Trop Dis 8:e3354) and (ii) an isolate from a traveler who had returned to Australia from the Caribbean (Asia genotype). Single production batches (aliquoted) of each virus were used for all assays. The two viruses behaved differently in the neutralization assays with the Caribbean isolate generating full cytopathic effect (CPE) after 6 days, whereas the La Reunion isolate showed full CPE after 5 days. The virus doses were adjusted to the minimum dose that provided about 100% CPE after 6 or 5 days, respectively, and approximated to a dose of 200 $CCID_{50}$ per well.

The neutralization assay was performed as follows. Mouse sera were heat inactivated and tested in duplicate starting at a 1-in-40 dilution with 3-fold serial dilutions. Sera were mixed with an equal volume of virus preparation (about 200 CCID50/well) and incubated prior to being transferred onto previously seeded Vero cells. Five to six days later, plates were stained with crystal violet, optical density (OD) was measured at 590 nm and titration curves were plotted. The 50% and 90% virus neutralization titers were interpolated from 2 point linear curve fitting, with 100% and 0% determined by 8 wells each for each 96-well plate. Occasionally 3 points were used for interpolation.

Immunogenicity results

Results of the immunogenicity assays are shown in Figure 9 (CHIKV VLPs) and Figure 10 (ChAd155-CHIKV). All vaccine groups induced CHIKV-neutralizing antibody (nAb) titers

above the detection threshold, for both the La Reunion and Caribbean CHIKV strains used in the neutralization assay. Immunogenicity of the 0.1 µg dose of CHIKV VLPs was enhanced by co-administration of adjuvants (Alum, AS01 or AS04). ChAd155-CHIKV induced high nAb titers after a single immunization with doses of 10^8 or 10^9 viral particles (Figure 10). The results indicate that neutralizing antibody responses elicited by the West African CHIKV strain have activity against the La Reunion strain (ECSA genotype) and the Caribbean strain (Asian genotype).

Example 5: Durability of immune response to ChAd155-CHIKV and VLP-CHIKV

Mouse study design

To evaluate the durability of the immune response to ChAd155-CHIKV and VLP-CHIKV immunizations, a study was designed as shown in Table 2. Specifically, C57BL/6 mice (4-6 weeks old; n=10/group) were immunized with either 1) ChAd155-CHIKV viral particles produced as described in Example 2 (single intramuscular immunization with $5x10^8$ viral particles); or 2) CHIKV VLPs produced as described in Example 3 (one or two immunizations with 1 ug/dose). Groups 2, 5 and 6 were also administered Adjuvant System AS01E, containing MPL, QS-21 and liposome (25 g MPL and 25 µg QS-21). See, e.g., Fochesato et al., Human Vaccines & Immunotherapeutics, 2016, Vol. 12, No. 8, 2092–2095. Control animals received phosphate buffered saline vehicle only.

Table 2:

Group	n	Number of immunizations (immunization day)	dose	Vaccine Format	Adjuvant
1	10	1 (d28)	$5x10^8$	ChAd155	n/a
2	10				AS01
3	10	1 (d28)	1ug	VLP	n/a
4	10	2 (d0, d28)	1ug		
5	10	1 (d28)	1ug		AS01
6	10	2 (d0, d28)	1ug		
7	10	N/A	N/A	Control	n/a

Neutralization assay

CHIKV-specific neutralizing antibody titers were determined using the La Reunion (LR) and Caribbean (CRBN) strains in the micro-neutralisation assays described in Example 4.

Immunogenicity results

As shown in Figure 11, a single dose of ChAd155-CHIKV ($5x10^8$ viral particles, i.m.) elicited high and durable neutralizing antibody titers. nAb titers above the detection threshold were observed at 3, 6 and 9 weeks post-immunization. In addition, antibodies elicited by the West-African CHIKV-based ChAd construct were capable of neutralizing both the La Reunion and Caribbean CHIKV strains. No difference was observed between the unadjuvanted and AS01E-adjuvanted groups.

CHIKV VLPs induced high nAb titers following 2 immunizations, as shown in Figure 12. As with the ChAd155-CHIKV construct, the West-African CHIKV VLPs were capable of eliciting nAbs against the La Reunion and Caribbean CHIKV strains. Elevated nAb titers were observed 3, 6 and 9 weeks after the second immunization. While a single immunization with CHIKV VLPs did not produce a robust nAb response, an adjuvanting effect was observed for the single immunization combined with AS01E.

These results demonstrate that a single immunization with ChAd155-CHIKV is capable of inducing CHIKV-specific neutralizing antibodies. Furthermore, immunization with the West African CHIKV strain elicited nAbs against the La Reunion and Caribbean CHIKV strains.

Example 6: Efficacy of ChAd155-CHIKV and VLP-CHIKV

10 weeks after the last immunization described in Example 4, animals were challenged with $1x10^4$ $CCID_{50}$ of the La Reunion (LR) CHIKV strain subcutaneously into the side of each hind foot to assess the efficacy of the immunizations. CHIKV viremia was measured for 5 days post-challenge, and foot pad swelling (a correlate of CHIKV infection in mice) was measured for 13 days post-challenge.

As shown in Figure 13, all immunized groups showed complete protection, except the group receiving a single dose of CHIKV VLPs, which showed low levels of viremia at d2 and d3 post-challenge. Furthermore, all immunized groups showed complete protection from disease as measured by foot pad swelling. A small but not significant trend in foot pad swelling was noted at d2 post challenge in the group immunized with a single dose of CHIKV VLPs.

These results demonstrate that a single immunization with ChAd155-CHIKV is capable of preventing viremia and clinical symptoms caused by challenge with live Chikungunya virus. Furthermore, immunization with a West African CHIKV strain was protective against infection with the La Reunion strain.

CLAIMS

1. A recombinant adenovirus comprising a polynucleotide encoding at least one polypeptide selected from the group consisting of:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1 or a functional derivative thereof,

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 3 or a functional derivative thereof, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 5 or a functional derivative thereof,

wherein the adenovirus further comprises at least one nucleic acid sequence encoding a *Chikungunya virus* antigen, wherein the nucleic acid sequence is operatively linked to one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell.

2. The adenovirus according to claim 1, wherein the polynucleotide encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 1.

3. The adenovirus according to claim 1, wherein the polynucleotide encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 1, wherein the functional derivative has an amino acid sequence which is at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length to the amino acid sequence of SEQ ID NO: 1.

4. The adenovirus according to any one of claims 1-3, wherein the polynucleotide encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 3.

5. The adenovirus according to any one of claims 1-3, wherein the polynucleotide encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 3, wherein the functional derivative has an amino acid sequence which is at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length to the amino acid sequence of SEQ ID NO: 3.

6. The adenovirus according to any one of claims 1-5, wherein the polynucleotide encodes a polypeptide having the amino acid sequence according to SEQ ID NO: 5.

7. The adenovirus according to any one of claims 1-5, wherein the polynucleotide encodes a functional derivative of a polypeptide having the amino acid sequence according to SEQ ID NO: 5, wherein the functional derivative has an amino acid sequence which is at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length to the amino acid sequence of SEQ ID NO: 5.

8. The adenovirus according to any one of claims 1-7, wherein the polynucleotide encodes at least two polypeptides selected from the group consisting of:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1 or a functional derivative thereof,

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 3 or a functional derivative thereof, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 5 or a functional derivative thereof.

9. The adenovirus according to any one of claims 1-8, wherein the polynucleotide encodes:

(a) a polypeptide having the amino acid sequence according to SEQ ID NO: 1 or a functional derivative thereof,

(b) a polypeptide having the amino acid sequence according to SEQ ID NO: 3 or a functional derivative thereof, and

(c) a polypeptide having the amino acid sequence according to SEQ ID NO: 5 or a functional derivative thereof.

10. The adenovirus according to any one of claims 1-9, comprising at least one polynucleotide selected from the group consisting of:

(a) a polynucleotide having the sequence of SEQ ID NO: 2;

(a) a polynucleotide having the sequence of SEQ ID NO: 4; and

(a) a polynucleotide having the sequence of SEQ ID NO: 6.

11. The adenovirus according to any one of claims 1-10, wherein the polynucleotide comprises at least one of the following:

(a) an adenoviral 5'-end, preferably an adenoviral 5' inverted terminal repeat;

(b) an adenoviral EIA region, or a fragment thereof selected from among the E1A_280R and E1A_243R regions;

(c) an adenoviral EIB or IX region, or a fragment thereof selected from among the group consisting of the E1B_19K, E1B_55K or IX regions;

(d) an adenoviral E2b region; or a fragment thereof selected from among the group consisting of the E2B_pTP, E2B_Polymerase and E2B_IVa2 regions;

(e) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1_13.6k protein, L1_52k and L1_IIIa protein;

(f) an adenoviral L2 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2_penton protein, L2_pVII, L2_V, and L2_pX protein;

(g) an adenoviral L3 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L3_pVI protein, L3_hexon protein and L3_protease;

(h) an adenoviral E2A region;

(i) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4_100k protein, the L4_33k protein and protein L4_VIII;

(j) an adenoviral E3 region, or a fragment thereof selected from the group consisting of E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, and E3 ORF9;

(k) an adenoviral L5 region, or a fragment thereof said fragment encoding the L5_fiber fiber protein;

(l) an adenoviral E4 region, or a fragment thereof selected from the group consisting of E4 ORF7, E4 ORF6, E4 ORF4, E4 ORF3, E4 ORF2, and E4 ORF1;

(m) an adenoviral 3'-end, preferably an adenoviral 3’ inverted terminal repeat; and

(n) an adenoviral VAI or VAII RNA region, preferably an adenoviral VAI or VAII RNA region from an adenovirus other than ChAd155, more preferably from Ad5.

12. The adenovirus according to claim 11, wherein the polynucleotide comprises at least one of the following:

(a) an adenoviral 5'-end, preferably an adenoviral 5’ inverted terminal repeat;

(b) an adenoviral L1 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L1_13.6k protein, L1_52k and L1_IIIa protein;

(c) an adenoviral L2 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L2_penton protein, L2_pVII, L2_V, and L2_pX protein;

(d) an adenoviral L3 region, or a fragment thereof, said fragment encoding an adenoviral protein selected from the group consisting of the L3_pVI protein, L3_hexon hexon protein and L3_protease;

(e) an adenoviral L4 region, or a fragment thereof said fragment encoding an adenoviral protein selected from the group consisting of the L4_100k protein, the L4_33k protein and protein L4_VIII;

(f) an adenoviral L5 region, or a fragment thereof said fragment encoding the L5_fiber fiber protein; and

(g) an adenoviral 3'-end, preferably an adenoviral 3' inverted terminal repeat.

13. The adenovirus according to any one of claims 1-12, wherein the polynucleotide comprises an adenoviral VAI or VAII RNA region.

14. The adenovirus according to claim 13, wherein the VAI or VAII RNA region is from an adenovirus other than ChAd155.

15. The adenovirus according to claim 14, wherein the VAI or VAII RNA region is from Ad5.

16. A composition comprising the recombinant adenovirus according to any one of claims 1-15, and a pharmaceutically acceptable excipient.

17. The adenovirus or composition according to any one of claims 1-16, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide at least 80%, at least 90%, at least 95% or at least 99% identical to amino acids 1 to 261 of SEQ ID NO: 23.

18. The adenovirus or composition according to any one of claims 1-17, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide at least 80%, at least 90%, at least 95% or at least 99% identical to amino acids 262 to 325 of SEQ ID NO: 23.

19. The adenovirus or composition according to any one of claims 1-18, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide at least 80%, at least 90%, at least 95% or at least 99% identical to amino acids 326 to 748 of SEQ ID NO: 23.

20. The adenovirus or composition according to any one of claims 1-19, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide at least 80%, at least 90%, at least 95% or at least 99% identical to amino acids 749 to 809 of SEQ ID NO: 23.

21. The adenovirus or composition according to any one of claims 1-20, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide at least 80%, at least 90%, at least 95% or at least 99% identical to amino acids 810 to 1248 of SEQ ID NO: 23.

22. The adenovirus or composition according to any one of claims 1-21, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide at least 80%, at least 90%, at least 95% or at least 99% identical to SEQ ID NO: 23.

22. The adenovirus or composition according to any one of claims 1-21, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a polynucleotide encoding a polypeptide fragment of at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 350 or at least 400, at least 450, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1100 or at least 1200 amino acids of SEQ ID NO: 23.

23. The adenovirus or composition according to any one of claims 1-22, wherein the nucleic acid sequence encoding a *Chikungunya virus* antigen comprises or consists of a

polynucleotide at least 80%, at least 90%, at least 95% or at least 99% identical to SEQ ID NOs: 21 or 22.

24. The adenovirus or composition according to any one of claims 1-23, wherein the recombinant adenovirus is replication-incompetent.

25. The adenovirus or composition according to any one of claims 1-24, wherein the polynucleotide comprises a mutation or deletion which renders non-functional at least one gene of an adenoviral genomic region selected from the group consisting of E1A, E1B, E2A, E2B, E3 and E4.

26. The adenovirus or composition according to claim 25, wherein the polynucleotide lacks at least one gene of an adenoviral genomic region selected from the group consisting of E1A, E1B, E2A, E2B, E3 and/or E4.

27. The adenovirus or composition according to either claim 25 or 26, wherein the adenoviral genomic regions are E1A and/or E1B.

28. The adenovirus or composition according to any one of claims 1-27, wherein the *Chikungunya virus* antigen is derived from a *Chikungunya virus* genotype selected from West African, Asian and East/Central/South African (ECSA).

29. The adenovirus or composition according to any one of claims 1-28, wherein the *Chikungunya virus* antigen is derived from *Chikungunya virus* strain #37997.

30. The adenovirus or composition according to any one of claims 1-29 wherein the *Chikungunya virus* antigen comprises a sequence which is an immunogenic fragment of at least 20 amino acid residues.

31. The adenovirus or composition of any one of claims 1-30, wherein the one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell includes a sequence selected from one or more of the group consisting of transcription initiation, transcription termination, promoter and enhancer sequences.

32. The adenovirus or composition of claim 31, wherein the one or more sequences which direct expression of said *Chikungunya virus* antigen in a host cell includes a promoter sequence.

33. The adenovirus or composition of claim 32, wherein the promoter sequence is selected from the group consisting of an internal promoter, a native promoter, RSV LTR promoter, CMV promoter, SV40 promoter, dihydrofolate reductase promoter, β-actin promoter, PGK promoter, EF1a promoter and CASI promoter.

34. The adenovirus or composition according to any one of claims 1-33, wherein the adenovirus has a seroprevalence of less than 10% in human subjects and preferably no seroprevalence in human subjects.

35. The adenovirus or composition according to any one of claims 1-34, wherein the adenovirus is capable of infecting a mammalian cell.

36. The composition according to any one of claims 16-35, comprising an adjuvant.

37. The adenovirus or composition according to any one of claims 1-36, for use as a medicament.

38. The adenovirus or composition according to claim 37, for use in the stimulation of an immune response.

39. The adenovirus or composition according to claim 38, for use as a vaccine.

40. The adenovirus or composition according to claim 39, for use in the prophylaxis, treatment or amelioration of a disease caused by a *Chikungunya virus* infection.

41. Use of the adenovirus or composition according to any one of claims 1-40 in the manufacture of a medicament for the prophylaxis of a disease caused by a *Chikungunya virus* infection.

42. A method of inducing an immune response in a subject comprising administering the adenovirus or composition according to any one of claims 1-40 to the subject.

43. The method according to claim 42, wherein the subject is infected with a *Chikungunya virus*.

44. The method according to claim 43, wherein the *Chikungunya virus* has a genotype selected from one or more of West African, Asian and East/Central/South African (ECSA).

45. A non-human simian adenovirus comprising the penton of SEQ ID NO: 3, the hexon of SEQ ID NO: 5 and/or the fiber of SEQ ID NO: 1 and also comprising a transgene encoding a *Chikungunya virus* antigen.

46. The non-human simian adenovirus according to claim 45, comprising the penton (SEQ ID NO: 3), hexon (SEQ ID NO: 5) and fiber (SEQ ID NO: 1) protein from ChAd155 and also comprising a transgene encoding a *Chikungunya virus* antigen.

47. The non-human simian adenovirus according to claim 45 or 46 wherein the encoded antigen comprises a sequence having at least 90% identity to SEQ ID NO: 23.

48. The non-human simian adenovirus according to any of claims 45-47, which is a replication deficient adenovirus.

49. The non-human simian adenovirus according to claim 48 wherein the adenovirus comprises a functional inactivation (such as deletion) of the E1 gene.

50. The non-human simian adenovirus according to claim 48 or 49 wherein the adenovirus comprises a functional inactivation (such as deletion) of the E4 gene.

51. The non-human simian adenovirus according to any of claims 47-50 wherein the adenovirus comprises a functional inactivation (such as deletion) of the E3 gene.

52. The non-human simian adenovirus according to any one of claims 48-51, wherein the adenovirus comprises an Ad5E4orf6 gene substitution.

53. An adenovirus comprising a polynucleotide having a sequence at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length to SEQ ID NO: 24.

54. An adenovirus comprising a polynucleotide having a sequence at least 80%, at least 90%, at least 95% or at least 99% identical over its entire length identical to SEQ ID NO: 25.

Figure 1

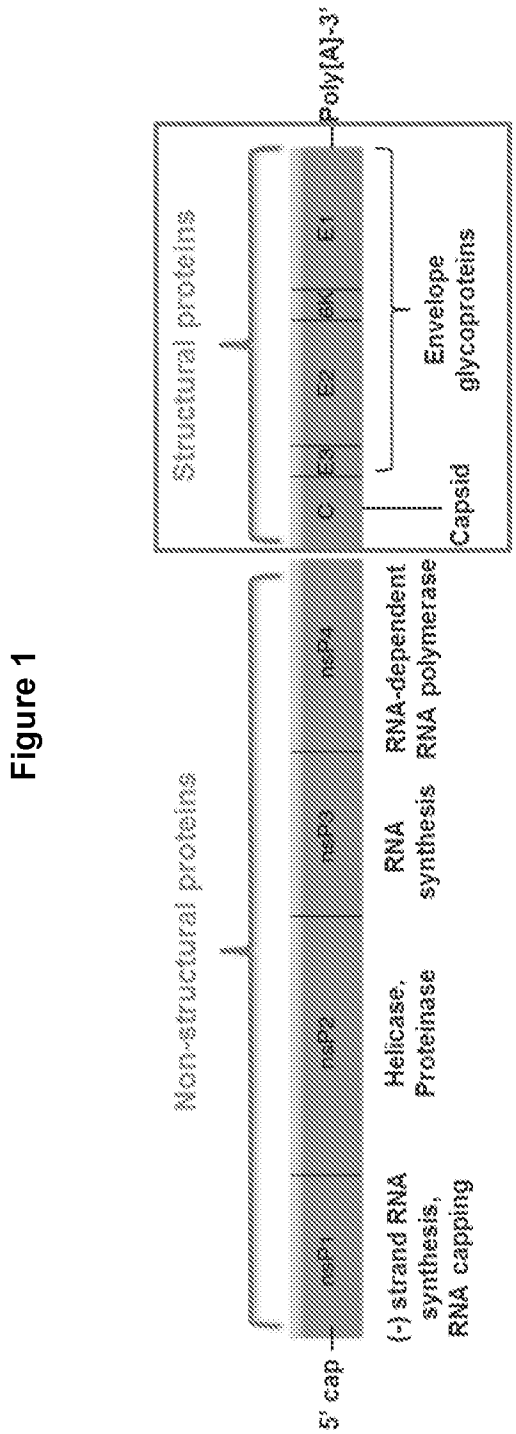

Poly(A)-3'
Structural proteins
Non-structural proteins
5' cap
(-) strand RNA synthesis, RNA capping
Helicase, Proteinase
RNA synthesis
RNA-dependent RNA polymerase
Capsid
Envelope glycoproteins

Figure 2A


ChAd3 (1)MKRTKTSDESFNPVYPYDTESGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDITTASPPLKKTKTNLSLE
PanAd3 (1)MKRAKTSDETFNPVYPYDTENGPPSVPFLTPPFVSPDGFQESPPGVLSLRLSEPLVTSHGMLALKMGNGLSLDDAGNLTSQDVTTVTPPLKKTKTNLSLQ
ChAd17 (1)MKRTKTSDESFNPVYPYDTESGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDITSTTPPLKKTKTNLSLE
ChAd19 (1)MKRTKTSDKSFNPVYPYDTENGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDVTTTTPPLKKTKTNLSLE
ChAd24 (1)MKRTKTSDESFNPVYPYDTENGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDVTTTTPPLKKTKTNLSLE
ChAd155 (1)MKRTKTSDESFNPVYPYDTESGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDITTASPPLKKTKTNLSLE
ChAd11 (1)MKRTKTSDESFNPVYPYDTENGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDVTTTTPPLKKTKTNLSLE
ChAd20 (1)MKRTKTSDESFNPVYPYDTESGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDITTASPPLKKTKTNLSLE
ChAd31 (1)MKRTKTSDESFNPVYPYDTESGPPSVPFLTPPFVSPDGFQESPPGVLSLNLAEPLVTSHGMLALKMGSGLSLDDAGNLTSQDITTASPPLKKTKTNLSLE
PanAd1 (1)MKRAKTSDETFNPVYPYDTENGPPSVPFLTPPFVSPDGFQESPPGVLSLRLSEPLVTSHGMLALKMGNGLSLDDAGNLTSQDVTTVTPPLKKTKTNLSLQ
PanAd2 (1)MKRAKTSDETFNPVYPYDTENGPPSVPFLTPPFVSPDGFQESPPGVLSLRLSEPLVTSHGMLALKMGNGLSLDDAGNLTSQDVTTVTPPLKKTKTNLSLQ
ChAd3 (101) TSSPLTVSTSGALTVAAAAPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSATPPTNVSSGSLGIDMEDPMYTH
PanAd3 (101) TSAPLTVS-SGSLTVAAAAPLAVAGTSLTMQSQAPLTVQDAKLGLATQGPLTVSEGKLTLQTSAPLTAADSSTLTVGTTPPTSVSSGSLGIDMEDPMYTH
ChAd17 (101) TSSPLTVSTSGALTVAAAAPLAVAGTSLTMQSEAPLAVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSSTPPTSVSSGSLGIDMEDPMYTH
ChAd19 (101) TSAPLTVSTSGALTLAAAAPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSATPPTSVSSGSLGIDMEDPMYTH
ChAd24 (101) TSAPLTVSTSGALTLAAAAPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSATPPTNVSSGSLGIDMENPMYTH
ChAd155(101) TSSPLTVSTSGALTVAAAAPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSATPPLSTSNGSLGIDMQAPIYTT
ChAd11 (101) TSAPLTVSTSGALTLAAAVPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTISATPPLSTSNGSLGIDMQAPIYTT
ChAd20 (101) TSSPLTVSTSGALTVAAAAPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSATPPLSTSNGSLGIDMQAPIYTT
ChAd31 (101) TSSPLTVSTSGALTVAAAAPLAVAGTSLTMQSEAPLTVQDAKLTLATKGPLTVSEGKLALQTSAPLTAADSSTLTVSATPPLSTSNGSLGIDMQAPIYTT
PanAd1 (101) TSAPLTVS-SGSLTVAAAAPLAVAGTSLTMQSQAPLTVQDAKLGLATQGPLTVSEGKLTLQTSAPLTAADSSTLTVSATPPLSTSNGSLSIDMQAPIYTT
PanAd2 (101) TSAPLTVS-SGSLTVAAAAPLAVAGTSLTMQSQAPLTVQDAKLGLATQGPLTVSEGKLTLQTSAPLTAADSSTLTVSATPPLSTSNGSLSIDMQAPIYTT

Figure 2B

Figure 2C

Figure 3

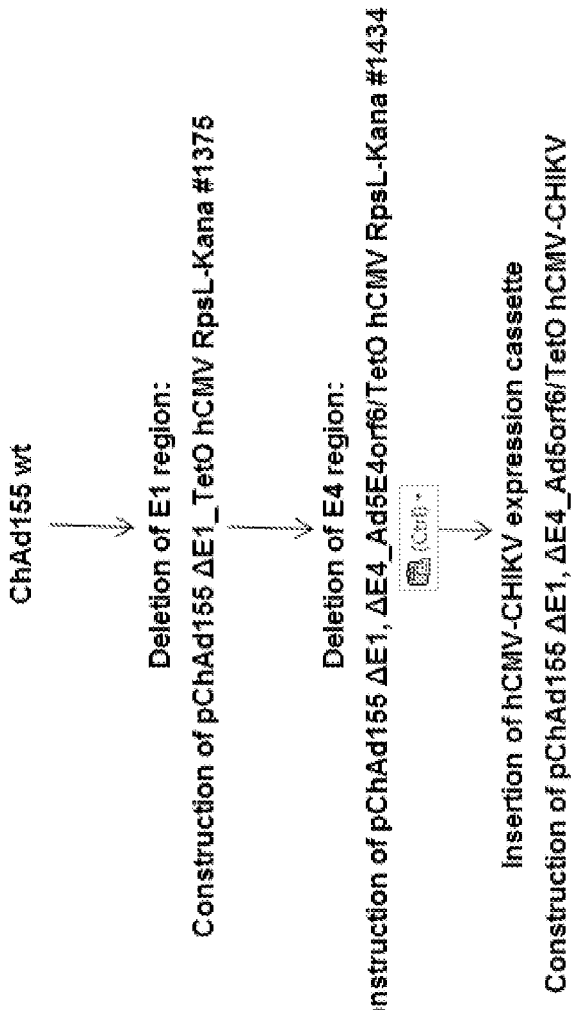

ChAd155 wt
Deletion of E1 region:
Construction of pChAd155 ΔE1_TetO hCMV RpsL-Kana #1375
Deletion of E4 region:
Construction of pChAd155 ΔE1, ΔE4_Ad5E4orf6/TetO hCMV RpsL-Kana #1434
Insertion of hCMV-CHIKV expression cassette
Construction of pChAd155 ΔE1, ΔE4_Ad5orf6/TetO hCMV-CHIKV

Figure 4

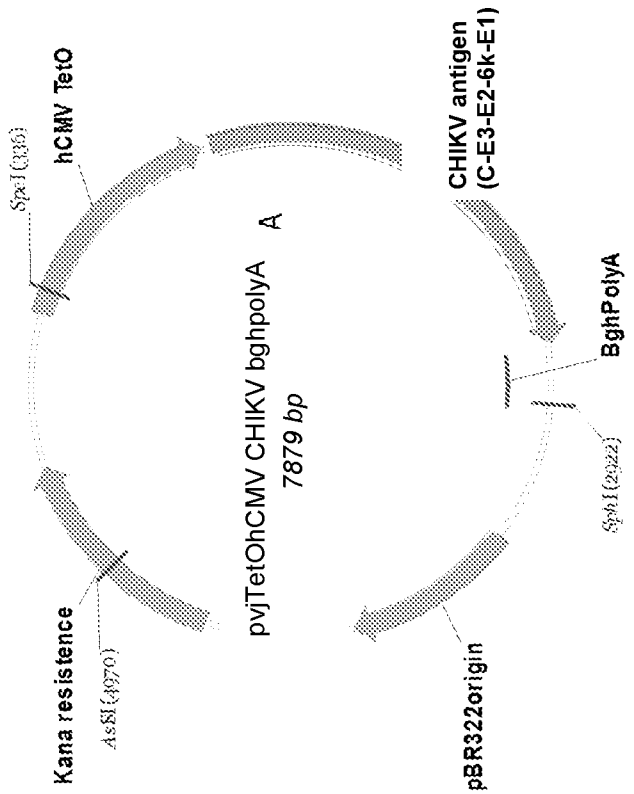

hCMV TetO
CHIKV antigen
(C-E3-E2-6k-E1)
pvjTetOhCMV CHIKV bghpolyA
7879 bp
A
Kana resistence
BghPolyA
pBR322origin

Figure 5

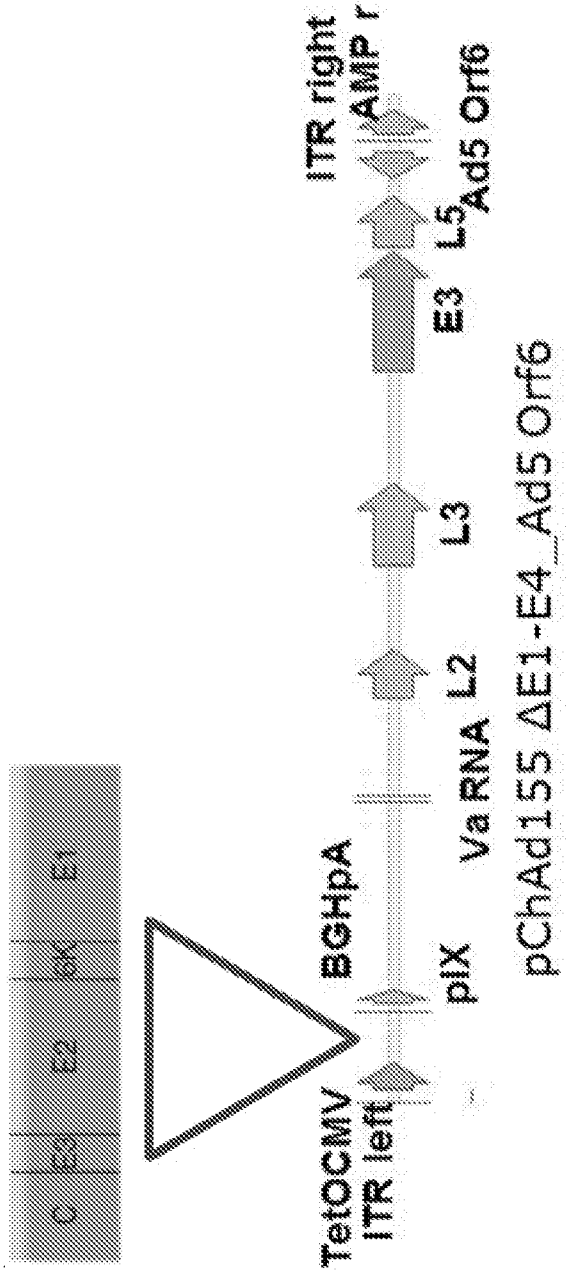

pChAd155 ΔE1-E4_Ad5 Orf6
TetOCMV
ITR left
pIX
BGHpA
Va RNA
L2
L3
E3
L5
Ad5 Orf6
ITR right
AMP r
E1
E2
E3
E4
ITR

Figure 6

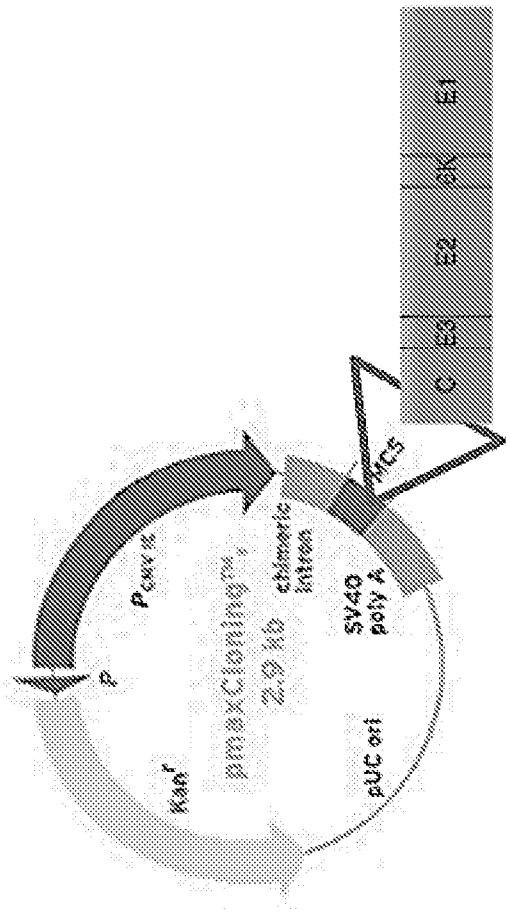

E1
E2
E3
C
HC5
SV40 poly A
chimeric intron
pmaxCloning™
2.9 kb
pUC ori
Kan^r
P

Figure 7

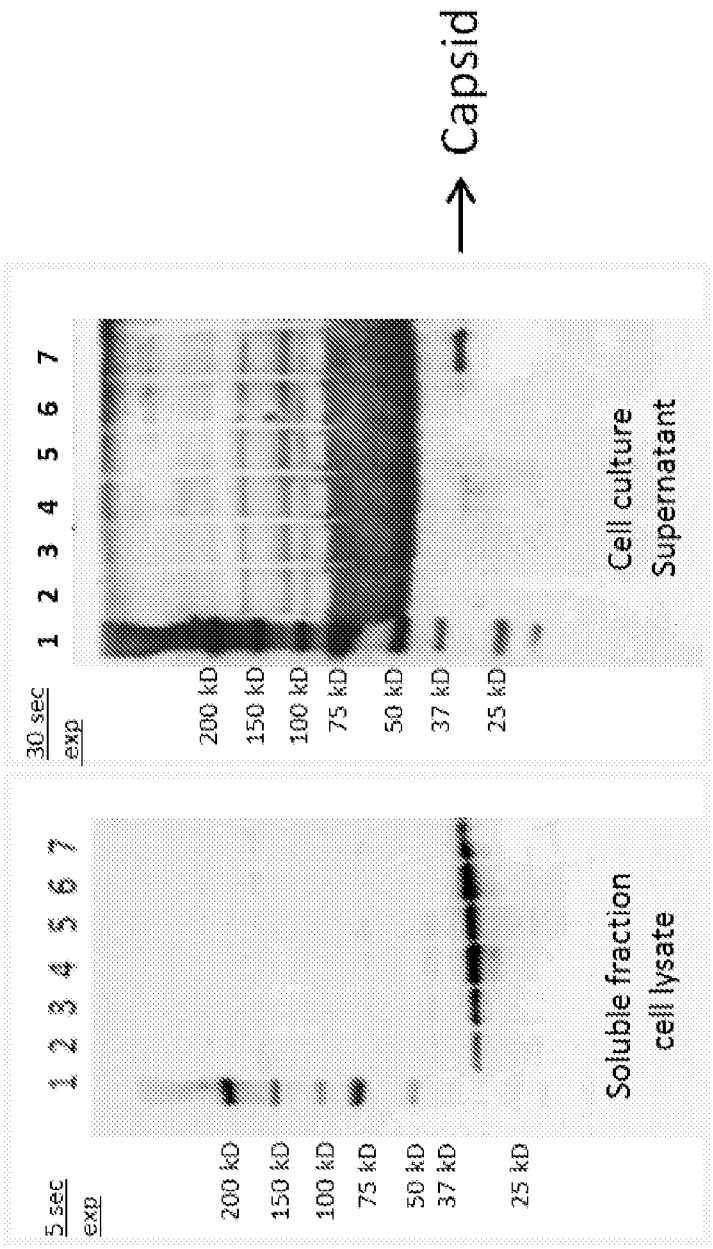

5 sec exp
30 sec exp
1 2 3 4 5 6 7
200 kD
150 kD
100 kD
75 kD
50 kD
37 kD
25 kD
Soluble fraction cell lysate
Cell culture Supernatant
Capsid

Figure 8

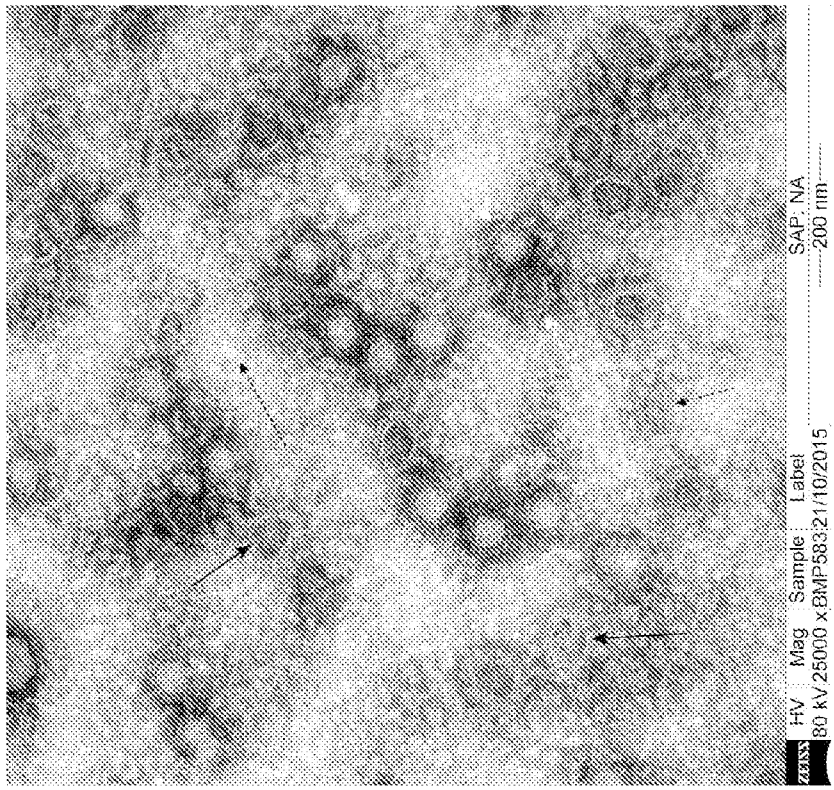

HV Mag Sample Label SAP: NA
80 kV 25000 x BMP583 21/10/2015 200 nm

Figure 9

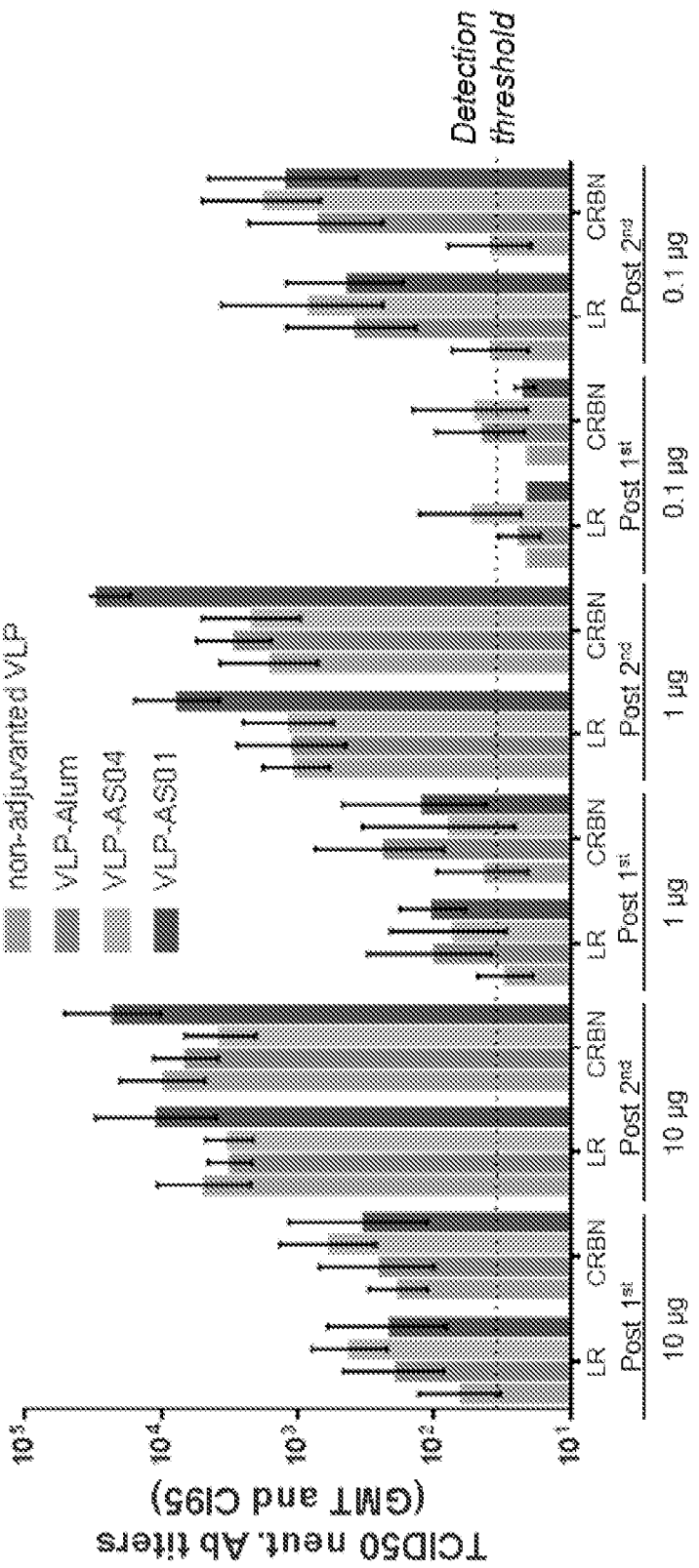

TCID50 neut. Ab titers (GMT and CI95)
non-adjuvanted VLP
VLP-Alum
VLP-AS04
VLP-AS01
Detection threshold
LR
CRBN
Post 1st
Post 2nd
10 µg
1 µg
0.1 µg

Figure 10

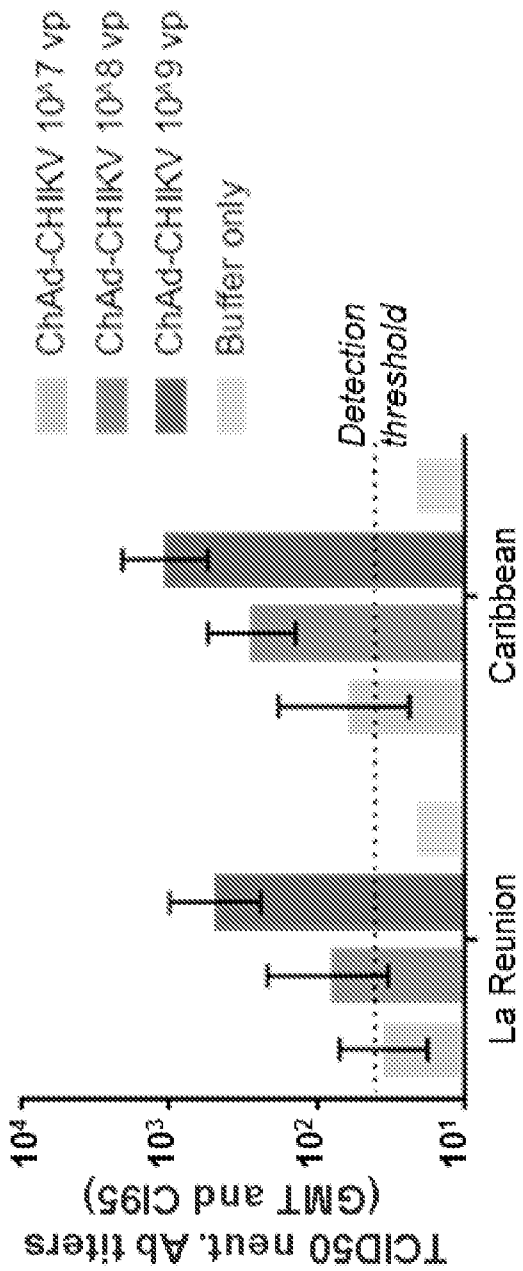

ChAd-CHIKV 10^7 vp
ChAd-CHIKV 10^8 vp
ChAd-CHIKV 10^9 vp
Buffer only
Detection threshold
TCID50 neut. Ab titers (GMT and CI95)
10^4
10^3
10^2
10^1
La Reunion
Caribbean

Figure 11

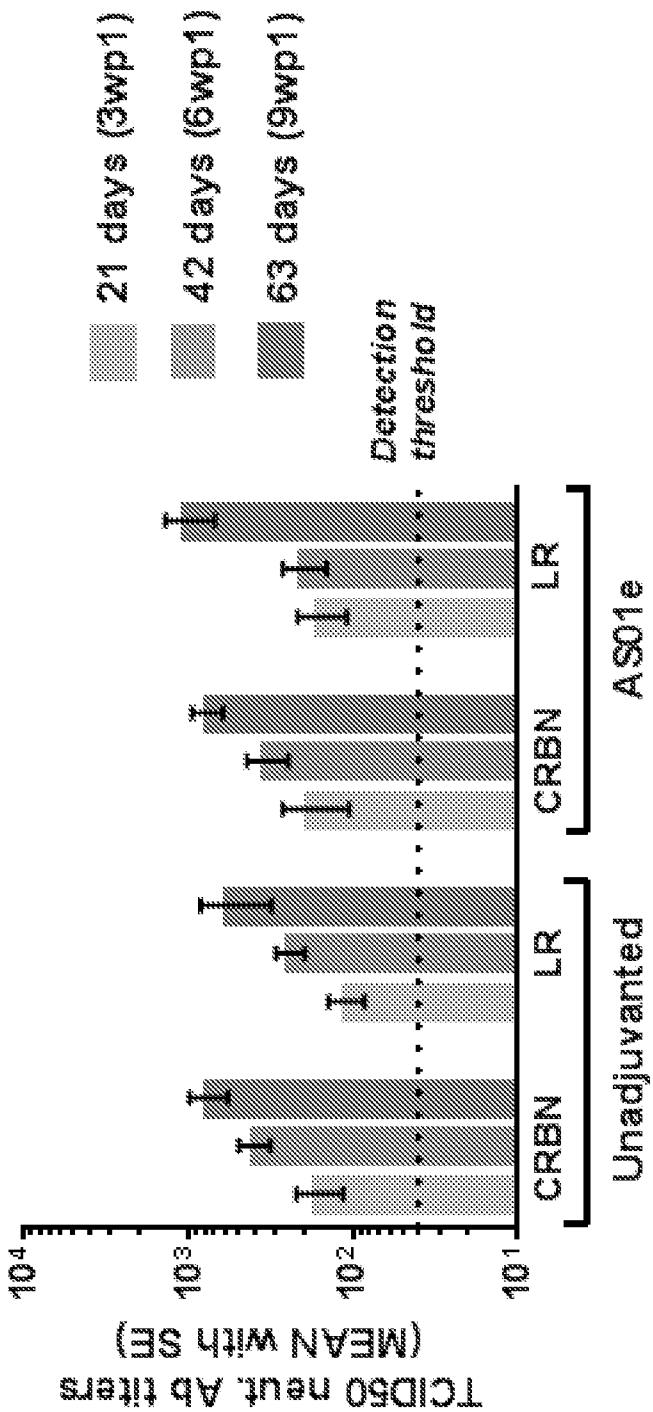

21 days (3wp1)
42 days (6wp1)
63 days (9wp1)
Detection threshold
TCID50 neut. Ab titers (MEAN with SE)
10^4
10^3
10^2
10^1
CRBN
LR
CRBN
LR
Unadjuvanted
AS01e

Figure 12

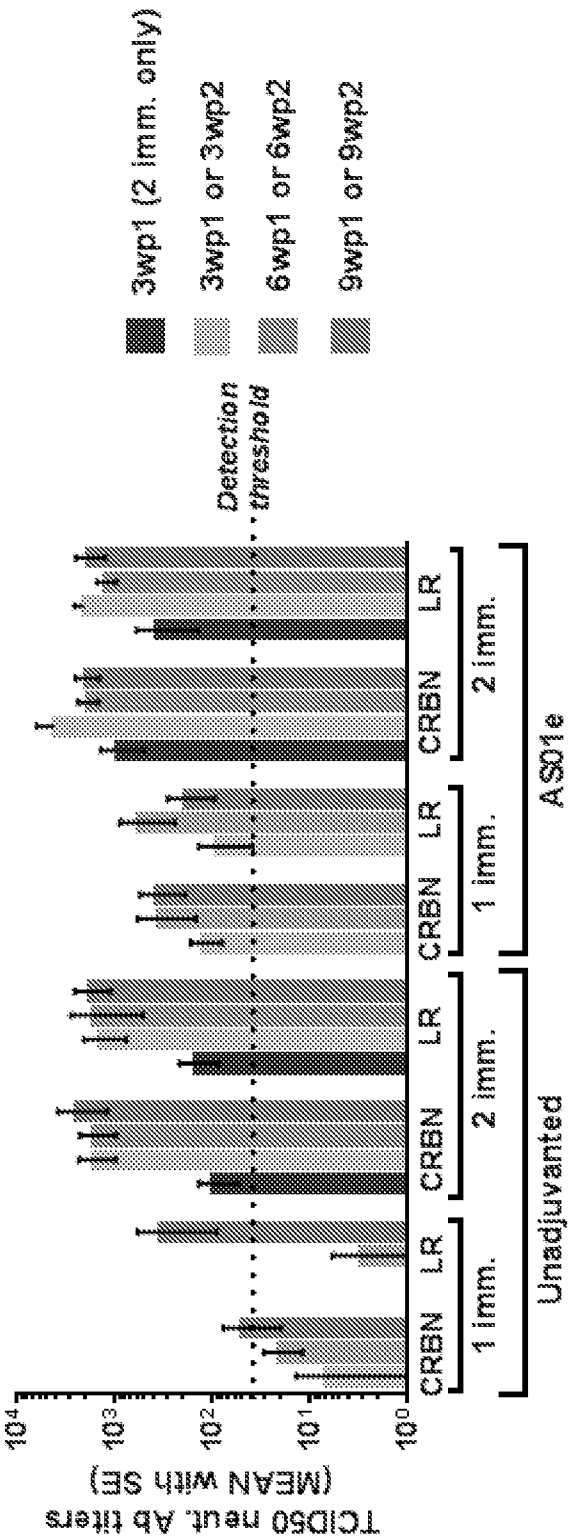
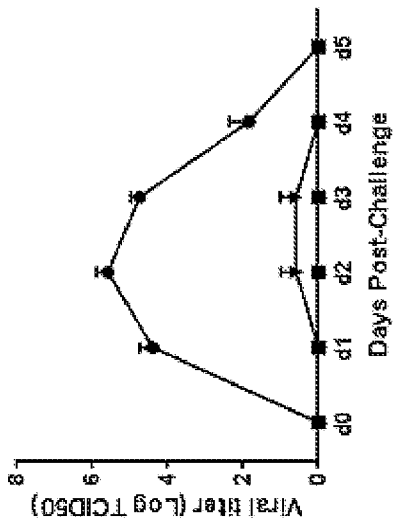
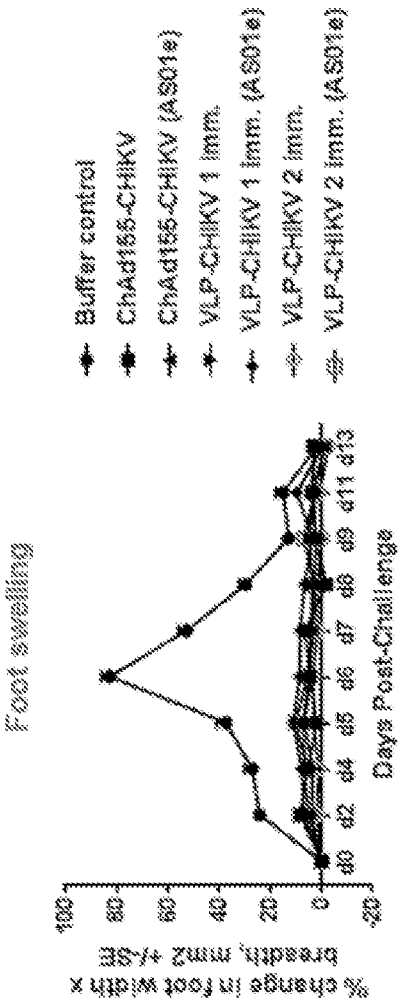

3wp1 (2 imm. only)
3wp1 or 3wp2
6wp1 or 6wp2
9wp1 or 9wp2
Detection threshold
TCID50 neut. Ab titers (MEAN with SE)
10^4
10^3
10^2
10^1
10^0
CRBN
LR
1 imm.
2 imm.
Unadjuvanted
AS01e

Figure 13


A
Viremia
Viral titer (Log TCID50)
0
2
4
6
8
d0
d1
d2
d3
d4
d5
Days Post-Challenge


B
Foot swelling
% change in foot width x breadth, mm2 +/-SE
-20
0
20
40
60
80
100
d0
d2
d4
d5
d6
d7
d8
d9
d11
d13
Days Post-Challenge
Buffer control
ChAd155-CHIKV
ChAd155-CHIKV (AS01e)
VLP-CHIKV 1 imm.
VLP-CHIKV 1 imm. (AS01e)
VLP-CHIKV 2 imm.
VLP-CHIKV 2 imm. (AS01e)

INTERNATIONAL SEARCH REPORT

International application No
PCT/IB2018/055389

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12N15/861 A61K39/12 C07K14/18
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DANHER WANG ET AL: "A complex adenovirus vaccine against chikungunya virus provides complete protection against viraemia and arthritis", VACCINE, ELSEVIER, AMSTERDAM, NL, vol. 29, no. 15, 30 January 2011 (2011-01-30), pages 2803-2809, XP028172366, ISSN: 0264-410X, DOI: 10.1016/J.VACCINE.2011.01.108 [retrieved on 2011-02-04] see sections 2.1, 3.1-3.4; page 2807, left-hand column, last paragraph; figures 1,4,5 ----- -/--	1,3,5, 7-9, 11-33, 35-44,53

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
24 September 2018	04/10/2018

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Brenz Verca, Stefano

INTERNATIONAL SEARCH REPORT

International application No
PCT/IB2018/055389

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2016/198621 A1 (GLAXOSMITHKLINE BIOLOGICALS SA [BE]) 15 December 2016 (2016-12-15) cited in the application	54
A	Simian adenovirus ChAd155; sequence 10	1-53

A	WO 2010/062396 A2 (US GOV HEALTH & HUMAN SERV [US]; NABEL GARY J [US]; AKAHATA WATARU [US) 3 June 2010 (2010-06-03) the whole document	1-54

X,P	WO 2018/014008 A1 (ETUBICS CORP [US]) 18 January 2018 (2018-01-18)	1,3,5, 7-9, 11-28, 30,31, 33,35, 37-44, 53,54
	paragraph [0125]; claims 15-20, 43-51; figures 2,4; examples 1-3,10-13,20; sequence 2	

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/IB2018/055389

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		EP 3307313 A1	18-04-2018
		EP 3307314 A1	18-04-2018
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		KR 20180011265 A	31-01-2018
		KR 20180012857 A	06-02-2018
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		MY 161495 A	14-04-2017
		SG 171828 A1	28-07-2011
		US 2012003266 A1	05-01-2012
		US 2016303221 A1	20-10-2016
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WO 2018014008 A1	18-01-2018	NONE	