(12) STANDARD PATENT (11) Application No. **AU 2015225553 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Recombinant Isfahan viral vectors

(51) International Patent Classification(s)
A61K 39/12 (2006.01) ***C12N 15/00*** (2006.01)

(21) Application No: **2015225553** (22) Date of Filing: **2015.02.27**

(87) WIPO No: **WO15/134332**

(30) Priority Data

(31) Number	(32) Date	(33) Country
61/946,734	**2014.03.01**	**US**

(43) Publication Date: **2015.09.11**
(44) Accepted Journal Date: **2020.02.27**

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(56) Related Art
US 20130023032 A1
US 20120244113 A1

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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 September 2015 (11.09.2015)

WIPO | PCT

(10) International Publication Number
WO 2015/134332 A3

(51) International Patent Classification:
A61K 39/12 (2006.01) *C12N 15/00* (2006.01)

(21) International Application Number:
PCT/US2015/018156

(22) International Filing Date:
27 February 2015 (27.02.2015)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/946,734 1 March 2014 (01.03.2014) US

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(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, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, 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).

Published:
— *with international search report (Art. 21(3))*
— *with sequence listing part of description (Rule 5.2(a))*

(88) Date of publication of the international search report:
28 January 2016

WO 2015/134332 A3

(54) **Title**: RECOMBINANT ISFAHAN VIRAL VECTORS

(57) **Abstract**: Certain embodiments are directed to recombinant vesiculovirus encoding a heterologous polynucleotide and methods of using the same.

RECOMBINANT ISFAHAN VIRAL VECTORS

PRIORITY

[001] This application claims priority to U.S. Provisional Patent Application serial number 61/946,734 filed March 1, 2014, which is incorporated herein by reference in its entirety.

STATEMENT REGARDING FEDERALLY FUNDED RESEARCH

[002] This invention was made with government support under N01-AI-30027, HHSN272201000040I, and HHSN2720004/D04 awarded by the National Institutes of Health/National Institute of Allergy and Infectious Disease. The government has certain rights in the invention.

REFERENCE TO SEQUENCE LISTING

[003] A sequence listing required by 37 CFR 1.821-1.825 is being submitted electronically with this application. The sequence listing is incorporated herein by reference.

BACKGROUND

[004] Recombinant vesicular stomatitis virus (rVSV) has been developed as a vector platform for a range of human pathogens (Finke and Conzelmann. *Current Topics in Microbiology and Immunology.* 2005, 292:165-200; Jones et al. *Nature Medicine.* 2005, 11(7):786-90; Kahn et al. *Journal of Virology.* 2001, 75(22):11079-87; Kapadia et al. *Virology.* 2005, 340(2):174-82; Reuter et al. *Journal of Virology.* 2002, 76(17):8900-9; Roberts et al. *Journal of Virology.* 1999, 73(5):3723-32; Roberts et al. *J Virol.* 1998, 72(6):4704-11; Rose et al. *Cell.* 2001, 106(5):539-49), and an optimized rVSV vector expressing HIV-1 gag protein has completed clinical evaluation (HVTN 090: accessible via the worldwide web at URL clinicaltrials.gov/). Despite these advances, challenges remain in the development of the rVSV vector platform, including potential immunity generated against vector proteins that may interfere with subsequent boosting immunizations with rVSV vectors. This potential problem may be overcome when rVSV vectors are used in heterologous prime-boost immunization regimens with other immunologically distinct vectors (Amara et al. *Science.* 2001, 292(5514):69-

74; Amara et al. *J Virol*. 2002, 76(15):7625-31; Egan et al. *AIDS Research and Human Retroviruses*. 2005, 21(7):629-43; Hanke et al. *J Virol*. 1999, 73(9):7524-32; Ramsburg et al. *Journal of Virology*. 2004, 78(8):3930-40; Santra et al. *J Virol*. 2007; Xu et al. *Journal of Virology*. 2009, 83(19):9813-23). Serotype switching of rVSV vectors, achieved by swapping the surface G protein with that of a different vesiculovirus serotype, also enhances immunogenicity in prime-boost regimens in mice (Rose et al. *Journal of Virology*. 2000, 74(23):10903-10). However, cross-reactivity of cellular immune responses directed towards rVSV core proteins may limit this approach.

[005] In view of these observations and potential limitations, there is a need for additional heterologous vectors for use either alone or in conjunction with rVSV vectors.

SUMMARY

[006] Embodiments of the invention include immunogenic compositions and methods related to vesiculoviruses, such as Isfahan virus (ISFV) alone or in combination with vesicular stomatitis virus (VSV) and their use as therapeutics and/or prophylactics. Certain aspects include methods and immunogenic compositions comprising a recombinant vesiculovirus encoding one or more heterologous polypeptides. “Recombinant virus” refers to any viral genome or virion that is the same as or different than a wild-type virus due to a rearrangement, deletion, insertion, or substitution of one or more nucleotides in the wild-type viral genome. In particular, the term includes recombinant viruses generated by the intervention of a human. In certain aspects the vesiculovirus is a recombinant Isfahan virus (rISFV). In certain aspects the rISFV is a replication competent virus. As applied to a recombinant virus, “replication competent” means that the virus is capable of cell infection; replication of the viral genome; and production and release of new virus particles; although one or more of these characteristics need not occur at the same rate as they occur in the same cell type infected by a wild-type virus, and may occur at a faster or slower rate.

[007] In a further aspect the rISFV comprises one or more of (i) an N protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID

NO:2, (ii) a P protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:3, (iii) an M protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:4, (iv) a G protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:5, or (v) an L protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:6.

[008] Certain embodiments are directed to a rISFV comprising 4 or 5 of an N protein gene, a P protein gene, an M protein gene, a G protein gene, and an L protein gene. In certain aspects the rISFV further comprises a heterologous polynucleotide sequence encoding a heterologous polypeptide. In certain embodiments the rISFV further comprises a heterologous transcription unit (TU). A transcription unit refers to a heterologous polynucleotide sequence (a) flanked by a transcription start signal and a transcription stop signal (including a polyadenylation sequence), and (b) encoding one or more target heterologous polypeptide(s). In certain embodiments the heterologous TU is the 1^{st}, 2^{nd}, 3^{rd}, 4^{th}, 5^{th} or 6^{th} TU in the virus genome. In certain aspects the heterologous TU encodes two or more heterologous polypeptides. In other aspects two heterologous TUs are included in the virus genome, with one heterologous TU inserted into one position in the virus genome and the second heterologous TU inserted into a different position in the virus genome.

[009] Another mechanism for expressing a heterologous polynucleotide sequence is to link the heterologous sequence to an ISF gene via a 2A peptide. The terms “2A”, “2A peptide” or “2A-like peptide” refer to peptides that have been used successfully to generate multiple proteins from a single open reading frame. These peptides are small (18-22 amino acids) and have divergent amino-terminal sequences, but all contain a PGP motif at the C-terminus. Through a ribosomal skip mechanism, the 2A peptide prevents normal peptide bond formation between a glycine and a proline residue at the C-terminus of the peptide. These 2A and 2A-like sequences are known in the art and may be readily selected for such use. See, *e.g.*, Szymczak-Workman et al, in Cold Spring Harbor Protocols 2012, doi 10.1101/pdb.ip067876; and Friedmann and Rossi (eds), Gene Transfer: Delivery and Expression of DNA and RNA, CSHL Press, Cold Spring

Harbor, NY USA, 2007, among others. One such 2A peptide is the peptide T2A, which is isolated from *Thosea asigna* virus and has the sequence EGRGSLLTCGDVEENPGP (SEQ ID NO:68). In further aspects an internal ribosome entry site (IRES) can be included in a gene encoding at least two polypeptides to enable cap independent transcription of the downstream coding region. A number of IRES sequence are known and can be selected from the IRESite database that is available on the worldwideweb at iresite.org.

[010] In certain aspects the rISFV G gene encodes a G protein having a carboxy-terminal truncation, in particular a truncation of 20 to 25 amino acids. In certain aspects the rISFV genome comprises 3' to 5' an ISFV leader sequence, an ISFV P protein open reading frame (ORF), an ISFV M protein ORF, an ISFV G protein ORF, an ISFV N protein ORF, an ISFV L protein ORF, and an ISFV trailer sequence, together with the heterologous polynucleotide sequence or the heterologous TU at any position within the rISFV genome. In certain aspects the heterologous TU is located at position 5 of the rISFV genome. In certain aspects the heterologous polynucleotide encodes an immunogenic polypeptide. In other aspects the heterologous polynucleotide encodes one or more antigens. The antigen(s) can be a viral antigen, a bacterial antigen, a tumor-specific or cancer antigen, a parasitic antigen, or an allergen.

[011] Certain embodiments are directed to a rISFV with a gene order, 3' to 5' relative to the (-) sense RNA, of N-P-M-G-L-(H), N-P-M-G-(H)-L, N-P-M-(H)-G-L, N-P-(H)-M-G-L, N-(H)-P-M-G-L, (H)-N-P-M-G-L, P-N-M-G-L-(H), P-N-M-G-(H)-L, P-N-M-(H)-G-L, P-N-(H)-M-G-L, P-(H)-N-M-G-L, (H)-P-N-M-G-L, P-M-N-G-L-(H), P-M-N-G-(H)-L, P-M-N-(H)-G-L, P-M-(H)-N-G-L, P-(H)-M-N-G-L, (H)-P-M-N-G-L, P-M-G-N-L-(H), P-M-G-N-(H)-L, P-M-G-(H)-N-L, P-M-(H)-G-N-L, P-(H)-M-G-N-L, (H)-P-M-G-N-L, P-M-G-L-N-(H), P-M-G-(H)-L-N, P-M-G-L(H)-N, P-M-(H)-G-L-N, P-(H)-M-G-L-N or (H)-P-M-G-L-N wherein (H) is a TU comprising at least one heterologous polynucleotide. In certain aspects the rISFV has a P-M-G-N-(H)-L gene order. In certain aspects the rISFV genome is encoded in an expression vector. In a further embodiment the expression vector is a DNA vector, e.g., a plasmid vector. The terms "gene shuffling", "shuffled gene", "shuffled", "shuffling", "gene rearrangement" and "gene

translocation" are used interchangeably, and refer to an alteration in the order of the vesiculovirus genes in the viral genome.

[012] Certain embodiments are directed to an expression vector encoding the recombinant negative sense RNA described above. In certain aspects the expression vector is a DNA vector.

[013] Other embodiments are directed to a host cell comprising the expression vector described above. As used herein, the term "expression vector" is intended to include a plasmid or virus that is capable of synthesizing a heterologous polynucleotide sequence encoded by the vector. In certain aspects a vector can replicate and express an encoded nucleic acid.

[014] Still other embodiments are directed to a virus particle comprising the recombinant RNA described above. As used herein a "virus particle" is an infective entity that provides a polynucleotide sequence encoding one or more polypeptides to be expressed in a host.

[015] Immunogenic compositions can include virus particles comprising the recombinant nucleic acids described herein. Certain aspects are directed to methods of inducing an immune response in a subject comprising administering the immunogenic compositions described herein.

[016] Methods and compositions of the invention can include a second therapeutic virus. A second virus can be selected from recombinant or oncolytic adenoviruses, vaccinia virus, Newcastle disease virus, herpes viruses, and rhabdoviruses. In other aspects, the composition is a pharmaceutically acceptable composition. In certain aspects the second therapeutic virus is an rVSV. In a further aspect the rVSV encodes the same antigen or a related antigen present in or on the same target cell or organism.

[017] A recombinant vesiculovirus (e.g., rISFV as described herein) can be administered to a subject in need of a therapeutic or prophylactic immune response. Recombinant vesiculovirus compositions can be administered 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more times with one or more recombinant vesiculoviruses. The composition administered can have 10, 100, 1000, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, or more viral particles or plaque forming units (pfu). Administration can be by the intraperitoneal, intravenous, intra-arterial, intratumoral (for

solid tumors), intramuscular, intradermal, subcutaneous, oral, or intranasal route. In certain aspects, the compositions are administered systemically, particularly by intravascular administration, which includes injection, perfusion and the like.

[018] The methods of the invention can further comprise administering a second anti-cancer or anti-microbial therapy. In certain aspects, a second anti-cancer agent is a chemotherapeutic, a radiotherapeutic, an immunotherapeutic, surgery or the like. In other aspects a second anti-microbial therapy is an antibiotic or an antiviral.

[019] rISFV is serologically and phylogenetically distinct from rVSV. This distinction can be utilized to optimize the protective efficacy and immunogenicity of an immune stimulating regimen. rISFV and rVSV vectors can be employed in prime-boost regimens. A first recombinant vesiculovirus can be used in any number of combinations with a second recombinant vesiculovirus.

[020] The term “providing” or “administering” is used according to its ordinary meaning “to supply or furnish for use.” In some embodiments, an antigen is provided by direct administration (for example, by intramuscular injection), while in other embodiments, the antigen is effectively provided by administering a nucleic acid encoding the antigen. In certain aspects the invention contemplates compositions comprising various combinations of nucleic acid, antigens, peptides, and/or epitopes.

[021] In certain aspects a viral particle, polypeptide, or nucleic acid can be an isolated viral particle, polypeptide, or nucleic acid. The term “isolated” can refer to a viral particle, nucleic acid, or polypeptide that is substantially free of cellular material, bacterial material, viral material, or culture medium (e.g., when produced by recombinant DNA techniques) of their source of origin, or chemical precursors or other chemicals (e.g., when chemically synthesized). Moreover, an isolated compound refers to one that can be administered to a subject as an isolated compound; in other words, the compound may not simply be considered “isolated” if it is adhered to a column or embedded in an agarose gel. Moreover, an “isolated nucleic acid

fragment" or "isolated peptide" is a nucleic acid or protein fragment that is not naturally occurring as a fragment and/or is not typically in the functional state.

[022] Other embodiments of the invention are discussed throughout this application. Any embodiment discussed with respect to one aspect of the invention applies to other aspects of the invention as well and vice versa. Each embodiment described herein is understood to be an embodiment of the invention that is applicable to all aspects of the invention. It is contemplated that any embodiment discussed herein can be implemented with respect to any method or composition of the invention, and vice versa. Furthermore, compositions and kits of the invention can be used to achieve methods of the invention.

[023] The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one", but it is also consistent with the meaning of "one or more", "at least one", and "one or more than one."

[024] Throughout this application, the term "about" is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value.

[025] The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or."

[026] As used in this specification and claim(s), the words "comprising" (and any form of comprising, such as "comprise" and "comprises"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including, such as "includes" and "include") or "containing" (and any form of containing, such as "contains" and "contain") are inclusive or open-ended and do not exclude additional, unrecited elements or method steps.

[027] Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit

and scope of the invention will become apparent to those skilled in the art from this detailed description.

DESCRIPTION OF THE DRAWINGS

[028] The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of the specification embodiments presented herein.

[029] FIG. 1 is a maximum-likelihood phylogenetic tree of the genus *Vesiculovirus* based on nucleotide sequences of the N gene.

[030] FIG. 2 depicts the restriction sites used in the cloning strategy for the generation of a complete Isfahan genomic cDNA clone.

FIG. 3A is a diagram of a rISFV vector [also designated rISFV-N4-G3-(VEEV ZPC E3-E1)5] encoding a Venezuelan equine encephalitis virus (VEEV) E3-E2-6K-E1 polyprotein; FIG. 3B is a Western blot depicting the expression of VEEV proteins (lane 3).

[031] FIG. 4 is an alignment of the amino acid sequences of the N protein of various vesiculoviruses. Regions of amino acid homology are shaded.

[032] FIG. 5 is a photograph of observed plaque sizes generated by various rISFVs expressing a modified HIV-1 gag protein.

[033] FIG. 6 depicts the percent survival of mice immunized with rISFV-N4 [also designated rISFV-N4-G3-(EEEV FL93 E3-E1)5] expressing eastern equine encephalitis virus (EEEV)-strain FL93 E3-E1 proteins, followed by lethal challenge with EEEV-FL93.

[034] FIG. 7 depicts the percent survival of mice immunized with rISFV-N4 [also designated rISFV-N4-G3-(VEEV ZPC E3-E1)5] expressing VEEV- strain ZPC E3-E1 proteins, followed by lethal challenge with VEEV-ZPC.

[035] FIG. 8 depicts the percent survival of mice immunized with rISFV-N4 [also designated rISFV-N4-G3-(VEEV ZPC E3-E1)5] expressing VEEV-ZPC E3-E1 proteins at 10^8 or 10^7 pfu and rVSV Indiana serotype N4CT1 ($rVSV_{IN}$N4CT1) [also designated $rVSV_{IN}$-N4-G3-(VEEV ZPC E3-E1)5] expressing VEEV-ZPC E3-E1 proteins at 10^8 or 10^7 pfu, followed by lethal challenge with VEEV-ZPC.

[036] FIG. 9 depicts the percent survival of mice immunized with rISFV-N4 expressing EEEV-FL93 E3-E1 proteins and rISFV-N4 expressing VEEV-ZPC E3-E1 proteins [together, also designated rISFV-N4G3-(VEEV ZPC E3-E1)5/rISFV-N4-G3-(EEEV FL93 E3-E1)5], followed by lethal challenge with EEEV-FL93.

[037] FIG. 10 depicts the percent survival of mice immunized with rISFV-N4 expressing EEEV-FL93 E3-E1 proteins and rISFV-N4 expressing VEEV-ZPC E3-E1 proteins [together, also designated rISFV-N4G3-(VEEV ZPC E3-E1)5/rISFV-N4-G3-(EEEV FL93 E3-E1)5], followed by lethal challenge with VEEV-ZPC.

[038] FIG. 11 illustrates the four amino acids that can be changed in the N protein sequence without negatively impacting biological function. A known epitope in BALB/c mice is underlined.

[039] FIG. 12 illustrates recombinant viruses tested in the PBS-Mu-062a study.

[040] FIG. 13 is a summary of the PBS-Mu-062a study design.

[041] FIG. 14 illustrates interferon gamma (IFN-γ) ELISpot responses to an HIV-1 gag epitope in the PBS-Mu-062a study.

[042] FIG. 15 illustrates rISFVs tested in the PBS-Mu-062b prime/boost study.

[043] FIG. 16 is a summary of the PBS-Mu-062b study design.

[044] FIG. 17 illustrates IFN-γ ELISpot responses to an HIV-1 Gag single dominant epitope in the PBS-Mu-062b study.

[045] FIG. 18 illustrates IFN-γ ELISpot responses to VSV-N in the PBS-Mu-062b study.

[046] FIG. 19 depicts body weights of mice immunized with rISFV-N4G-CTΔ25(CHIKV GP)1 versus unimmunized mice after challenge with the LaReunion isolate of CHIKV.

[047] FIG. 20 depicts footpad swelling of mice immunized with rISFV-N4G-CTΔ25(CHIKV GP)1 versus unimmunized mice after challenge with the LaReunion isolate of CHIKV.

[048] FIG. 21 depicts viremia of mice immunized with rISFV-N4G-CTΔ25(CHIKV GP)1 versus unimmunized mice after challenge with the LaReunion isolate of CHIKV.

[049] FIG. 22 depicts the survival of mice immunized with rISFV-N4G-CTΔ25(CHIKV GP)1, followed by lethal challenge with the LaReunion isolate of CHIKV.

DESCRIPTION

[050] Isfahan virus (ISFV) and vesicular stomatitis virus (VSV) are members of the *Vesiculovirus* genus in the family *Rhabdoviridae*. The prototypical rhabdoviruses are rabies virus (RV) and VSV. The *Rhabdoviridae* is a family of bullet shaped viruses having single strand non-segmented (-) sense RNA genomes. There are more than 250 known Rhabdoviruses that infect mammals, fish, insects, or plants. The family comprises at least 5 genera: (1) *Lyssavirus*: including RV, other mammalian viruses, and some insect viruses; (2) *Vesiculovirus*: including VSV; (3) *Ephemerovirus*: including bovine ephemeral fever virus; (4) *Cytorhabdovirus*: including lettuce necrotic yellow virus; and (5) *Nucleorhabdovirus*: including potato yellow dwarf virus.

[051] The rhabdovirus negative-sense viral RNA (vRNA) genome is approximately 11 - 15kb in length with an approximately 50 nucleotide 3' leader sequence and an approximately 60 nucleotide non-translated 5' trailer sequence. Rhabdovirus viral genomic RNA (vRNA) generally contains 5 genes encoding 5 major proteins: nucleocapsid protein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), and large protein (L)(also known as the polymerase).

Rhabdoviruses have a conserved polyadenylation signal at the 5' end of each gene and a short untranscribed intergenic region between each of the 5 genes. Typically these genes are in the order 3'-N-P-M-G-L-5' of the viral genome. The order of the genes dictates the levels of protein expression in the infected cell. Any manipulations of a Rhabdovirus genome to produce an infectious virus will typically include at least five transcription units (TU) encoding at least 4, and usually 5, of the major virus proteins to maintain the ability to infect and replicate at high levels.

I. RECOMBINANT VESICULOVIRUS

[052] Vesiculovirus genomes have been shown to accommodate more than one foreign gene spanning at least three kilobases (kb) of additional nucleotide sequence. Vesiculovirus vectors, which have been sufficiently attenuated (by, for example, gene shuffling and/or truncation of viral proteins), have demonstrated genetic stability, and the virus genome does not undergo detectable recombination. In addition, since viral replication is cytoplasmic, viral genomic RNA does not integrate into the host cell genome. Also, these negative-strand RNA viruses possess relatively simple, well-characterized transcriptional control sequences, which permit robust foreign gene expression. The level of foreign gene expression can be modulated by changing the position of the foreign gene relative to the single viral 3' transcription promoter (see, *e.g.*, US Patent No. 6,136,585 and 8,287,878, among others). The 3' to 5' gradient of gene expression reflects the decreasing likelihood that the transcribing viral RNA-dependent RNA polymerase will successfully traverse each transcription stop/start signal encountered at gene junctions as it progresses along the genome template. Thus, foreign genes placed in proximity to the 3' terminal transcription promoter are expressed abundantly, while those inserted in more distal genomic positions, less so.

[053] VSV replicates to high titers in a large array of different cell types, and viral proteins are expressed in great abundance. This not only means that VSV will act as a potent functional foreign gene expression vector, but also, that relevant rVSV vectors can be scaled to manufacturing levels in cell lines approved for the production of human biologicals. This replication-competent virus vector produces little to no disease symptoms or pathology in

healthy humans, even in the face of substantial virus replication (Tesh, R. B. *et al*, 1969 *Am. J. Epidemiol.*, *90*:255-61). Additionally human infection with, and thus pre-existing immunity to, VSV is rare. Therefore, rVSV is useful as a vector.

[054] While a variety of rVSVs have been disclosed in the art with their genes "shuffled" to genome positions different from those of wild-type VSV (see US Patent No. 8,287,878; US Patent No. 6,596,529, and references cited therein), it may be useful for the N gene to be in the fourth position (N4) in the VSV gene order as part of a combination of mutations, so that the virus is sufficiently attenuated. In order to further attenuate rVSV, the cytoplasmic tail of the G protein may be truncated (G-CT).

[055] Various embodiments of the rVSV described above employ VSV sequences derived from VSV serotype Indiana. However, other known vesiculoviruses (e.g., Isfahan virus) or VSV serotypes may be readily substituted for the exemplified sequences of the described embodiments given the teachings of this specification.

[056] Suitable promoters for use in generating vectors described herein may be selected from constitutive promoters, inducible promoters, tissue-specific promoters and others. Examples of constitutive promoters that are non-specific in activity and employed in the expression of nucleic acid molecules of this invention include, without limitation, those promoters identified in International Patent Application No. WO2004/093906 and US Patent No. 8,287,878. The hCMV promoter is used to express VSV proteins for rVSV rescue purposes in a reverse genetics technique. Other pol II promoters that may be used include, inter alia, the ubiquitin C (UbiC) promoter, the phosphoglycerate kinase (PGK) promoter, the bovine cytomegalovirus (bCMV) promoter, a beta-actin promoter with an upstream CMV IV enhancer (CAGGS), and the elongation factor 1 alpha promoter (EF1A). In certain embodiments, the T7 RNA polymerase promoter is used.

[057] Certain embodiments of the invention are directed to recombinant vesiculoviruses, including recombinant Isfahan virus (rISFV) alone or in combination with recombinant vesicular stomatitis virus (rVSV) for example in a prime/boost regimen, as well as vectors encoding

recombinant vesiculoviruses and methods of using such recombinant vesiculoviruses and vectors. Recombinant vesiculoviruses can be produced (1) using cDNA transfections or (2) cDNAs transfected into a cell, which is further infected with a minivirus providing in trans the remaining components or activities needed to produce a recombinant vesiculovirus. Using any of these methods (e.g., minivirus, helper cell line, or cDNA transfection), the minimum components for producing a packaged RNA require an RNA molecule containing the cis-acting signals for (1) encapsidation of the genomic RNA by the N protein, and (2) replication of a genomic RNA equivalent.

[058] A replicating element or replicon is a strand of RNA minimally containing at the 3' and 5' ends the leader sequence and the trailer sequence of a vesiculovirus; in the (-) sense genome, the leader is at the 3' end and the trailer is at the 5' end. RNA placed between these two replication signals can be replicated. The leader and trailer regions contain the minimal cis-acting elements for purposes of encapsidation by the N protein and for polymerase binding needed to initiate transcription and replication.

[059] For any gene contained within a recombinant vesiculovirus genome, the gene can be flanked by the appropriate transcription initiation and termination signals that enable expression of those genes and production of encoded protein products. In particular, a heterologous polynucleotide is used, which is not encoded by the virus as isolated from nature or contains a coding region in a position, form, or context that is not naturally found in a virus.

[060] A recombinant vesiculovirus for use as a therapeutic or an immunogenic composition can, in certain aspects, include rearranging the virus' gene order. In certain aspects the N gene is moved away from 3' promoter-proximal position, position 1. In a further aspect the N gene is moved to position 2, 3, 4, or 5. In certain aspects the N gene is at position 4 in the genome.

[061] In certain embodiments the recombinant vesiculovirus comprises a heterologous polynucleotide. In certain aspects, a heterologous polynucleotide encodes an antigen. In other aspects the heterologous polynucleotide or polygene coding for the selected heterologous

immune response-inducing antigen or antigens is located in position 1, 2, 3, 4, 5, or 6 of the gene order.

A. Recombinant Vesiculovirus Production

[062] The transcription and replication of negative-sense, single stranded, non-segmented, viral RNA genomes are achieved through the enzymatic activity of a multimeric protein complex acting on the ribonucleoprotein core (nucleocapsid). The viral sequences are recognized when they are encapsidated by the N protein into the nucleocapsid structure. The genomic and antigenomic terminal promoter sequences of the nucleocapsid structure are recognized to initiate the transcriptional or replication pathways.

[063] Thus, a genetically modified and attenuated recombinant vesiculovirus as described herein is produced according to rescue methods known in the art and more specifically as described in the examples below. Any suitable Isfahan virus, VSV strain or serotype may be used, including, but not limited to, VSV Indiana, VSV New Jersey, VSV Chandipura, VSV Glasgow, and the like. As described above, in addition to polynucleotide sequences encoding attenuated forms of Isfahan virus or VSV, the polynucleotide sequence also encodes heterologous polynucleotide sequences or open reading frames (ORFs) encoding a selected heterologous protein(s).

[064] The typical (although not necessarily exclusive) circumstances for rescue include an appropriate mammalian cell in which T7 polymerase is present in the cell cytoplasm to drive transcription of the antigenomic (or genomic) single-stranded RNA from the viral genomic cDNA-containing transcription vector. Either co-transcriptionally or shortly thereafter, this viral anti-genome (or genome) RNA transcript is encapsidated into functional templates by the nucleoprotein and engaged by the required polymerase components produced concurrently from co-transfected plasmids expressing the required virus-specific trans-acting proteins. These events and processes lead to the prerequisite transcription of viral mRNAs, the replication and amplification of new genomes and, thereby, the production of novel vesiculovirus progeny, *i.e.*, rescue.

[065] The transcription and expression vectors are typically plasmid vectors designed for expression in the host cell. Expression vectors that comprise at least one isolated nucleic acid molecule encoding the trans-acting proteins necessary for encapsidation, transcription, and replication express these proteins from one expression vector or at least two different vectors.

[066] A cloned DNA equivalent of a vesiculovirus genome can be placed between a suitable DNA-dependent RNA polymerase promoter (*e.g.*, the T7 RNA polymerase promoter) and a self-cleaving ribozyme sequence (*e.g.*, the hepatitis delta ribozyme), and inserted into a suitable transcription vector (*e.g.*, a bacterial plasmid). This transcription vector provides a readily manipulable DNA template from which the RNA polymerase (*e.g.*, T7 RNA polymerase) can faithfully transcribe a single-stranded RNA copy of the vesiculovirus cDNA with 5' and 3' termini. The orientation of the virus cDNA copy and the flanking promoter and ribozyme sequences determine whether anti-genome or genome RNA equivalents are transcribed. Also required for rescue of new vesiculovirus progeny are the vesiculovirus-specific trans-acting support proteins needed to encapsidate the naked, single-stranded anti-genome or genome RNA transcripts into functional nucleocapsid templates, and to start viral transcription and replication: the viral nucleocapsid (N) protein, the polymerase-associated phosphoprotein (P) and the polymerase (L) protein.

[067] Briefly, one method of generating a recombinant vesiculovirus comprises introducing into a host cell a viral cDNA expression vector comprising a nucleic acid sequence described herein. In certain aspects, the expression vector comprises a T7 promoter upstream of position 1 (P_1), and a hepatitis delta virus ribozyme site (HDV Rz) and T7 terminator sequence downstream of the last position of a selected recombinant vesiculovirus nucleic acid sequence. The T7 promoter directs synthesis of viral RNA anti-genome transcripts from the expression vector when in the presence of the T7 RNA polymerase.

[068] In some embodiments, the method further comprises transiently transfecting a host cell with a plasmid expressing the T7 RNA polymerase. In other embodiments, the method further involves co-transfecting the host cell with one or more plasmids expressing at least the viral proteins N, P, and L of a vesiculovirus (and optionally M and G). In some embodiments,

these vesiculovirus proteins are expressed in the host cell using an RNA polII-dependent expression system. Other embodiments include steps such as heat-shocking the host cells containing the expression vector, T7 polymerase, and viral proteins of a recombinant vesiculovirus after plasmid DNA (pDNA) transfection. The transfected host cells or supernatant obtained from the transfected host cells may be transferred into a culture of fresh expansion cells. Assembled, infectious recombinant vesiculovirus can then be recovered from the culture.

[069] In other aspects, a replication-competent recombinant vesiculovirus may be isolated and "rescued" using techniques known in the art (Ball, L. A. *et al.* 1999 *J. Virol.*, 73:4705-12; Conzelmann, 1998, *Ann. Rev. Genet.*, *32*:123-162; Roberts and Rose, 1998, *Virol., 247*:1-6). See, also, *e.g.*, US Patents 8,287,878; 6,168,943; and 6,033,886; and International Patent Publication No. WO99/02657, each of which is incorporated herein by reference. Methods of producing recombinant RNA virus are referred to in the art as "rescue" or "reverse genetics" methods. Exemplary rescue methods for VSV are described in U.S. Patents 6,033,886 and 6,596,529, and PCT publication WO 2004/113517, each incorporated herein by reference.

[070] Additional techniques for conducting rescue of viruses such as VSV are described in U.S. Patent 6,673,572 and U.S. publication number US2006/0153870, which are hereby incorporated by reference.

[071] The host cells used in the rescue of vesiculoviruses are those that permit the expression from the vectors of the requisite constituents necessary for the production of recombinant vesiculovirus. Such host cells can be selected from a eukaryotic cell, such as a vertebrate cell. In general, host cells are derived from a human cell, such as a human embryonic kidney cell (*e.g.*, 293). Vero cells, as well as many other types of cells are also used as host cells as described in the US patents and published application cited above. In certain embodiments, a transfection-facilitating reagent is added to increase DNA uptake by cells. Many of these reagents are known in the art (*e.g.*, calcium phosphate, LIPOFECTAMINE® cationic lipid (Life Technologies, Gaithersburg, MD) and EFFECTENE® cationic lipid (Qiagen, Hilden, Germany).

[072] The rescued vesiculovirus is then tested for its desired phenotype (plaque morphology and transcription and replication attenuation), first by *in vitro* means. The vesiculovirus is also tested *in vivo* in an animal neurovirulence model. For example, mouse and/or ferret models are established for detecting neurovirulence. Briefly, groups of ten mice are injected intra-cranially (IC) with each of a range of virus concentrations that span the anticipated LD_{50} dose (a dose that is lethal for 50% of animals). For example, IC inoculations containing virus at 10^2, 10^3, 10^4 and 10^5 pfu are used where the anticipated LD_{50} for the virus is in the range 10^3 -10^4 pfu. Virus formulations are prepared by serial dilution of purified virus stocks in PBS. Mice are then injected through the top of the cranium with the requisite dose, in 25 μl of PBS. Animals are monitored daily for weight loss, morbidity and death. The LD_{50} for a virus vector is then calculated from the cumulative death of mice over the range of concentrations tested.

[073] To determine immunogenicity or antigenicity by detecting humoral immune responses, various immunoassays known in the art are used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), “sandwich” immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, immunoprecipitation reactions, agglutination assays (*e.g.*, gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, neutralization assays, etc. In one embodiment, antibody binding is measured by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by measuring binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. In still another embodiment for detecting immunogenicity, T cell-mediated responses are assayed by standard methods, *e.g.*, *in vitro* or *in vivo* cytoxicity assays, tetramer assays, ELISpot assays or *in vivo* delayed-type hypersensitivity assays.

[074] The terms “isolation” or “isolating” a vesiculovirus means the process of culturing and purifying the virus particles from cellular debris and the like. One example would be to take

the virus containing supernatant of a cell culture producing vesiculovirus and pass it through a 0.1-0.2 micron pore size filter (e.g., Millex-GS, Millipore) to remove cellular debris. Alternatively, virions can be purified using a gradient, such as a sucrose gradient. Recombinant virus particles can then be pelleted and resuspended in whatever excipient or carrier is desired. Titers can be determined by standard plaque assay or by indirect immunofluorescence using antibodies specific for particular proteins.

[075] In certain aspects, vesiculoviruses that encode or contain one or more protein components (N, P, M, G, and/or L proteins) and a heterologous polynucleotide have been constructed with one or more mutations or variations as compared to a wild-type virus or viral proteins such that the virus has desirable properties for expressing heterologous polynucleotide(s), while having characteristics that are not present in the virus as originally isolated. The methods described herein provide various examples of protocols for implementing methods and compositions of the invention. They provide background for generating mutated or variant viruses through the use of recombinant DNA or nucleic acid technology.

B. Isfahan Virus (ISFV) Constructs

[076] Isfahan virus (ISFV) is a member of the *Vesiculovirus* genus in the *Rhabdoviridae* family. ISFV was first isolated from sand flies in Iran in 1975 (Tesh et al. *The American journal of tropical medicine and hygiene.* 1977; 26(2):299-306). ISFV appears to be geographically restricted to Iran and some neighboring countries, where there is serological evidence for human infection (Tesh et al., *The American journal of tropical medicine and hygiene.* 1977, 26(2):299-306; Gaidamovich et al., *Voprosy Virusologii.* 1978, (5):556-60). Infection with ISFV has not been linked to human disease and, unlike the prototypical *Vesiculovirus*, vesicular stomatitis virus (VSV), ISFV does not appear to cycle in livestock and/or to cause vesicular lesions in experimentally inoculated animals (Wilks and House, *J Hyg (Lond).* 1986, 97(2):359-68). ISFV is morphologically similar to VSV (Tesh et al. *The American journal of tropical medicine and hygiene.* 1977; 26(2):299-306) and has a similar genomic organization, including highly conserved replication and transcription regulatory sequences (Marriott, *Arch Virol.* 2005, 150(4):671-80). However, both viruses are serologically distinct (Tesh et al. *The American*

journal of tropical medicine and hygiene. 1977; 26(2):299-306) and a phylogenetic analysis of vesiculoviruses shows substantial evolutionary divergence (FIG. 1), based upon an amino acid alignment of virus proteins.

[077] Isfahan virus comprises an approximately 11 kb non-segmented, negative-strand RNA genome that encodes five major viral proteins abbreviated N, P, M, G, and L. The nucleotide sequence of the complement (5' to 3') to the Isfahan viral genome is provided in SEQ ID NO:1. The 3' to 5' genomic order in the negative sense RNA genome encodes proteins designated as nucleocapsid (N), phosphoprotein (P), matrix protein (M), transmembrane glycoprotein (G) and polymerase (L), *i.e.*, 3'- N-P-M-G-L-5'. The nucleocapsid is involved in genome encapsidation. An amino acid sequence of an example of the Isfahan virus N protein is provided as SEQ ID NO:2. The P protein is a phosphoprotein involved in RNA synthesis. The amino acid sequence of an example of the Isfahan virus P protein is provided as SEQ ID NO:3. The M protein is a matrix protein. The amino acid sequence of an example of the Isfahan virus M protein is provided as SEQ ID NO:4. The G protein is a glycoprotein. The amino acid sequence of an example of the Isfahan virus G protein is provided as SEQ ID NO:5. The L protein is a large polymerase involved in RNA synthesis. The amino acid sequence of an example of the Isfahan virus L protein is provided as SEQ ID NO:6.

[078] The divergence of ISFV from VSV can be used to aid therapeutic and prophylactic regimens by (1) using rISFV as a vector in place of rVSV, and thus avoiding potential anti-vector immunity with repeated administration of VSV vector; and (2) providing a second Vesiculovirus vector so as to constitute a heterologous prime-boost regimen with rVSV.

C. Vesicular Stomatitis Virus (VSV) Constructs

[079] Vesicular stomatitis virus (VSV) comprises an approximately 11 kb non-segmented, negative-strand RNA genome that encodes five major viral proteins abbreviated N, P, M, G, and L. The nucleotide sequences encoding VSV G, M, N, P, and L proteins are known in the art (Rose and Gallione, 1981, *J. Virol.* 39, 519-28; Gallione et al., 1981 *J. Virol.* 39:529-35). A number of VSV serotypes are known and have been sequenced. The genomic sequence of VSV (Indiana) is provided under Accession No. NC001560 in the NCBI database (see SEQ ID NO:7-

12), which is incorporated herein as of the priority date of this application. Other sequences for VSV, including VSV (Chandipura) sequences, are available in that database; for example, see Accession Nos. Ay382603, Af128868, V01208, V01207, V01206, M16608, M14715, M14720 and J04350, all of which are incorporated herein as of the priority date of this application. VSV serotypes, such as New Jersey, are also available from depositories such as the American Type Culture Collection, Rockville, Maryland (see, *e.g.*, Accession Nos. VR-1238 and VR-1239, which are incorporated herein as of the priority date of this application). Other known VSV sequences and serotypes are described in the art or referenced in the documents cited throughout this specification, see, *e.g.*, International Patent Application No. WO2004/093906 and US Patent No. 8,287,878, which are incorporated herein as of the priority date of this application.

II. IMMUNOGENIC COMPOSITIONS

[080] Certain embodiments are directed to recombinant vesiculovirus compositions and methods for inducing an antigen-specific immune response to an antigen when administered to a mammalian subject. An immunogenic composition useful in this invention is a replication-competent, attenuated, recombinant Isfahan virus (rISFV) or a vector encoding the same. In certain embodiments, the immunogenic composition contains a recombinant vesiculovirus described herein. Certain aspects are directed to rISFV as described herein. In a further aspect a rISFV comprises a heterologous polynucleotide encoding one or more antigens.

A. Antigens

[081] In certain embodiments a vesiculovirus (e.g., rISFV alone, or in a prime/boost regimen with rVSV) encodes a heterologous antigen. As used herein, the term “antigen” or “targeted antigen” refers to any substance, including complex antigens (e.g. tumor cells, virus infected cells, etc.) that is capable of being the target of an immune response. An antigen may be the target of, for example, a cell-mediated and/or humoral immune response of a subject administered or provided an immunogenic composition described herein. The term “antigen” or “targeted antigen” encompasses for example all or part of viral antigens, bacterial antigens, tumor-specific or tumor-related antigens, parasitic antigens, allergens, and the like. An antigen is capable of being bound by an antibody or T-cell receptor. An antigen is additionally capable

of inducing a humoral and/or cellular immune response leading to the production of B- and/or T-lymphocytes. The structural aspect of an antigen, e.g., three-dimensional conformation or modification (e.g., phosphorylation), giving rise to a biological response is referred to herein as an "antigenic determinant" or "epitope." The antigenic determinants or epitopes are those parts of an antigen that are recognized by antibodies, or in the context of an MHC, by T-cell receptors.

[082] Viral antigens include for example antigens from rhabdoviruses (e.g., *Lyssavirus* including rabies virus), alphaviruses, hepatitis viruses A, B, C, D and E, HIV, herpes viruses, cytomegalovirus, varicella zoster, papilloma viruses, Epstein Barr virus, parainfluenza viruses, adenoviruses, Coxsakie viruses, picornaviruses, rotaviruses, pox viruses, rhinoviruses, rubella virus, papovavirus, mumps virus, measles virus; some non-limiting examples of known viral antigens include the following: antigens derived from alphaviruses such as nsP1–nsP4, capsid, E3, E2, 6K, and E1 proteins; HIV-1 such as tat, nef, gp120 or gp160, gp40, p24, gag, env, vif, vpr, vpu, rev or part and/or combinations thereof; antigens derived from human herpes viruses such as HSV-2 with antigens such as gH, gL, gM, gB, gC, gK, gE or gD, Immediate Early proteins such as ICP27, ICP47, ICP4, ICP36 and ICP0, VP16, US6, US8, UL7, UL19, UL21, UL25, UL46, UL47, UL48, UL49 and UL50, or part and/or combinations thereof; antigens derived from cytomegalovirus, especially human cytomegalovirus such as gB or derivatives thereof; antigens derived from Epstein Barr virus such as gp350 or derivatives thereof; antigens derived from Varicella Zoster Virus such as gpl, 11, 111 and IE63; antigens derived from a hepatitis virus such as hepatitis B, hepatitis C or hepatitis E virus antigen (e.g. env proteins E1 or E2, core protein, NS2, NS3, NS4a, NS4b, NS5a, NS5b, p7, or part and/or combinations thereof of HCV); antigens derived from human papilloma viruses (for example, proteins, e.g., L1, L2, E1, E2, E3, E4, E5, E6, E7, or part and/or combinations thereof); antigens derived from other viral pathogens, such as Respiratory Syncytial virus (e.g. F and G proteins or derivatives thereof), flaviviruses (e.g. Yellow Fever Virus, Dengue Virus, Tick-borne encephalitis virus, Japanese Encephalitis Virus) or Influenza viruses (e.g. HA, NP, NA, or M proteins, or part and/or combinations thereof).

[083] Tumor-specific, tumor-related, or cancer antigens include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. Expression of such antigens by rISFV provides both the induction of a cell-mediated immune response against the cancer cell and direct cancer cell lysis by rISFV. More particular examples of such cancers include breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer, renal cancer, malignant melanoma, laryngeal cancer, prostate cancer. Cancer antigens are antigens that can potentially stimulate tumor-specific immune responses. Some of these antigens are encoded, although not necessarily expressed, by normal cells. These antigens can be characterized as those that are normally silent (i.e., not expressed) in normal cells, those that are expressed only at certain stages of differentiation and those that are temporally expressed such as embryonic and fetal antigens. Other cancer antigens are encoded by mutant cellular genes, such as oncogenes (e.g., activated ras oncogene), suppressor genes (e.g., mutant p53), fusion proteins resulting from internal deletions or chromosomal translocations. Still other cancer antigens are encoded by viral genes, such as those carried on RNA and DNA tumor viruses. Some non-limiting examples of tumor-specific or tumor-related antigens include MART-1/Melan-A, gp100, Dipeptidyl peptidase IV (DPPIV), adenosine deaminase-binding protein (ADAbp), cyclophilin b, Colorectal associated antigen (CRC)-0017-1A/GA733, Carcinoembryonic Antigen (CEA) and its immunogenic epitopes CAP-1 and CAP-2, etv6, aml1, Prostate Specific Antigen (PSA) and its immunogenic epitopes PSA-1, PSA-2, and PSA-3, prostate-specific membrane antigen (PSMA), T-cell receptor/CD3-zeta chain, MACE-family of tumor antigens (e.g., MAGE-A1, MAGE-A2, MAGE-A3, MAGE-A4, MAGE-A5, MAGE-A6, MAGE-A7, MAGE-A8, MAGE-A9, MAGE-A10, MAGE-A11, MAGE-A12, MAGE-Xp2 (MAGE-B2), MAGE-Xp3 (MAGE-B3), MAGE-Xp4 (MAGE-B4), MAGE-C1, MAGE-C2, MAGE-C3, MAGE-C4, MAGE-05), GAGE-family of tumor antigens (e.g., GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, GAGE-7, GAGE-8, GAGE-9), BAGE, RAGE, LAGE-1, NAG, GnT-V, MUM-1, CDK4, tyrosinase, p53, MUG family (e.g. MUC-1), HER2/neu, p21ras, RCAS1, alpha-fetoprotein, E-cadherin, alpha-

catenin, beta-catenin and gamma-catenin, p120ctn, gp100Pme1117, PRAME, NY-ESO-1, cdc27, adenomatous polyposis coli protein (APC), fodrin, Connexin 37, Ig-idiotype, p15, gp75, GM2 and GD2 gangliosides, viral products such as human papilloma virus proteins, Smad family of tumor antigens, Imp-1, P1A, EBV-encoded nuclear antigen (EBNA)-1, brain glycogen phosphorylase, SSX-1, SSX-2 (HOM-MEL-40), SSX-1, SSX-4, SSX-5, SCP-1 and CT-7, and c-erbB-2.

[084] In another embodiment, an attenuated rISFV is utilized *per se*, that is without the inclusion of a heterologous polynucleotide sequence, as an anti-cancer (oncolytic) therapeutic. ISFV possesses tumor cell killing properties *in vitro* and *in vivo*. The term "oncolytic" typically refers to an agent that is capable of killing, lysing, or halting the growth of a cancer cell. In terms of an oncolytic virus the term refers to a virus that can replicate to some degree in a cancer cell, cause the death, lysis, or cessation of cancer cell growth and typically have minimal toxic effects on non-cancer cells. The rISFV is attenuated using any of the methods described herein.

[085] Bacterial antigens include for example antigens from Mycobacteria causing TB and leprosy, pneumococci, aerobic gram-negative bacilli, *mycoplasma*, staphylococcus, streptococcus, salmonellae, chlamydiae, or neisseriae.

[086] Other antigens include for example antigens from parasites such as malaria, leishmaniasis, trypanosomiasis, toxoplasmosis, schistosomiasis, filariasis, as well as antigens that are allergens.

[087] In another aspect the ISFV G gene may be replaced in its entirety by one or more of the heterologous polynucleotide sequences described above. In still another aspect the ISFV G gene may be replaced by a heterologous G gene of a second vesiculovirus, i.e., pseudotyped. In certain aspects a rISFV can be pseudotyped with a G gene from VSV. The VSV G gene can be selected from among the VSV serotypes listed above.

[088] According to variants of the invention, the immunogenic composition comprises at least two targeted antigens, or a heterologous nucleotide sequence encoding at least two targeted

antigens, or at least two heterologous nucleotide sequences encoding at least two targeted antigens, or any combination thereof.

[089] In certain embodiments the heterologous antigen is an alphavirus antigen. Most alphaviruses infect terrestrial vertebrates via mosquito-borne transmission and exhibit a broad host range (Strauss et al., 1994 *Microbiol Rev.* 58(3):491-562). Occasionally, these cycles spill over into humans and domesticated animals to cause disease. Human infections with Old World viruses such as Ross River virus, chikungunya virus, and SINV are typically characterized by fever, rash, and polyarthritis, whereas infections with the New World viruses Venezuelan Equine Encephalitis virus (VEEV), Eastern Equine Encephalitis virus (EEEV), and Western Equine Encephalitis virus (WEEV) can cause fatal encephalitis (Strauss et al., 1994 *Microbiol Rev.* 58(3):491-562). As a consequence the latter viruses were developed as biological weapons during the cold war, and recent aerosol infections of primates confirm their highly debilitating and/or lethal properties (Reed et al., 2007 *The Journal of Infectious Diseases* 196:441-450; Reed et al., 2005 *The Journal of Infectious Diseases* 192:1173-1182; Reed et al., 2004 *The Journal of Infectious Diseases* 189:1013-1017; Smith et al., 2009 Alphaviruses, p. 1241-1274. In D. D. Richman, R. J. Whitley, and F. G. Hayden (ed.), Clinical Virology. ASM Press, Washington, D.C.). EEEV is uniformly lethal for cynomolgus macaques after high dose aerosol infection and causes one of the highest natural human case-fatality rates (>50%) of any viral infection (Reed et al., 2007 *The Journal of Infectious Diseases* 196:441-450). VEEV infection of humans is not typically fatal, but this virus is one of the most infectious viruses by aerosol and is highly debilitating as well as immunosuppressive (Reed et al., 2004 *The Journal of Infectious Diseases* 189:1013-1017; Smith et al., 2009 *Alphaviruses*, p. 1241-1274. In D. D. Richman, R. J. Whitley, and F. G. Hayden (ed.), Clinical Virology. ASM Press, Washington, D.C.; Weaver et al., 2004. *Annu. Rev. Entomol.* 49:141-174). Furthermore, it causes extensive endemic disease throughout Latin America, and its intentional introduction could result in equine amplification and mosquito transmission to infect hundreds of thousands of persons. These traits have resulted in the assignment of the encephalitic alphaviruses to the NIAID category B pathogen list.

[090] Because there are no licensed antiviral treatments or immunogenic compositions for alphaviral diseases, the U.S. population remains vulnerable to a biological attack as well as to natural infections with the 3 encephalitides. Development of an effective antiviral treatment is particularly challenging because diagnoses generally occur only after the prodromal illnesses have progressed to encephalitis about one week after infection. Therefore, immunization is the best approach to protecting against fatal disease.

[091] To address this unmet need, rISFV has been modified to express the E3-E1 glycoproteins of VEEV and EEEV for use as a stand-alone immunogenic composition for both alphaviruses, and/or for use in heterologous prime-boost immunization regimens with rVSV vectors expressing VEEV and EEEV E3-E1 glycoproteins, should such a immunization modality be necessary for optimal efficacy.

B. Formulation of Recombinant Vesiculoviruses

[092] The immunogenic compositions useful in this invention, e.g., rISFV alone or in a prime/boost regimen with rVSV compositions, further comprise an immunologically or pharmaceutically acceptable diluent, excipient or carrier, such as sterile water or sterile isotonic saline. The immunogenic compositions may also be mixed with such diluents or carriers in a conventional manner. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with administration to humans or other vertebrate hosts. The appropriate carrier is evident to those skilled in the art and will depend in large part upon the route of administration. Thus, the immunogenic compositions useful in this invention may comprise a recombinant replicable ISFV comprising one or more of an N protein gene, a P protein gene, an M protein gene, a G protein gene, and an L protein gene; and further comprising a heterologous polynucleotide sequence, wherein said heterologous polynucleotide sequence (a) is flanked by a transcription start signal and a transcription stop signal, and (b) encodes a heterologous polypeptide; and a pharmaceutically acceptable diluent, excipient or carrier.

[093] Additional components may be present in the immunogenic compositions, including, but not limited to preservatives, surface-active agents, and chemical stabilizers, suspending or dispersing agents. Typically, stabilizers, adjuvants, and preservatives are optimized to determine the best formulation for efficacy in the target human or animal. Suitable exemplary preservatives include chlorobutanol, potassium sorbate, sorbic acid, sulfur dioxide, propyl gallate, the parabens, ethyl vanillin, glycerin, phenol, and parachlorophenol.

[094] Suitable stabilizing ingredients that may be used include, for example, casamino acids, sucrose, gelatin, phenol red, N-Z amine, monopotassium diphosphate, lactose, lactalbumin hydrolysate, and dried milk. Suitable surface-active substances include, without limitation, Freund's incomplete adjuvant, quinone analogs, hexadecylamine, octadecylamine, octadecyl amino acid esters, lysolecithin, dimethyl-dioctadecylammonium bromide, methoxyhexadecylgylcerol, and pluronic polyols; polyamines, *e.g.*, pyran, dextran sulfate, poly IC, carbopol; peptides, *e.g.*, muramyl peptide and dipeptide, dimethylglycine, tuftsin; oil emulsions; and mineral gels, *e.g.*, aluminum phosphate, etc. and immune stimulating complexes (ISCOMS). The rISFVs and rVSVs or any of their polypeptide components may also be incorporated into liposomes for use as an immunogenic composition. The immunogenic compositions may also contain other additives suitable for the selected mode of administration of the composition. The compositions of the invention may also involve lyophilized formulations, which can be used with other pharmaceutically acceptable excipients for developing powder, liquid or suspension dosage forms. See, *e.g.*, Remington: The Science and Practice of Pharmacy, Vol. 2, 19th edition (1995), *e.g.*, Chapter 95 Aerosols; and International Patent Publication No. WO99/45966, the teachings of which are hereby incorporated by reference.

[095] These immunogenic compositions can contain additives suitable for administration via any conventional route of administration. In some embodiments, the immunogenic composition of the invention is prepared for administration to human subjects in the form of, for example, liquids, powders, aerosols, tablets, capsules, enteric-coated tablets or capsules, or suppositories. Thus, the immunogenic compositions may also include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-

release or biodegradable formulations. In one embodiment of a formulation for parenteral administration, the active ingredient is provided in dry (*i.e.*, powder or granular) form for reconstitution with a suitable vehicle (*e.g.*, sterile pyrogen-free water) prior to parenteral administration of the reconstituted composition. Other useful parenterally-administrable formulations include those which comprise the active ingredient in microcrystalline form, in a liposomal preparation, or as a component of a biodegradable polymer system. Compositions for sustained release or implantation may comprise pharmaceutically acceptable polymeric or hydrophobic materials such as an emulsion, an ion exchange resin, a sparingly soluble polymer, or a sparingly soluble salt.

[096] The immunogenic compositions described herein are not limited by the selection of the conventional, physiologically acceptable carriers, adjuvants, or other ingredients useful in pharmaceutical preparations of the types described above. The preparation of these pharmaceutically acceptable compositions, from the above-described components, having appropriate pH isotonicity, stability and other conventional characteristics is within the skill of the art.

[097] For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous, intratumoral, and intraperitoneal administration. In this connection, sterile aqueous media that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards required by governments of the countries in which the compositions are being used.

[098] As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

[099] The phrase "pharmaceutically acceptable" or "pharmacologically acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a virus particle as an active ingredient is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared.

[0100] As described above, any of the embodiments of the recombinant vesiculoviruses may be used in these methods of treatment. Desirably, this composition is admixed with a pharmaceutically acceptable diluent or other components as described above. In one embodiment, the treatment or prevention of an infection caused by a pathogen involves administration of one or more effective amounts of one or a combination of the recombinant vesiculoviruses described herein.

C. Administration of Recombinant Vesiculovirus

[0101] The antigenic or immunogenic compositions of this invention are administered to a human or to other mammalian subjects by a variety of routes including, but not limited to, intramuscular, intratumoral, intraperitoneal, subcutaneous, intravenous, intraarterial, intranasal, oral, sublingual, buccal, vaginal, rectal, parenteral, intradermal, and transdermal (*see*, *e.g.*, International patent publication No. WO 98/20734, which is hereby incorporated by reference). The appropriate route is selected depending on the nature of the immunogenic composition used, and an evaluation of the age, weight, sex and general health of the patient and the antigens present in the immunogenic composition, and similar factors by an attending physician.

[0102] In the examples provided below, both the immunogenic rISFV compositions and rVSV compositions are administered intramuscularly (i.m.) either individually or in combination in a prime/boost regimen. In other embodiments, it is desirable to administer the rISFV compositions and rVSV compositions by different routes. For example, the rISFV composition may be administered by conventional means, including intramuscular and intranasal administration. However, the selection of dosages and routes of administration are not limitations upon this invention.

[0103] The order of immunogenic composition administration and the time periods between individual administrations may be selected by the attending physician or one of skill in the art based upon the physical characteristics and precise responses of the host to the application of the method. Such optimization is expected to be well within the skill of the art.

[0104] In general, selection of the appropriate "effective amount" or dosage for the components of the immunogenic composition(s) of the present invention will also be based upon whether the administration is rISFV only or prime/boost with an rVSV composition, as well as the physical condition of the subject, most especially including the general health, age and weight of the immunized subject. The method and routes of administration and the presence of additional components in the immunogenic compositions may also affect the dosages and amounts of the rISFV and rVSV compositions. Such selection and upward or downward adjustment of the effective dose is within the skill of the art. The amount of rISFV and rVSV required to induce an immune response, such as a protective response, or produce a therapeutic effect in the patient without significant adverse side effects varies depending upon these factors.

[0105] A suitable dose is formulated in a pharmaceutical composition, as described above (*e.g.*, dissolved in about 0.1 ml to about 2 ml of a physiologically compatible carrier) and delivered by any suitable means. The treatments may include various "unit doses." Unit dose is defined as containing a predetermined quantity of the therapeutic composition. The quantity to be administered, and the particular route and formulation, are within the skill of those in the clinical arts. A unit dose need not be administered as a single injection but may comprise continuous infusion over a set period of time. Unit dose of the present invention may conveniently be described in terms of plaque forming units (pfu) or viral particles for viral constructs. Unit doses range from 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13} pfu or infectious viral particles (vp) and higher. Alternatively, depending on the virus and the titer attainable, one will deliver 1 to 100, 10 to 50, 100-1000, or up to about $1x10^4$, $1x10^5$, $1x10^6$, $1x10^7$, $1x10^8$, $1x10^9$, $1x10^{10}$, $1x10^{11}$, $1x10^{12}$, $1x10^{13}$, $1x10^{14}$, or $1x10^{15}$ or higher vp to the patient or to the patient's cells. A suitable dose is formulated in a pharmaceutical composition as described (for example, dissolved in about 0.1 ml to about 2 ml of a physiologically compatible carrier) and delivered by any suitable means.

[0106] In one embodiment, the single or boosting dosages for rISFV are the same. Such dosages are generally between $1x10^7$ pfu (or measured as viral particles) and $1x10^9$ pfu/viral particles/ml. However, any suitable dose is readily determined by persons skilled in the art.

[0107] In the second embodiment of the methods described herein, the administration of a recombinant vesiculovirus (e.g., rISFV) is preceded by administering to a mammalian subject an effective amount of a priming composition comprising a second recombinant vesiculovirus (e.g., rVSV) comprising one or more open reading frames encoding the same or heterologous antigens as those encoded by the first virus. Alternatively, the administration of the first virus is followed by the administration of the second virus. In either regimen, more than one dose of the first virus and/or the second virus may be administered.

[0108] According to the present invention, for example, the rVSV immunogenic composition may be administered as a boosting composition subsequent to the administration of the priming rISFV immunogenic composition that presents the selected heterologous antigen or antigens to the host. The mammalian subject is administered an effective amount of a priming composition comprising a rISFV comprising one or more open reading frames encoding one or more heterologous proteins under the control of regulatory sequences directing expression thereof and a pharmaceutically acceptable diluent prior to the immunogenic rVSV composition. When used as a priming composition, this rISFV composition is administered once or more than once prior to the boosting rVSV composition.

[0109] In another embodiment of the prime/boost method, the priming rISFV composition is administered at least once prior to the immunogenic rVSV composition, or administered both prior to and after the rVSV immunogenic composition.

[0110] In still further embodiments of the prime/boost regimen, multiple rVSV compositions are administered as later boosters. In one embodiment at least two rVSV compositions are administered following the priming compositions.

[0111] Each subsequent vesiculovirus composition may have a different serotype selected from known serotypes and from among any synthetic serotypes provided by manipulation of the vesiculovirus G protein. For example, one rVSV may be the Indiana serotype and the other may be the Chandipura serotype or the New Jersey serotype. In another embodiment, additional rVSV boosters are of the same serotype. When used as a boosting composition, the rVSV compositions are administered serially, after the priming rISFV immunogenic compositions. rISFVs and rVSVs displaying a desired balance of attenuation and immunogenicity are useful in this invention.

[0112] In still another embodiment, administration of one or more of the rISFV immunogenic compositions is followed by one or more administrations of the rVSV immunogenic compositions, and then followed by one or more additional administrations of the rISFV immunogenic compositions.

[0113] In yet another embodiment, administration of one or more of the rISFV immunogenic compositions is preceded or followed by administration of one or more plasmid DNA immunogenic compositions, wherein the plasmid DNA(s) encode the same or different heterologous polypeptides as the rISFV immunogenic compositions.

III. PROTEINACEOUS COMPOSITIONS

[0114] Proteinaceous compositions of the invention include viral particles and compositions including the viral particles. In certain embodiments, vesiculoviruses will be engineered to include polypeptide variants of viral proteins N, P, M, G, and/or L; and/or heterologous polynucleotides. As used herein, a “protein” or “polypeptide” refers to a polymer of amino acid residues. In some embodiments, a wild-type version of a protein or polypeptide are employed, however, in many embodiments, all or part of a viral protein or polypeptide is absent or altered so as to render the virus more useful for therapy.

[0115] A “modified protein” or “modified polypeptide” or “variant protein” or “variant polypeptide” refers to a protein or polypeptide whose chemical structure or amino acid sequence is altered with respect to the wild-type or a reference protein or polypeptide. In some embodiments, a modified protein or polypeptide has at least one modified activity or function (recognizing that proteins or polypeptides may have multiple activities or functions). The modified activity or function may be reduced, diminished, eliminated, enhanced, improved, or altered in some other way with respect to that activity or function in a wild-type protein or polypeptide, or the characteristics of virus containing such a polypeptide. It is contemplated that a modified protein or polypeptide may be altered with respect to one activity or function yet retain wild-type or unaltered activity or function in other respects. Alternatively, a modified protein may be completely nonfunctional or its cognate nucleic acid sequence may have been altered so that the polypeptide is no longer expressed at all, is truncated, or expresses a different amino acid sequence as a result of a frame-shift or other modification.

[0116] It is contemplated that polypeptides may be modified by truncation, rendering them shorter than their corresponding unaltered form or by fusion or domain shuffling which may render the altered protein longer.

[0117] Amino acid sequence variants of the polypeptides of the present invention can be substitutional, insertional, or deletion variants. A mutation in a gene encoding a polypeptide may affect 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500 or more non-contiguous or contiguous amino acids (i.e., segment) of a polypeptide, as compared to a wild-type or unaltered polypeptide or other reference polypeptide. Various polypeptides encoded by vesiculoviruses may be identified by reference to sequence listing filed with this application or GenBank Accession Numbers and related public database entries provided herein.

[0118] Deletion variants lack one or more residues of the native, unaltered, or wild-type protein. Individual residues can be deleted, or all or part of a domain (such as a catalytic or binding domain) can be deleted. The cytoplasmic tail of the vesiculovirus G protein may be truncated so as to attenuate the virus. For example, the rISFV G protein may have a carboxy-terminal truncation of 20 to 25 amino acids, while the rVSV G protein may have a carboxy-terminal truncation of 20 to 28 amino acids. Further attenuation may be achieved by also shuffling the N gene away from its native first position in the vesiculovirus genome, or by a non-cytopathic (ncp) M gene mutation at amino acid positions 33 and 51, as described in U.S. Patent 8,287,878. A stop codon may be introduced (by substitution or insertion) into an encoding nucleic acid sequence to generate a truncated protein. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide, a specific type of insert is a chimeric polypeptide that include homologous or similar portions of a related protein in place of the related portion of a target protein. This may include the insertion of an immunoreactive epitope or simply one or more residues. Terminal additions, typically called fusion proteins, may also be generated.

[0119] Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, with or without the loss of other functions or properties. Substitutions may be conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine;

serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine. Alternatively, substitutions may be non-conservative such that a function or activity of the polypeptide is affected. Non-conservative changes typically involve substituting a residue with one that is chemically dissimilar, such as a polar or charged amino acid for a nonpolar or uncharged amino acid, and vice versa.

[0120] The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers to codons that encode biologically equivalent amino acids. Amino acids codons include: Alanine (Ala, A) GCA, GCC, GCG, or GCU; Cysteine (Cys, C) UGC or UGU; Aspartic acid (Asp, D) GAC or GAU; Glutamic acid (Glu, E) GAA or GAG; Phenylalanine (Phe, F) UUC or UUU; Glycine (GIy, G) GGA, GGC, GGG or GGU; Histidine (His, H) CAC or CAU; Isoleucine (Ile, I) AUA, AUC, or AUU; Lysine (Lys, K) AAA or AAG; Leucine (Leu, L) UUA, UUG, CUA, CUC, CUG, or CUU; Methionine (Met, M) AUG; Asparagine (Asn, N) AAC or AAU; Proline (Pro, P) CCA, CCC, CCG, or CCU; Glutamine (Gln, Q) CAA or CAG; Arginine (Arg, R) AGA, AGG, CGA, CGC, CGG, or CGU; Serine (Ser, S) AGC, AGU, UCA, UCC, UCG, or UCU; Threonine (Thr, T) ACA, ACC, ACG, or ACU; Valine (Val, V) GUA, GUC, GUG, or GUU; Tryptophan (Trp, W) UGG; and Tyrosine (Tyr, Y) UAC or UAU.

[0121] It also will be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids, or 5' or 3' sequences, and yet still be essentially as set forth herein, including having a certain biological activity. The addition of terminal sequences particularly applies to nucleic acid sequences that may, for example, include various non-coding sequences flanking either the 5' or 3' portions of the coding region or may include various internal sequences, i.e., introns, which are known to occur within genes.

[0122] The following is a discussion based upon changing of the amino acids of a protein described herein to create an equivalent, or even an improved, molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on receptor molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid substitutions can be made in a protein sequence, and in its underlying polynucleotide sequence, and nevertheless produce a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the nucleic acid sequences of vesiculovirus or an encoded heterologous polynucleotide without appreciable loss of biological utility or activity of interest.

[0123] In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring a biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. It also is understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (0.5); histidine *-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still produce a biologically equivalent and immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those that are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

[0124] As outlined above, amino acid substitutions generally are based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Examples of substitutions that take into consideration the various foregoing characteristics are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine. In making such changes, the phylogenetic analysis of functionally related proteins may be considered (see Fig. 11 and the four amino acid changes made in the rISFV N protein, as depicted therein).

IV. NUCLEIC ACID MOLECULES

[0125] Certain embodiments are directed to compositions and methods that include polynucleotides that are capable of expressing all or part of a heterologous protein or polypeptide. In some embodiments all or parts of a viral genome are mutated or altered to generate a virus, viral polypeptide, heterologous polynucleotide, or heterologous polypeptide with certain properties and/or characteristics. The polynucleotides may encode a peptide or polypeptide containing all or part of a viral or heterologous amino acid sequence, or be engineered so they do not encode a viral polypeptide or encode a viral polypeptide having at least one function or activity added, increased, reduced, or removed.

[0126] As used herein, the term an isolated "RNA, DNA, or nucleic acid segment" refers to a RNA, DNA, or nucleic acid molecule that has been isolated from total genomic DNA or other contaminants. In certain embodiments the polynucleotide has been isolated free of other nucleic acids. A "vesiculovirus genome" or a "VSV genome," or a "ISFV genome" refers to a polynucleotide that can be provided to a host cell to yield a viral particle, in the presence or absence of a helper virus or complementing coding regions supplying other factors in trans.

[0127] The term "complementary DNA" or "cDNA" refers to DNA prepared using RNA as a template. There may be times when the full or partial genomic sequence is preferred.

[0128] Similarly, a polynucleotide encoding a polypeptide refers to a nucleic acid segment including coding sequences and, in certain aspects, regulatory sequences, isolated substantially away from other naturally occurring genes or protein encoding sequences. In this respect, the term "gene" is used for simplicity to refer to a nucleic acid unit encoding a protein, polypeptide, or peptide (including any sequences required for proper transcription, post-translational modification, or localization). As will be understood by those in the art, this functional term includes genomic sequences, cDNA sequences, and smaller engineered nucleic acid segments that express, or may be adapted to express, proteins, polypeptides, domains, peptides, fusion proteins, and mutants.

[0129] The nucleic acid segments used in the present invention, regardless of the length of the coding sequence itself, may be combined with other nucleic acid sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant nucleic acid protocol.

[0130] It is contemplated that the nucleic acid constructs of the present invention may encode full-length polypeptide(s) from any source or encode a truncated or modified version of the polypeptide(s), for example a heterologous peptide fragment. A nucleic acid sequence may encode a full-length polypeptide sequence with additional heterologous coding sequences, for example to allow for purification of the polypeptide, transport, secretion, post-translational modification, or for therapeutic benefits such as targeting or efficacy. A tag or other heterologous polypeptide may be added to a polypeptide-encoding sequence. The term “heterologous” refers to a polypeptide, polynucleotide, or segment thereof that is not the same as the modified polypeptide, polynucleotide, or found associated with or encoded by the naturally occurring virus.

[0131] In a non-limiting example, one or more nucleic acid constructs may be prepared that include a contiguous stretch of nucleotides identical to or complementary to a particular viral segment, such as a vesiculovirus N, P, M, G, or L gene.

[0132] The nucleic acid segments used in the present invention encompass modified nucleic acids that encode modified polypeptides. Such sequences may arise as a consequence of codon redundancy and functional equivalency. Functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by humans may be introduced through the application of site-directed mutagenesis techniques, e.g., to introduce improvements to the antigenicity or lack thereof. A protein can be modified to reduce toxicity effects of the protein in vivo, or to increase the efficacy of any treatment involving the protein or a virus comprising such a protein.

[0133] Recombinant vesiculovirus vectors can be manipulated using a variety of techniques including insertional mutations, point mutations, deletions, and gene shuffling.

[0134] A recombinant vesiculovirus may be designed to reduce the N mRNA synthesis in cells infected with virus by shuffling the N (nucleocapsid protein) gene to a position in the genome that is further away (distal) from the native 3' transcription promoter. Because VSV is not considered a human pathogen, and pre-existing immunity to VSV is rare in the human population, the development of VSV-derived vectors has been a focus in areas such as immunogenic compositions and gene therapy. For example, studies have established that VSV can serve as an effective vector for immunogenic compositions, expressing influenza virus hemagglutinin (Roberts et al., 1999 *J. Virol*, 73:3723-3732), measles virus H protein (Schlereth et al., 2000 *J. Virol*, 74:4652-57) and HIV-1 env and gag proteins (Rose et al., 2001 *Cell*, 106:539-549).

[0135] In certain other embodiments, the invention concerns isolated nucleic acid segments and recombinant vectors that include within their sequence a contiguous nucleic acid sequence from that shown in sequences identified herein (and/or incorporated by reference).

[0136] It also will be understood that this invention is not limited to the particular nucleic acid and amino acid sequences of these identified sequences. Recombinant vectors and isolated nucleic acid segments may therefore variously include vesiculovirus-coding regions, coding regions bearing selected alterations or modifications in the basic coding region, or they may encode larger polypeptides that nevertheless include vesiculovirus-coding regions, or may encode biologically functional equivalent proteins or peptides that have variant amino acids sequences.

[0137] In various embodiments, the vesiculovirus polynucleotide and/or a heterologous polynucleotide may be altered or mutated. Alterations or mutations may include insertions, deletions, substitutions, rearrangement, inversions, and the like and may result in the modulation, activation, and/or inactivation of certain proteins or molecular mechanisms, as well as altering the function, location, or expression of a gene product. Where employed, mutagenesis of a polynucleotide can be accomplished by a variety of standard, mutagenic procedures (Sambrook et al, 2001). Mutation is the process whereby changes occur in the function or structure of an organism or molecule. Mutation can involve modification of the nucleotide sequence of a single gene, blocks of genes or whole genomes. Changes in single genes may be the consequence of point mutations that involve the removal, addition, or substitution of a single nucleotide base within a DNA sequence, or they may be the consequence of changes involving the insertion or deletion of large numbers of nucleotides.

[0138] Insertional mutagenesis is based on the modification of a gene via insertion of a known nucleotide or nucleic acid fragment. Because it involves the insertion of some type of nucleic acid fragment, the mutations generated are generally loss-of-function, rather than gain-of-function mutations. However, there are examples of insertions generating gain-of-function mutations. Insertional mutagenesis may be accomplished using standard molecular biology techniques.

[0139] Structure-guided site-specific mutagenesis represents a powerful tool for the dissection and engineering of protein-ligand interactions (Wells, 1996; Braisted et al., 1996). The technique provides for the preparation and testing of sequence variants by introducing one or more nucleotide sequence changes into a selected DNA.

[0140] As used herein, "G-CT" refers to a mutated VSV G gene wherein the encoded G protein is truncated or deleted of some of the amino acids in its cytoplasmic domain (carboxy-terminus), also referred to as the "cytoplasmic tail region" of the G protein. G-CT1 is truncated of its last carboxy terminal 28 amino acids, resulting in a protein product that retains only one amino acid from the twenty-nine amino acid wild-type cytoplasmic domain. Other G gene truncations are identified in US Patent No. 8,287,878, *e.g.*, G-CT9, having the last twenty carboxy-terminal amino acid residues of the cytoplasmic domain deleted, relative to the wild-type. Among known methods for altering the G protein of rVSV are the technologies described in International Publication No. WO99/32648 and Rose, N. F. *et al.* 2000 *J. Virol.,74*:10903-10.

[0141] The term "expression vector" refers to a vector containing a nucleic acid sequence coding for at least part of a gene product capable of being transcribed. In some cases, RNA molecules are translated into a protein, polypeptide, or peptide. In other cases, these sequences are not translated, for example, in the production of antisense molecules or ribozymes. Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described *infra*.

[0142] A "promoter" is a control sequence that is a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements that bind regulatory proteins and molecules, such as RNA polymerase and other transcription factors. The phrases "operatively positioned," "operatively coupled," "operatively linked," "under control," and "under transcriptional control" mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and/or expression of that sequence. A promoter may or may not be used in conjunction with an "enhancer," which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

[0143] A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences. Heterologous translational control signals, including the ATG initiation codon, may need to be provided. The translational control signal and initiation codons can be either natural or synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements.

[0144] In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent translation and begin translation at internal sites (Pelletier and Sonnenberg, 1988). IRES elements from two members of the picornavirus family (polio and encephalomyocarditis) have been described (Pelletier and Sonnenberg, 1988), as well as an IRES from a mammalian message (Macejak and Sarnow, 1991). By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation.

[0145] Vectors can include a multiple cloning site (MCS), which is a nucleic acid region that contains multiple restriction enzyme sites any of which can be used in conjunction with standard recombinant technology to digest the vector. (See Carbonelli et al., 1999, Levenson et al., 1998, and Cocea, 1997, incorporated herein by reference.) "Restriction enzyme digestion" refers to catalytic cleavage of a nucleic acid molecule with an enzyme that functions only at specific locations in a nucleic acid molecule. Many of these restriction enzymes are commercially available. A vector can be linearized or fragmented using a restriction enzyme that cuts within the MCS to enable heterologous sequences to be ligated to the vector. "Ligation" refers to the process of forming phosphodiester bonds between two nucleic acid fragments, which may or may not be contiguous with each other.

[0146] The vectors or constructs can comprise at least one termination signal. A "termination signal" or "terminator" is comprised of the nucleic acid sequences involved in specific termination of an RNA transcript by an RNA polymerase. Thus, in certain embodiments a termination signal that ends the production of an RNA transcript is contemplated. A terminator may be necessary in vivo to achieve desirable message levels. Terminators contemplated for use in the invention include any known terminator of transcription described herein or known to one of ordinary skill in the art, including but not limited to, for example, the termination sequences of genes, such as for example the bovine growth hormone terminator or viral termination sequences, such as for example the SV40 terminator. In certain embodiments, the termination signal may be a lack of transcribable or translatable sequence, such as due to a sequence truncation.

[0147] A polyadenylation signal can be used to effect proper polyadenylation of a transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention. Embodiments include the SV40 polyadenylation signal and/or the bovine growth hormone polyadenylation signal. Polyadenylation may increase the stability of the transcript or may facilitate cytoplasmic transport.

[0148] In certain embodiments of the invention, cells containing a nucleic acid construct of the present invention may be identified *in vitro* or *in vivo* by including a marker in the expression vector. Such markers would confer an identifiable change to the cell permitting easy identification of cells containing the expression vector. Generally, a selectable marker is one that confers a property that allows for selection. A positive selectable marker is one in which the presence of the marker allows for its selection, while a negative selectable marker is one in which its presence prevents its selection. An example of a positive selectable marker is a drug resistance marker. Usually the inclusion of a drug selection marker aids in the cloning and identification of transformants, for example, genes that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin and histidinol are useful selectable markers. In addition to markers conferring a phenotype that allows for the discrimination of transformants based on the implementation of conditions, other types of markers including screenable markers such as GFP, whose basis is colorimetric analysis, are also contemplated. Alternatively, screenable enzymes such as herpes simplex virus thymidine kinase (tk) or chloramphenicol acetyltransferase (CAT) may be utilized. One of skill in the art would also know how to employ immunologic markers, possibly in conjunction with FACS analysis. The marker used is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a gene product. Further examples of selectable and screenable markers are well known to one of skill in the art.

V. KITS RELATED TO RECOMBINANT VESICULOVIRUS

[0149] In still another embodiment, the present invention provides a pharmaceutical kit for ready administration of an immunogenic, prophylactic, or therapeutic regimen. This kit is designed for use in a method of inducing a high level of antigen-specific immune response in a mammalian or vertebrate subject. The kit may contain at least one immunogenic composition comprising a rISFV composition as described herein. For example, multiple prepackaged dosages of the rISFV immunogenic composition are provided in the kit for multiple administrations. The kit also contains at least one immunogenic composition comprising a rVSV immunogenic composition as described herein. In one embodiment, multiple prepackaged dosages of the rVSV immunogenic composition are provided in the kit for multiple administrations.

[0150] The kit also contains instructions for using the immunogenic compositions in a prime/boost method as described herein. The kits may also include instructions for performing certain assays, various carriers, excipients, diluents, adjuvants and the like above-described, as well as apparatus for administration of the compositions, such as syringes, electroporation devices, spray devices, etc. Other components may include disposable gloves, decontamination instructions, applicator sticks or containers, among other compositions.

VI. EXAMPLES

[0151] The following examples as well as the figures are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples or figures represent techniques discovered by the inventors to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLE 1
ANALYSIS AND RECOVERY OF ISFAHAN VIRUS (ISFV)

[0152] A system has been developed for recovery of recombinant Isfahan virus (rISFV) from plasmid DNA encoding ISFV genomic cDNA. The safety of wild-type (wt) rISFV and the attenuated variant rISFVN4ΔCT25gag1 was studied in a highly sensitive 4-5-week-old NIH Swiss Webster mouse intracranial neurovirulence model. Unmodified rISFV wt exhibited an $LD_{50}>10^3$ PFU, in contrast to $wtVSV_{IN}$ with an LD_{50} of <10 PFU. rISFVN4ΔCT25gag1 exhibited an $LD_{50}>10^7$, in contrast to $rVSV_{IN}N2CT1$ with an LD_{50} of 10^4. These results indicate that rISFV is fundamentally less pathogenic than VSV_{IN} and may not require the utilization of multiple attenuation strategies (N-shuffle, truncation of cytoplasmic tail of G-protein) to achieve similar safety and immunogenicity as $rVSV_{IN}$ vectors.

[0153] *Isfahan phylogenetic analysis.* Available sequences of the genus *Vesiculovirus* were downloaded from GenBank. N gene sequences were aligned in SeaView (PBIL (Pôle Bio-Informatique Lyonnais), France) utilizing the MUSCLE algorithm (Gouy et al., 2010, *Molecular Biology and Evolution* 27:221-24; Edgar, 2004. *Nucleic Acids Research* 32:1792-97). The sequences were aligned by deducing amino acid sequences from open reading frames (ORFs) and then returning to nucleotide sequences for subsequent analyses (Gouy et al., 2010, *Molecular Biology and Evolution* 27:221-24; Edgar, 2004. *Nucleic Acids Research* 32:1792-97). Maximum-likelihood (ML) analysis was performed utilizing the PHYLIP package (Felsenstein, 1989, *Cladistics* 5, 164–1663). The robustness of ML phylogeny was evaluated by bootstrap re-sampling of 100 replicates. The analysis revealed two main clusters within the genus (FIG. 1). The first cluster consists of VSV_{IN} and its subtypes, and VSV_{NJ}, whereas the second cluster is comprised of ISFV, Chandipura, and Piry viruses. These data are in congruence with previous serological analyses to determine the relationship of ISFV within the genus, and taken together indicate that ISFV is distantly related to VSV_{IN} (Tesh et al., *Am J Trop Med Hyg*. 1977, Mar 26(2):299-306).

[0154] *Generation of Isfahan cDNA clone.* A low tissue culture passaged ISFV isolate was obtained from the World Reference Center for Emerging Viruses and Arboviruses at the University of Texas Medical Branch. Viral genomic RNA was isolated from culture supernatants and cDNA fragments spanning the complete ISFV genome were generated by reverse transcription (RT) and PCR amplification (RT-PCR) (FIG. 2). RT-PCR products (fragments 3-5) were cloned step-wise into a plasmid containing the full-length genomic cDNA of VSV New Jersey (pVSV$_{NJ}$N4CT1 HIVgag1) (FIG. 2). The remaining fragments (1-2) were cloned into the pBlueScript plasmid (Invitrogen).

[0155] Support plasmids for rescue, expressing individual ISFV proteins (N, P, M, G and L), were generated by cloning the respective open reading frames (ORF) into the Nco I and Sac I sites of the pVSV$_{IN}$ P plasmid (Witko et al., *J Virol Methods*. 2006 Jul, 135(1):91-101). Cohesive ends compatible with Nco I were generated via BspH I (N and M genes), Pci I (P gene) and BsmB I (G and L genes). The L gene ORF was assembled by joining two cDNA fragments: fragment #1 (BsmB I to Avr II), and fragment #2 (Avr II to Sac I). All resulting rescue support plasmids were verified by nucleotide sequence analysis.

[0156] *rISFV and rVSV$_{IN}$ constructs encoding Alphavirus envelope genes*. The envelope genes (encompassing E3-E2-6K-E1) of EEEV strain FL93 and VEEV strain ZPC738 were cloned into pPBS-ISFV-38 (whose construction is described below). In addition, VEEV-ZPC E3-E1 genes were cloned into pVSV$_{IN}$ N4CT1 HIVgag5. In each case the alphavirus genes were inserted at the fifth position of the vector genome using restriction sites Xho I and Not I in such a way as to place the inserted genes under control of the rISFV or rVSV transcriptase (FIG. 3A). All vectors were verified by full-length nucleotide sequence analysis and expression of alphavirus proteins was confirmed by Western blot (FIG. 3B).

[0157] A 3' to 5' gradient in gene expression has been well documented for the vesiculoviruses (Ball and White, *PNAS*. 1976, 73(2):442-6; Villarreal et al., *Biochemistry*. 1976, 15(8):1663-7) and other negative sense RNA viruses (Conzelmann, *Annual review of genetics*. 1998, 32:123-62). Therefore, maximal expression of a target antigen is achieved by insertion of the transgene in the first position of the genome, immediately adjacent to the single strong 3' transcription promoter. However, high expression levels of some antigens can be toxic to rVSV replication, leading to transgene instability and loss of antigen expression (unpublished). Down regulation of expression of toxic antigens, such as HIV-1 Env proteins, by moving the trans gene(s) further away from the 3' transcription promoter has been successful in maintaining genetic stability of Env expression and all target antigens from a range of different pathogens tested thus far in the rVSV platform. To take into account the possibility that the E2/E1 glycoproteins could be toxic to rVSV and rISFV replication if expressed at very high levels, attenuated rVSV and rISFV vectors were generated which expressed E2/E1 from the fifth position in the genome.

[0158] Generation of Full Length Recombinant Isfahan Virus pDNA.

[0159] Starting material for constructing full length Isfahan virus (ISFV) consisted of two subcloning plasmids that encoded the following:

[0160] UTMB Plasmid #1 (renamed pPBS-ISFV-001): The nucleic acid sequences of T7 promoter, VSV Leader, ISFV Leader, N, M, P, G and a partial sequence of L inserted into pBlueScript II SK+ via the XhoI/KpnI sites. The sequences were inserted in a 3' to 5'direction.

[0161] UTMB Plasmid #2 (renamed pPBS-ISFV-002): Nucleic acid sequence of partial 3' sequence of ISFV L and terminator inserted into VSV_{NJ} N4CT1 backbone via XhoI/RsrII sites.

[0162] In addition to the above, support plasmids encoding individual ISFV genes (M, P, N, G, and L) under the control of a T7 promoter were provided.

[0163] Construction of pPBS-ISFV-008 Containing Full-Length ISFV Genomic cDNA

[0164] *Insertion of ISFV L Deleted Sequence.* The missing 2.4 kb nucleic acid sequence of ISFV L was inserted into pPBS-ISFV-001 and pPBS-ISFV-002. The missing fragment was generated by PCR using primers ISF_59- GTGCGTGGAAGACCGGTACCTCCCATTTGG (SEQ ID NO:13)/ ISF_60- TAATGTTATTGCCGGCGAATTCGAAACTGAATAAATC (SEQ ID NO:14) with pT7-IRES-ISFV L support plasmid as the template. The PCR cycle used was: 95°C, 2 min; (95°C, 30 sec denaturation/ 50°C, 30 sec annealing/ 72°C, 2.5 min elongation) at 40 cycles; 72°C, 2 min. To ensure the highest fidelity of the sequence, Pfx50 DNA polymerase (Invitrogen) was used. Next, the PCR product was digested with restriction enzymes KpnI and NgoMIV alongside pPBS-ISFV-001. This restriction digest product was ligated to generate pPBS-ISFV-003. The 2.4kb was also generated by PCR using primers ISF_62- AATAACATTACTCGAGTTCGGTACCTCCCATTTGG (SEQ ID NO:15)/ ISF 63- CAACTTTAAATTCGAAACTGAATAAATCTATC (SEQ ID NO:16) with pT7-IRES-L support plasmid as the template and inserted into pPBS-ISFV-002 via XhoI and BstBI, respectively, to generate pPBS-ISFV-005. Full length ISFV L was restored by combining pPBS-ISFV-001 and pPBS-ISFV-005 via XhoI/ KpnI restriction sites to generate pPBS-ISFV-006.

[0165] *Construction of T7 promoter adjacent to ISFV Leader.* In order to generate a suitable construct for ISFV rescue, the T7 promoter (TAATACGACTCACTATAGG (SEQ ID NO:17)) had to be placed immediately upstream of the ISFV leader sequence (ACGGAGAAAAACAAACCAATTCACGC (SEQ ID NO:18)). Therefore, the PCR amplification of the T7 promoter adjacent to the ISFV leader sequence was achieved using primers ISF_65- TTGAGCACCTGGTACAGGTATGAATTGATGTGACAC (SEQ ID NO:19)/ ISF_66- GCGTGAATTGGTTTGTTTTTCTCCGTCCTATAGTGAGTCGTATTAGCCGGCCTCGAGTAAATTAATT (SEQ ID NO:20) with pPBS-ISFV-001 as the template. The resulting PCR amplification generated a fragment that served as a template for a second round of amplification using primers ISF_65- TTGAGCACCTGGTACAGGTATGAATTGATGTGACAC (SEQ ID NO:21) / ISF_67- CGTATTAGCCGGCCTCGAGTAAATTAATT (SEQ ID NO:22) to create EcoNI/ NgoMIV restriction sites. The PCR product was then inserted into pPBS-ISFV-001 via EcoNI/ NgoMIV restriction sites to generate pPBS-ISFV-007.

[0166] ***Construction of a pDNA Containing a Full Length Isfahan Virus cDNA.*** A pDNA containing full length ISFV genomic cDNA was generated by digesting pPBS-ISFV-006 and pPBS-ISFV-007 with restriction enzymes NgoMIV/ SanDI to construct pPBS-ISFV-008 with the nucleic acid sequence 5'-N_1-P_2-M_3-G_4-L_5 -3' and the T7 promoter adjacent to ISFV leader sequence.

[0167] rISFV Rescue Procedure

[0168] *Preparation of pDNA.* For each electroporation, the following plasmid DNAs as listed in Table 1 were combined in a microfuge tube under sterile conditions:

Table 1

Plasmids *	Amounts **
pCMV-Neo-T7	50 µg
pT7-IRES-ISFV-N	10 µg
pT7-IRES-ISFV-P	4 µg
pT7-IRES-ISFV-L	1 µg
pT7-IRES-ISFV-M	1 µg
pT7-IRES-ISFV-G	2 µg
pPBS-ISFV full genome	12 µg

* All viral proteins were expressed from wild type nucleotide sequences and transcription was under control of a T7 promoter

** The pDNA amounts are calculated for one electroporation.

[0169] The DNA volume was adjusted to 300 µL with sterile, nuclease-free water. Next, 60 µl of 3M sodium acetate and 900 µL 100% ethanol were added and the mixture was stored overnight at -20°C. The DNA was pelleted by centrifugation at 14000 rpm for 30 minutes at 4°C. The supernatant was aspirated and the DNA pellet was air dried and resuspended in 50 µL sterile, nuclease-free water for each electroporation.

[0170] *Preparation of Vero Cells.* The following media as listed in Table 2 were used for the rescue of ISFV:

Table 2	
Rescue Medium #1	**Rescue Medium #2**
Dulbecco's Modified Eagle Medium (DMEM)	Iscove's Modified Dulbecco's Medium (IMDM)
10 % Fetal Bovine Serum (FBS)	1% DMSO
0.22 mM β-Mercaptoethanol	0.22 mM β-Mercaptoethanol
1% Nonessential Amino Acid	1% Nonessential Amino Acid
1% Sodium Pyruvate	1% Sodium Pyruvate

[0171] Each electroporation requires cells from approximately 1.3 near-confluent T-150 flasks or one confluent flask. The cell monolayers of each T150 flask were washed with Dulbecco's Phosphate Buffered Saline (DPBS) without Ca^{2+} or Mg^{2+}. DPBS was aspirated and trypsinized with 5 ml of trypsin-EDTA solution, and then incubated at 37°C for up to 5 minutes. After dislodging the cells by tapping the flask, 10 mL of Rescue Medium 1 were added to each flask to suspend the cells and 2 flasks each were transferred to a 50 mL conical tube containing 10 mL Rescue Medium 1. The cells were centrifuged at 1200 rpm for 5 minutes at 4°C. The supernatant was aspirated and the cells resuspended with 10 mL of Rescue Medium 2 per 50 mL conical tube, followed by centrifugation at 1200 rpm for 5 minutes at 4°C. The wash was discarded and the cell pellet resuspended in 0.7 mL of Rescue Medium 2. The cell suspension was transferred to a microfuge tube aliquoted with 50 µl of the plasmid DNA solution and gently mixed, followed by transferring the cells/DNA to an electroporation cuvette.

[0172] *Electroporation.* Cells were electroporated in a BTX820 Electroporator as follows:

Mode:	Low Voltage
Voltage:	140 V
Number of Pulses:	4
Pulse Length:	70 msec
Pulse Interval:	500 msec

[0173] After electroporation, all samples were left at room temperature for 10 minutes, then 1 mL of Rescue Medium 1 was added to the cuvette with gentle mixing to resuspend electroporated cells. The cell suspension was then transferred from the cuvette to a 15 mL centrifuge tube containing 10 mL of Rescue Medium 1 and centrifuged at 1200 rpm for 5 minutes at 4°C. The medium was aspirated and cells resuspended in 10 mL Rescue Medium 1 and transferred to T-150 flasks containing 20 mL Rescue Medium 1. The flasks were incubated at 37°C (5% CO_2) for 3 hours, followed by heat-shock at 43°C (5% CO_2) for 3-5 hours and then returned to 32°C for long-term incubation. After overnight incubation supernatant was replaced with 25 ml of fresh Rescue Medium 1. Positive rISFV rescues showed a cytopathic effect (CPE), characterized by regions of rounded up cells, after 5-10 days. Rescue supernatant was collected; flash frozen in an ethanol/dry ice bath and a single virus clone(s) was isolated by plaque picking followed by two rounds of amplification in Vero cells to generate a virus working stock.

[0174] ISFV/Vesiculovirus Nucleoprotein Amino Acid Alignment

[0175] The amino acid sequence of ISFV nucleoprotein was aligned with other vesiculovirus nucleoprotein sequences (Table 3). The percent matches are based on amino acid identities to the ISFV nucleoprotein sequence. Detailed homology in the sequences can be seen in FIG. 4. Regions of amino acid homology are shaded.

Table 3

Nucleoprotein Sequence from	% Match Compared to ISFV
VSV Indiana serotype	51
VSV NJ serotype	51
Chandipura	58
Piry	60
Cocal	50
Alagoas	51
Spring viraemia of carp virus	43
vesiculo_Pike Fry	45

EXAMPLE 2
CONSTRUCTION OF ATTENUATED rISFV VECTORS USING GENE SHUFFLES AND TRUNCATIONS OF THE CYTOPLASMIC TAIL OF ISFV G

[0176] *Construction of rISFV-N4G5-MCS1.* Plasmid pPBS-ISFV-008 comprises the nucleic acid sequence 5'-N_1-P_2-M_3-G_4-L_5-3' [anti-genome of rISFV]. The subscript numbers indicate the genomic position of each ISFV gene, P (encoding the phosphoprotein), M (encoding the matrix protein), G (encoding the attachment protein), N (encoding the nucleocapsid protein) and L (encoding the polymerase protein).

[0177] Plasmid pPBS-ISFV-009 comprises the nucleic acid sequence 5'-MCS_1-N_2-P_3-M_4-G_5-L_6 -3' (anti-genome of an rISFV with an additional transcriptional cassette in position 1). According to this formula, MCS (multiple cloning site) is an empty transcriptional unit (TU) in the rISFV anti-genome at position 1 immediately upstream of ISFV N. The subscript numbers indicate the anti-genomic position of each ISFV gene, P (encoding the phosphoprotein), M (encoding the matrix protein), G (encoding the attachment protein), N (encoding the nucleocapsid protein) and L (encoding the polymerase protein).

[0178] First, the internal NheI site in ISFV L was removed for cloning purposes: A PCR fragment was generated with primers ISF_68 –

AATCTGGAcgcgtctcGCTAGtCAGGCTGATTATTTGAGG (SEQ ID NO:23) / ISF_48 – TTGATATTTCCCCAACTCTAC (SEQ ID NO:24) and using pPBS-ISFV-008 as a template and was inserted into pPBS-ISFV-008 via AfeI/BsmBI and AfeI/NheI -restriction sites, respectively, to generate pPBS-ISFV-010.

[0179] A second PCR fragment containing partial ISFV M – ISFV G – partial ISFV L sequence was generated with primers ISF_73 – CGCATGCCGTCTCCTTATGTTGATTG (SEQ ID NO:25) / ISF28 – AGCATTCATTATAAGTATGAC (SEQ ID NO:26) and using pPBS-ISFV-008 as a template. This fragment was inserted into a modified pT7Blue cloning vector (Novagen) via SphI/AgeI restriction sites to generate pPBS-ISFV-011.

[0180] Starting from pPBS-ISFV-011, two consecutive mutagenesis reactions were performed using primer pairs ISF_71 – GCTTTTCACAGATGAAGCTAGCTGAAAGTATGAAAAAAACG (SEQ ID NO:27) / ISF_72 – GTTTTTTTCATACTTTCAGCTAGCTTCATCTGTGAAAAGCTTG (SEQ ID NO:28) and ISF_69 – AACAGAGGTCAAACGCGTGTCAAAATGACTTCAGTTTTATTCATG (SEQ ID NO:29) / ISF_70 – GAATAAAACTGAAGTCATTTTGACACGCGTTTGACCTCTGTTAAT (SEQ ID NO:30) to generate pPBS-ISFV-013. pPBS-ISFV-013 was then digested using BsmBI/AgeI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-009. The resulting construct pPBS-ISFV-014 comprised therefore the nucleic acid sequence 5'-MCS_1-N_2-P_3-M_4-G_5-L_6 -3', but unlike pPBS-ISFV-009 the ISFV G gene is flanked by MluI/NheI restriction sites allowing the easy exchange with ISFV G variants comprising, for example, truncations of the cytoplasmic tail of ISFV G.

[0181] In order to shuffle the N-gene into position 4 and therefore to attenuate rISFV as a vector, a PCR fragment was generated with primers ISF_84 – CAGCTGGCGGCCGCTAGGAATTCAAATCAACATATATGAAAAAAATCAACAGAGAT ACAACAATG (SEQ ID NO:31) / ISF20 – ACATAGTGGCATTGTGAACAG (SEQ ID NO:32) and using pPBS-ISFV-008 as a template and was inserted into a modified pT7Blue cloning vector (Novagen) via HindIII/NotI restriction sites to generate pPBS-ISFV-017. pPBS-

ISFV-017 and pPBS-ISFV-014 were combined by swapping the BsmBI/NotI-insert from pPBS-ISFV-017 into the corresponding vector fragment of pPBS-ISFV-014 to generate pPBS-ISFV-019.

[0182] At the same time, pPBS-ISFV-015 was generated by PCR amplification of a fragment with primers ISF_73 – CGCATGCCGTCTCCTTATGTTGATTG (SEQ ID NO:33) / ISF_82 – AGTCATACCGGTCTCGTTAATTTTTTTCATATCTTTCTTCTGCATGTTATAATTC (SEQ ID NO:34) and using pPBS-ISFV-008 as a template and inserting it into a modified pT7Blue cloning vector (Novagen) via SphI/AgeI-restriction sites. A second PCR fragment was generated with ISF_80 – TCGAGAACGCGTTTGACCTCTGTTAATTTTTTTCATATATGTTGATTTGAATTC (SEQ ID NO:35) / ISF_81 – ATTCCAACGCGTCTCGTTAACAGGGATCAAAATGACTTCTGTAGTAAAG (SEQ ID NO:36) and using pPBS-ISFV-008 as a template and inserted into pPBS-ISFV-015 via BsmBI/MluI and BsaI/MluI -restriction sites, respectively, to generate pPBS-ISFV-016.

[0183] Finally, pPBS-ISFV-016 and pPBS-ISFV-019 were combined by swapping the BsmBI/Mlul-insert from pPBS-ISFV-016 into the corresponding vector fragment of pPBS-ISFV-019. The resulting construct pPBS-ISFV-020 comprises therefore the nucleic acid sequence 5'-MCS_1-P_2-M_3-N_4-G_5-L_6 -3', where compared to pPBS-ISFV-014 the N gene has been shuffled to position 4 of the rISFV.

[0184] *Construction of rISFV-N4G3-MCS5.* Starting from pPBS-ISFV-013, a mutagenesis reaction was performed with primers ISF_90 – GCTTTTCACAGATGAAGCTAGCGCATGCGGCCGCTGAAAGTATGAAAAAAACG (SEQ ID NO:37) / ISF_91 – GTTTTTTTCATACTTTCAGCGGCCGCATGCGCTAGCTTCATCTGTGAAAAGCTTG (SEQ ID NO:38) to generate pPBS-ISFV-022. An oligonucleotide linker generated from ISF_92 – CTAGCTGAAAGTATGAAAAAAATTAACAGAGGTCAAACTCGAGGATATCGGTACCGAAGGCGCGCCCAGCTGTGCGGCC (SEQ ID NO:39) and ISF_93 –

GGCCGCACAGCTGGGCGCGCCTTCGGTACCGATATCCTCGAGTTTGACCTCTGTTAA TTTTTTTCATACTTTCAG (SEQ ID NO:40) was then ligated with the NheI/NotI-vector fragment of pPBS-ISFV-022 to generate pPBS-ISFV-023. A PCR fragment was generated with primers ISF_98 - GAATTCCTCGAGTTGACCTCTGTTAATTTTTTCATATATGTTGATTTGAATTC (SEQ ID NO:41) and ISF_99 - GATGAA GCTAGCTGAAAGTATGAAAAAAATTAACAGGGATCAAAATGACTTCTGTAG (SEQ ID NO:42) and using pPBS-ISFV-016 as a template and inserted into pPBS-ISFV-023 via XhoI/NheI restriction sites to generate pPBS-ISFV-024.

[0185] In addition, a PCR fragment was generated with primers ISF16 - ATCATTCCTTTATTTGTCAGC (SEQ ID NO:43) and ISF_100 - TATATGGCTAGC GAAGACAGAGGGATCAAAATGTCTCGACTCAACCAAAT (SEQ ID NO:44) and using pPBS-ISFV-017 as a template and inserted into pPBS-ISFV-017 via BsmBI/NheI restriction sites to generate pPBS-ISFV-025.

[0186] Two oligonucleotide linkers generated from ISF_101 – CTAGCCCGGCTAATACGACTCACTATAGGACGGAGAAAAACAAA (SEQ ID NO:45) / ISF_102 – TTGGTTTGTTTTTCTCCGTCCTATAGTGAGTCGTATTAGCCGGCG (SEQ ID NO:46) and ISF_103 – CCAATTCACGCATTAGAAGATTCCAGAGGAAAGTGCTAAC (SEQ ID NO:47) / ISF_104 – CCCTGTTAGCACTTTCCTCTGGAATCTTCTAATGCGTGAA (SEQ ID NO:48), respectively, were then ligated with the NheI/BbsI-vector fragment of pPBS-ISFV-025 (to generate pPBS-ISFV-026). To generate pPBS-ISFV-030, a plasmid comprising the nucleic acid sequence 5'-P_1-M_2-N_3-G_4-L_5-3', pPBS-ISFV-026 was digested using BsmBI/NgoMIV restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-020.

[0187] Finally, pPBS-ISFV-024 and pPBS-ISFV-030 were combined by swapping the BsmBI/AgeI-insert from pPBS-ISFV-024 into the corresponding vector fragment of pPBS-ISFV-030. The resulting construct pPBS-ISFV-031 comprises therefore the nucleic acid sequence 5'-P_1-M_2-G_3-N_4-MCS_5-L_6 -3', where compared to pPBS-ISFV-014 the N gene has been shuffled to position 4 of the rISFV.

[0188] *Construction of rISFV-N*4G5-MCS1.* Although an amino acid sequence alignment of rISFV and rVSV N proteins revealed only an overall 52% homology, the alignment demonstrated a very close homology for a strong, known H2d restricted epitope (MPYLIDFGL; see Fig. 11). Further alignments with additional N proteins from other vesiculoviruses were therefore used to ablate or at least to reduce the homology between rISFV and rVSV for this stretch of amino acids. Starting from pPBS-ISFV-016, a mutagenesis reaction was performed with primers ISF_127 – GAAAGACAAGAAGTGGACCAGAGCGATTCCTACATGCCTTACATGATTGATATGGGGATCTCAACCAAATC (SEQ ID NO:49) / ISF_128 – GGTTGAGATCCCCATATCAATCATGTAAGGCATGTAGGAATCGCTCTGGTCCACTTCTTGTCTTTCTTTC (SEQ ID NO:50) to generate pPBS-ISFV-033 containing the following amino acid changes in ISFV N: K271Q, A272S, L279M, F282M (ISFV N*) (see Fig. 11). pPBS-ISFV-033 was digested using SanDI/BsrGI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-024 to generate pPBS-ISFV-037. Finally, pPBS-ISFV-037 and pPBS-ISFV-031 were combined by swapping the NheI/AgeI-insert from pPBS-ISFV-037 into the corresponding vector fragment of pPBS-ISFV-031. The resulting construct pPBS-ISFV-038 comprises therefore - like pPBS-ISFV-031 - the antigenomic nucleic acid sequence 5'-P_1-M_2-G_3-N_4-MCS_5-L_6-3', however, the encoded ISFV N protein carries the four amino acids changes K271Q, A272S, L279M, F282M (ISFV N*).

[0189] *Attenuated rISFV N vectors expressing model antigen HIV-1 gag SDE.* Plasmid pPBS-HIV-055 is a standard cloning vector comprising a truncated HIV-1 gag gene called HIV-1 gag SDE (single dominant epitope). The amino acid sequence of HIV-1 gag SDE is as follows: ^{1}MVARASVLGGELDRWEKEEERPGGKKKYKLKEEEWASRELERFAVNPGLETSEGCRQ ^{60}I-^{192}GGHQAAMQMLKETINEEA^{210}A-^{333}ILKALGPAATLEEMMTACQGVGGYPYDVPDYAPGHKARV^{363}L (SEQ ID NO:51) The numbers indicate the amino acid positions in the native HIV-1 gag protein. The peptide

“AMQMLKETI” (SEQ ID NO:52) was found to be a strong inducer of a T-cell response in BALB/c mice and HIV-1 gag SDE was therefore used a model antigen testing immunogenicity of different vector designs.

[0190] First, pPBS-HIV-055 was digested using XhoI/NotI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-014. The resulting construct pPBS-ISFV-HIV-013 comprises therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-N_2-P_3-M_4-G_5-L_6 -3’ and was used to create the corresponding rISFV.

[0191] Plasmid pPBS-HIV-055 was digested using XhoI/NotI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-020. The resulting construct pPBS-ISFV-HIV-014 comprises therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-P_2-M_3-N_4-G_5-L_6 -3’. Therefore the corresponding rISFV virus comprises a single attenuation marker - an ISFV N shuffle into position 4 of the rISFV.

[0192] A PCR fragment was generated with primers ISF_83 – TTTTTTGCTAGCTTCACCTGCATAATAGTGGCAAC (SEQ ID NO:53) / ISF_69 – AACAGAGGTCAAACGCGTGTCAAAATGACTTCAGTTTTATTCATG (SEQ ID NO:54) and using pPBS-ISFV-HIV-014 as a template and was inserted into pPBS-ISFV-HIV-014 via MluI/NheI to generate pPBS-ISFV-HIV-015, now comprising the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-P_2-M_3-N_4-(GΔCT25)$_5$-L_6-3’. Therefore the corresponding rISFV virus comprises two attenuation markers: (1) shuffling of ISFV N into position 4 of the rISFV antigenome and (2) truncating the distal end of the cytoplasmic tail (CT) of ISFV G by 25 amino acids. The precise length of the CT and transmembrane (TM) domains of ISFV G protein have not been as well characterized as those of VSV_{IN}, but an approximate 18 amino acid (aa) hydrophobic domain near the carboxyl terminus is predicted as the ISFV G protein TM anchor. The remaining downstream 33 aa residues represent the G protein CT.

[0193] In addition, pPBS-ISFV-033 was digested using BsmBI/MluI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-HIV-015. The resulting construct pPBS-ISFV-HIV-018 comprised therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-P$_2$-M$_3$- N*$_4$-(GΔCT25)$_5$-L$_6$ -3'. Compared to rISFV-HIV-015, the encoded ISFV N gene in the corresponding rISFV-HIV-003 carried the four amino acids changes K271Q, A272S, L279M, F282M within the known, strong T cell epitope for BALB/c mice.

[0194] Plasmid pPBS-ISFV-HIV-015 was digested using MluI/NheI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-HIV-013. The resulting construct pPBS-ISFV-HIV-017 comprised therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-N$_2$-P$_3$-M$_4$-(GΔCT25)$_5$-L$_6$-3'. Therefore the corresponding rISFV virus comprises a single attenuation marker - the truncation of the ISFV G cytoplasmic tail.

[0195] Finally, an attenuated rISFV vector was generated in which the truncated ISFV GΔCT25 gene was replaced by VSV$_{NJ}$ GCT1 gene, which encoded a modified VSV G from the NJ serotype with similar truncation at the cytoplasmic tail of 28 amino acids. To generate pPBS-ISFV-HIV-016 [comprising the nucleotide sequence 5'-(HIV-1 gag SDE)$_1$-P$_2$-M$_3$-N$_4$-(VSV$_{NJ}$ GCT1)$_5$-L$_6$-3'], pPBS-VSV-HIV-054 (rVSV cloning vector containing a VSV$_{NJ}$ GCT1 gene flanked by MluI/NheI restriction enzyme sites) was digested using MluI/NheI restriction enzymes. The isolated insert was then ligated with a corresponding vector fragment derived from pPBS-ISFV-HIV-015. The resulting construct pPBS-ISFV-HIV-016 comprised therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-N$_2$-P$_3$-M$_4$-(VSV$_{NJ}$ G CT1)$_5$-L$_6$-3' and was used to rescue the corresponding rISFV.

[0196] The attenuation of all the rISFVs expressing HIV-1 gag SDE was tested in vitro by plaque assay. The observed plaque sizes were as follows (FIG. 5): rISFV-HIV-013 = rISFV-HIV-14 > rISFV-HIV-15 = rISFV-HIV-017 ≥ rISFV-HIV-018 = rISFV-HIV-016.

[0197] In addition to the rISFV constructs described above, two attenuated rVSV vectors generated from the following plasmids were used in the prime-boost immunization experiments:

[0198] pPBS-VSV-HIV-106 comprises the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-P$_2$-M$_3$-N$_4$-(G CT1)$_5$-L$_6$-3' and all vector genes (P, M , N, G CT1 and L) are derived from VSV

Indiana serotype. The $rVSV_{IN}$ derived from this plasmid was used in the study depicted in FIG. 16.

[0199] pPBS-VSV-HIV-122 comprises the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-P_2-M_3-N_4-(G CT1)$_5$-L_6-3', vector genes (P, M , N, and L) are derived from VSV Indiana serotype, and vector gene G CT1 is derived from VSV NJ serotype. The $rVSV_{NJ}$ derived from this plasmid was used in the study depicted in FIG. 16.

[0200] *Stabilizing the truncation of the cytoplasmic tail of ISFV G.* Numerous attenuated rISFVs comprising an ISFV GΔCT25 gene (e.g. rISFV-HIV-015 and rISFV-HIV-018) were extensively passaged in Vero cell culture to determine the stability of this attenuation marker. At passage 10 virtually all rISFVs extended the cytoplasmic tail by two amino acids to contain essentially a rISFV GΔCT23 gene. Thereby, the tested rISFVs changed the stop codon of the ISFV GΔCT25 gene into a codon for an amino acid and then used an alternative in frame stop codon two codons further downstream. Two manipulations of ISFV GΔCT25 - L gene junction were therefore examined for their ability to stabilize the attenuation marker ISFV GΔCT25 in rISFV:

[0201] A) Combining the transcriptional (underscored) and translational (bold) stop signal for the transcriptional cassette containing ISFV GΔCT25:

```
…gtgcgtatga aaaaaacgaa tcaacagagt tcatcatgga tgagtactct gaagaaaagt ggggcgattc…
…cacgcatact tttttgcttt agttgtctca agtagtacct actcatgaga cttcttttca ccccgctaag…
 >.......>> ISF G deltaCT25 (SEQ ID NO:55)
 l  c  v  -
                                             >>..............ISF L................>
                              (SEQ ID NO:56)  m   d  e  y  s   e  e  k   w  g  d
```

[0202] The last amino acid of ISFV GΔCT25 changes from arginine to valine.

[0203] B) Using the 3'-NCR of VSV_{IN} G CT1 present in prototypical $rVSV_{IN}$-N4CT1 vectors as 3'-NCR for the ISFV GΔCT25 expressing cassette:

```
                 NheI
               ~+~~~~
~ gtgcaggtga gctagccgcc tagccagatt cttcatgttt ggaccaaatc aacttgtgat accatgctca
  cacgtccact cgatcggcgg atcggtctaa gaagtacaaa cctggtttag ttgaacacta tggtacgagt
  >.......>> ISF G CTdelta25
  l  c  r  -

~  aagaggcctc aattatattt gagtttttaa ttttatgaa aaaaacgaat caacagagtt catcatggat
   ttctccggag ttaatataaa ctcaaaaatt aaaatactt ttttgctta gttgtctcaa gtagtaccta
                                                                  ISF L >>...>
                                                                        m   d
```

(SEQ ID NO:57)

[0204] Results showed that only approach (B) stabilized the ISFV GΔCT25 attenuation marker during extensive passage of corresponding rISFV viruses (e.g. rISF-HIV-020) in Vero cell culture.

[0205] Approach A – Construction

[0206] In order to manipulate the ISFV GΔCT25 - L gene junction, pPBS-ISFV-HIV-018 was digested using MluI/NheI restriction enzymes and inserted into a corresponding vector fragment derived from a modified pT7Blue cloning vector (Novagen) to generate pPBS-ISFV-049.

[0207] First, a mutagenesis reaction was performed on pPBS-ISFV-049 with primers ISF_140 – CTATTATGCGTATGCGAGACGCGTCTCGTATGAAAAAAACGAATCAACAGAG (SEQ ID NO:58) / ISF_141 – CTGTTGATTCGTTTTTTTCATACGAGACGCGTCTCGCATACGCATAATAGTG (SEQ ID NO:59) to generate pPBS-ISFV-051. In addition, a PCR fragment was generated with primers ISF_146 - AATTAACGTCTC AGAGATTGCAGCGAACCCCAGTGCGGCTGCTGTTTCTTTC (SEQ ID NO:60) / ISF_69 – AACAGAGGTCAAACGCGTGTCAAAATGACTTCAGTTTTATTCATG (SEQ ID NO:61) and using pPBS-ISFV-031 as a template. Together with an oligonucleotide linker generated from ISF_144 - TCTCTGTGATCCTGATCATCGGACTGATGAGGCTGCTGCCACTACTGTGCAGGTGAG (SEQ ID NO:62) and ISF_145 –

CTAGCTCACCTGCACAGTAGTGGCAGCAGCCTCATCAGTCCGATGATCAGGATCACA (SEQ ID NO:63) the PCR fragment (MluI/BsmBI) was then inserted into pPBS-ISFV-049 via MluI/NheI to generate pPBS-ISFV-056. Compared to pPBS-ISFV-049, the nucleotide sequence encoding the transmembrane region of ISFV GΔCT25 in pPBS-ISFV-056 has been silently modified to reduce A/T richness. A PCR fragment was generated with primers ISF_147 – CTAGGCGCGTCTCGCATACGCACAGTAGTGGCAG (SEQ ID NO:64) / ISF_69 – AACAGAGGTCAAACGCGTGTCAAAATGACTTCAGTTTTATTCATG (SEQ ID NO:65) and using pPBS-ISFV-056 as a template and inserted into pPBS-ISFV-051 via MluI/BsmBI to generate pPBS-ISFV-059.

[0208] Plasmid pPBS-ISFV-059 was digested using MluI/AgeI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-HIV-018. The resulting construct pPBS-ISFV-HIV-021 comprises therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-N*$_2$-P$_3$-M$_4$-G$_5$-L$_6$-3', has silent nucleotide changes in the transmembrane region of ISFV GΔCT25 to reduce A/T richness compared to the native sequence, and the Stop codon of ISFV GΔCT25 is part of the transcriptional stop in the ISFV GΔCT25 – L gene junction.

[0209] Approach B – Construction

[0210] Plasmid pPBS-ISFV-056 was digested using MluI/NheI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-VSV-HIV-020, which contains an anti-genomic sequence of an attenuated rVSV vector (N4CT1) expressing HIV-1 gag from the first transcriptional cassette. The resulting construct pPBS-ISFV-057 therefore comprises the nucleic acid sequence 5'-(HIV-1 gag)$_1$-VSV P$_2$-VSV M$_3$-VSV N$_4$- ISFV GΔCT25$_5$-VSV L$_6$ -3' and thereby the 3'-NCR of VSV G CT1 is linked to the open reading frame encoding ISFV GΔCT25.

[0211] A PCR fragment was generated with primers ISF_148 – TGTTAGCGTCTCTCATAAAAATTAAAAACTCAAATATAATTG (SEQ ID NO:66) and ISF_69 – AACAGAGGTCAAACGCGTGTCAAAATGACTTCAGTTTTATTCATG (SEQ ID

NO:67) and using pPBS-ISFV-057 as a template and inserted into pPBS-ISFV-051 via MluI/BsmBI to generate pPBS-ISFV-058.

[0212] Finally, pPBS-ISFV-058 was digested using MluI/AgeI restriction enzymes and the isolated insert was ligated with a corresponding vector fragment derived from pPBS-ISFV-HIV-018. The resulting construct pPBS-ISFV-HIV-021 comprises therefore the nucleic acid sequence 5'-(HIV-1 gag SDE)$_1$-N*$_2$-P$_3$-M$_4$-G$_5$-L$_6$ -3’, has silent nucleotide changes in the transmembrane region of ISFV GΔCT25 to reduce A/T richness compared to the native sequence, and comprises the 3’-NCR of VSV GCT1 in the ISFV GΔCT25 – L gene junction.

EXAMPLE 3
ANIMAL STUDIES

[0213] A series of mouse studies was performed to investigate the relative safety and efficacy of immunogenic compositions comprising rISFV vectors expressing alphavirus proteins. The mouse intra-cranial (IC) LD_{50} model was used for a primary assessment of vector safety due to the known neurovirulence properties of vesiculoviruses and related viruses (Olitsky et al., *Journal of Experimental Medicine.* 1934, 59:159–71; Frank et al., *Am J Vet Res.* 1945, Jan:28–38; Sabin et al., *Journal of Experimental Medicine.* 1937, 66:15–34; Rao et al., *Lancet.* 2004, 364(9437):869–74). Efficacy was assessed in stringent VEEV and EEEV challenge models.

[0214] *Neurovirulence of rISFV vectors.* A pilot study was performed to investigate the neurovirulence properties of unmodified rISFV and a highly attenuated variant expressing HIV-1 gag (rISFV-N4 GΔCT25 HIVgag1). An $rVSV_{IN}$ N2CT1 vector with a known LD_{50} from previous studies was utilized as a positive control (Clarke et al., *J Virol.* 2007, Feb;81(4):2056-64). Groups of 10 five-week-old, female Swiss Webster mice were inoculated IC with 25 μL of serial 10-fold dilutions of each virus via the intracerebral (IC) route and animals were observed for lethality for 21 days. PBS was used as a control for the injection process (Table 4).

[0215] Limited lethality was observed in animals injected with rISFV vectors and consequently an LD_{50} could not be determined (Table 4). In contrast, $rVSV_{IN}$ N2CT1 did cause lethality and an LD_{50} (10^4 pfu) similar to that determined in previous studies was determined

(Table 4). These data suggest that rISFV is inherently less neurovirulent than $rVSV_{IN}$, which demonstrated an LD_{50} of 5-10 plaque forming units (PFU) in its unmodified form (Clarke et al., *J Virol.* 2007, Feb;81(4):2056-64).

Table 4. LD_{50} titer of rISFV and $rVSV_{IN}$ vectors in Swiss Webster mice

Viral Construct	N	Dose (pfu)	Survival (%)	LD_{50} (pfu)
	10	10^7	100	
	10	10^6	100	
rISFV N4ΔCT25 HIVgag1	10	10^5	100	$>10^7$
	10	10^4	100	
	10	10^3	100	
	10	10^4	50	
$rVSV_{IN}$ N2CT1	10	10^3	90	10^4
	10	10^2	90	
	10	10^3	80	
rISFV	10	10^2	100	$>10^3$
	10	10^1	100	
PBS	10		100	

[0216] *Protective Efficacy of rISFV vectors.* A series of studies was performed to investigate the potential of rISFV as a vector for protection against alphavirus infection and disease. For these studies, 4-6-week-old female CD-1 mice were immunized by the intramuscular route using a 50 μL dose volume. Mice were then challenged with 10^4 PFU of either VEEV-ZPC or EEEV-FL93 injected subcutaneously. All animal care and procedures conformed to Institutional Animal Care and Use Committee guidelines.

[0217] *Short term protection against VEEV and EEEV challenge.* To determine whether rISFV-N4G3 vectors encoding E3-E1 of VEEV-ZPC or EEEV-FL93 in the fifth position could protect against lethal challenge with VEEV and EEEV, cohorts of CD-1 mice were immunized with 10^8 PFU of the vectors and then challenged 3-4 weeks post-immunization (Table 5). Following immunization, a neutralizing antibody response was readily detected in mice immunized with rISFV-N4G3-(EEEV-FL93 E3-E1)5, whereas little neutralizing antibody was detected in animals immunized with rISFV-N4G3-(VEEV-ZPC)5 (Tables 6, 7). Regardless of the antibody response, all animals were protected against lethal EEEV-FL93 and VEEV-ZPC challenge (FIG. 6 and FIG. 7).

Table 5. Study design for VEEV-ZPC and EEEV-FL93 challenge studies

Immunization					Challenge		
Group	Immunization Construct	Dose (pfu)	Route	Number of Animals	Virus	Dose (pfu)	Route
1	rISF-N4G3-(VEEV ZPC E3-E1)5	10^8	IM	10	VEEV ZPC	10^4	SC
2	PBS		IM	10	VEEV ZPC	10^4	SC
3	rISF-N4G3-(EEEV FL93 E3-E1)5	10^8	IM	10	EEEV FL93	10^4	SC
4	PBS		IM	12	EEEV FL93	10^4	SC

Table 6. Neutralizing antibody response in mice immunized with rISFV-N4G3-(EEEV-FL93 E3-E1)5

	$PRNT_{80}$	
Animal #	**Day 14**	**Day 21**
1	40	80
2	0	0
3	40	20
4	40	320
5	40	160
6	40	80
7	80	80
8	0	80
9	160	40
10	40	160
Mean	48	102
SD	45	93

Table 7. Neutralizing antibody response in mice immunized with rISFV-N4G3-(VEEV-ZPC E3-E1)5

	$PRNT_{80}$	
Animal #	**Day 21**	**Day 28**
1	0	0
2	0	0
3	0	0
4	0	40
5	0	0
6	0	0
7	0	0
8	0	0
9	0	0
10	0	0

[0218] *Dose Titration and Long-term Immunity study.* Animals were immunized with either 10^8 or 10^7 PFU of rISFV-N4G3-(VEEV-ZPC E3-E1)5 or $rVSV_{IN}$ $N4G_{(CT-1)}3$-(VEEV-ZPC E3-

E1)5 (Table 8). Following immunization, a VEEV neutralizing antibody response could be detected in most rISFV-N4G3-(VEEV-ZPC E3-E1)5-immunized animals at both doses (Table 9). More robust neutralizing antibody responses were detected in all animals immunized with $rVSV_{IN}$ $N4G_{(CT-1)}3$-(VEEV-ZPC E3-E1)5 (Table 10). However, as observed in the previous study, regardless of neutralizing antibody response to VEEV, all animals were protected following lethal challenge (FIG. 8).

Table 8. Dose Titration and Long-term Immunity study design

Immunization					Challenge (4 & 30 weeks post-infection)			
Group	Immunization Construct	Dose (pfu)	Route	No. of Animals	Virus	Dose (pfu)	Route	No. of Animals
1	rISF-N4G3-(VEEV ZPC E3-E1)5	10^8	IM	10	VEEV ZPC	10^4	SC	5
2	rISF-N4G3-(VEEV ZPC E3-E1)5	10^7	IM	10	VEEV ZPC	10^4	SC	5
3	rVSV$_{IN}$ N4G$_{(CT-1)}$3-(VEEV-ZPC E3-E1)5	10^8	IM	10	VEEV ZPC	10^4	SC	5
4	rVSV$_{IN}$ N4G$_{(CT-1)}$3-(VEEV-ZPC E3-E1)5	10^7	IM	10	VEEV ZPC	10^4	SC	5
5	PBS		IM	10	VEEV ZPC	10^4	SC	5

Table 9. Neutralizing antibody response in mice immunized with rISFV-N4G3-(VEEV-ZPC E3-E1)5

10^7 PFU				10^8 PFU		
	PRNT$_{80}$				PRNT$_{80}$	
Animal #	Day 25	Day 35		Animal #	Day 25	Day 35
1	80	80		1	80	640
2	80	640		2	80	20
3	80	0		3	80	0
4	40	0		4	40	0
5	40	80		5	20	20
6	20	20		6	20	20
7	80	320		7	20	40
8	40	20		8	20	20
9	80	320		9	0	0
10	0	80		10	20	20
Mean	54	156		Mean	38	78
SD	30	208		SD	30	198

Table 10. Neutralizing antibody response in mice immunized with rVSV$_{IN}$-N4G$_{(CT-1)}$3-(VEEV-ZPC E3-E1)5

10^7 PFU				10^8 PFU		
	PRNT$_{80}$				PRNT$_{80}$	
Animal #	Day 25	Day 35		Animal #	Day 25	Day 35
1	640	640		1	80	20
2	640	640		2	40	640
3	640	320		3	0	20
4	640	640		4	640	640
5	640	640		5	640	40
6	320	160		6	640	640
7	640	640		7	80	160
8	640	320		8	640	40
Mean	600	500		Mean	344	288
SD	113	199		SD	313	306

[0219] *Efficacy of blended immunogenic compositions.* Since an immunogenic composition should provide protection from more than one alphavirus, a study was designed to investigate if animals simultaneously immunized with rISFV-N4G3-(VEEV-ZPC E3-E1)5 and rISFV-N4G3-(EEEV-FL93 E3-E1)5 could be protected against lethal challenge against both EEEV-FL93 and VEEV-ZPC (Table 11). As in previous studies, neutralizing antibodies to both EEEV-FL93 and VEEV-ZPC were detected in almost all mice (Tables 12 and 13) and all immunized animals were protected against lethal EEEV-FL93 (FIG. 9) or VEEV-ZPC (FIG. 10) challenge. These results demonstrate that blended immunogenic compositions can provide protection against lethal challenge from multiple alphaviruses.

Table 11. Blended Immunization study design

Immunization					Challenge VEEV-ZPC			Challenge EEEV-FL93		
Group	Immunization Construct	Dose* (pfu)	Route	Number of Animals	Dose (pfu)	Route	No. of Animals	Dose (pfu)	Route	No. of Animals
1	rISF-N4G3-(VEEV ZPC E3-E1)5 & rISF-N4G3-(EEEV FL93 E3-E1)5	10^8	IM	20	10^4	SC	10	10^5	IP	10
2	PBS		IM	20	10^4	SC	10	10^5	IP	11

*Group 1 animals were immunized with 10^8 pfu of each virus

Table 12. Neutralizing antibody response against EEEV-FL93 in mice immunized with rISFV-N4G3-(EEEV-FL93 E3-E1)5 and rISFV-N4G3-(VEEV ZPC E3-E1)5

	$PRNT_{80}$	
Animal #	Day 14	Day 21
1	80	160
2	40	80
3	80	80
4	80	320
5	40	80
6	80	160
7	80	80
8	40	80
9	80	160
10	40	320
Mean	64	152
SD	21	96

Table 13. Neutralizing antibody response against VEEV-ZPC in mice immunized with rISFV-N4G3-(EEEV-FL93 E3-E1)5 and rISFV-N4G3-(VEEV ZPC E3-E1)5

	$PRNT_{80}$	
Animal #	Day 14	Day 21
1	0	20
2	0	20
3	20	40
4	40	20
5	40	20
6	20	20
7	80	80
8	0	0
9	80	80
10	0	20
Mean	28	32
SD	32	27

EXAMPLE 4
PRIME/BOOST STUDY PBS-MU-062 WITH RVSV AND RISFV VECTORS IN BALB/C MICE

[0220] A series of mouse studies was performed to assess a prime/boost regimen using rVSV and rISFV encoding an HIV Gag single dominant epitope (SDE) in Balb/c mice. These studies were designed to meet two study objectives: (a) PBS-Mu-062a: to study the immunogenicity of two new rISFV-HIV gag SDE vectors in mice, and to select the preferred candidate for a future prime/boost study with $rVSV_{IN}$ N4CT1Gag, and (b) PBS-Mu-062b: to compare the immune responses elicited using the prime/boost combination of $rVSV_{NJ}$/$rVSV_{IN}$ and rISFV/$rVSV_{IN}$.

[0221] PBS-Mu-062a: For this study, the relative immunogenicity of two candidate rISFV-based HIV gag expressing vectors were compared with the goal of advancing the most immunogenic construct into future prime/boost studies with $rVSV_{IN}$ based HIV gag-expressing vectors. A summary of the PBS-Mu-062a study design is provided in FIG. 13. For this study, BALB/c mice (n=5/group) were immunized by intramuscular injection with 10^7 pfu of the HIV gag-expressing vectors outlined in FIG. 12 and ten days later, splenocytes were collected and tested for HIV gag SDE and $rVSV_{IN}$ N peptide pool-specific IFN-γ secretion by ELISpot analysis (FIG. 14). In this study, immunization with rISFV-HIV-016 (rISFV) resulted in a mean HIV gag SDE-specific interferon-γ ELISpot response of 236±74 SFC/10^6 splenocytes, a response which was not significantly different than the HIV gag SDE-specific ELISpot response (147±32 SFC/10^6 splenocytes) elicited by the other rISFV-HIV gag candidate rISFV-HIV-018 (rISFVN*)(FIG. 14, left). Importantly, the vector rISFV-HIV-018, which encodes a viral N protein with a series of mutations in a known H2d-restricted epitope, showed a reduced tendency to elicit anti-vector $rVSV_{IN}$ N peptide-pool specific ELISpot responses (45±15 SFC/10^6 splenocytes) compared to the rISFV-HIV gag candidate rISFV-HIV-016 (140±59 SFC/10^6 splenocytes) which encodes a wild-type viral N gene (FIG. 14, right). Based on these results, rISFVN* (rISFV-HIV-018) was chosen for use in subsequent rVSV/rISFV prime/boost experiments.

[0222] PBS-Mu-062b: For this experiment, the relative immunogenicity was compared of various prime/boost immunization regimens using rVSV based vectors exclusively versus a combination of rISFV and rVSV based vectors. A summary of the PBS-Mu-062b study design is provided in FIG. 16. For this experiment, BALB/c mice (n=5/group) were immunized by intramuscular injection with 10^7 pfu of the rISFV HIV gag SDE expressing vectors outlined in FIG. 15 in combination with the $rVSV_{IN}$ HIV gag SDE construct (FIG. 12). Mice were immunized on a schedule of 0 and 4 weeks. One week after the final immunization, splenocytes were collected and tested for HIV gag SDE-specific (FIG. 17) and $rVSV_{IN}$ N peptide pool-specific (FIG. 18) IFN-γ secretion by ELISpot analysis. In this study, mice immunized with the $rVSV_{NJ}$ / $rVSV_{IN}$ prime/boost regimen demonstrated an HIV gag SDE-specific ELISpot response (2,330±412 SFC/10^6 splenocytes) which was significantly lower ($p<0.05$) than the response seen in mice immunized with the heterologous rISFVN*/$rVSV_{IN}$ prime/boost regimen (4,758±183 SFC/10^6 splenocytes)(FIG. 17). This significant two-fold increase in the HIV gag SDE-specific IFN-γ ELISpot response compared to the $rVSV_{NJ}$/$rVSV_{IN}$ immunized mice was unaffected by switching the order of the heterologous regimen ($rVSV_{IN}$/ rISFVN*; 5,870±1,258 SFC/10^6 splenocytes) or by the presence of a wild-type viral N gene in the rISFV vector (rISFV/ $rVSV_{IN}$; 5,061±890 SFC/10^6 splenocytes) (FIG. 17). As shown in FIG. 18, the heterologous rISFVN*/$rVSV_{IN}$ and $rVSV_{IN}$/ rISFVN* prime/boost regimens elicited significantly lower ($p<0.05$) mean $rVSV_{IN}$ N peptide pool-specific IFN-γ ELISpot responses (451±67 and 408±55 SFC/10^6 splenocytes, respectively) compared to the $rVSV_{NJ}$ / $rVSV_{IN}$ (2,794±456 SFC/10^6 splenocytes) or the rISFV/$rVSV_{IN}$ (1,459±238 SFC/10^6 splenocytes) regimen.

[0223] The above mentioned studies clearly demonstrate that the heterologous rISFV/rVSV$_{IN}$ and rVSV$_{IN}$/rISFV prime/boost immunization regimens elicited significantly higher IFN-γ ELISpot responses than did the rVSV$_{NJ}$/rVSV$_{IN}$ immunization regimen in mice. Furthermore, the rISFV N* mutation reduced cross-reactive responses to rVSV N, although this did not result in an increase in the HIV gag SDE-specific IFN-γ ELISpot response.

EXAMPLE 5
STUDY OF rISFV VECTOR EXPRESSING CHIKUNGUNYA VIRUS GLYCOPROTEIN IN A129 MICE

[0224] Chikungunya virus (CHIKV) is a mosquito borne virus of the Alphavirus genus in the *Togaviridae* family. CHIKV infection in humans results in high fever, headache, vomiting, skin rash and painful arthritis. Arthritis, which can persist for months or even years (Powers and Logue. *J. Gen. Virol.* 2007, 88:2363-2377), is the hallmark of a generally self-limiting CHIKV infection. However, in recent epidemics in the Indian subcontinent and Indian Ocean islands, which affected over 1.5 million people, some people have displayed more severe symptoms including encephalitis, hemorrhagic disease, and mortality (Schwartz and Albert. *Nature Rev. Microbiol.* 2010, 8:491-500). The more recent and rapid spread of CHIKV into the Caribbean islands and the Americas (Powers. *J. Gen. Virol.* 2015, 96:1-5) has generated an even more urgent need for immunogenic compositions against CHIKV.

[0225] CHIKV has a single, positive sense, 11.8 kb RNA genome, which encodes four non-structural proteins (nsP 1-4) and five structural proteins (C, E3-E2-6K-E1). The structural proteins are cleaved from a precursor to generate the capsid and envelope glycoproteins (Strauss and Strauss. *Microbiol. Rev.* 1994, 58:491-562). The E2 and E1 proteins form a stable heterodimer and E2-E1 heterodimers interact to form the spike that is found on the virus surface. E2 is formed as a precursor called PE2 or p62 that is cleaved into E2 and E3. There is a small hydrophobic peptide called 6K that is produced as a linker between E2 and E1. When the E3-E2-6K-E1 polyprotein is processed, the E2 and E1 glycoproteins are produced, which then form the E2-E1 glycoprotein heterodimers (Strauss and Strauss. pages 497-499).

[0226] The starting point for constructing an attenuated rISFV vector expressing the E2-E1 glycoprotein was the plasmid designated pVSVΔG-CHIKV, which was received from Dr. John Rose (Yale University) (Chattopadhyay et al. *J. Virol.* 2013, 87:395-402). This plasmid contained an optimized Chikungunya E3-E2-6K-E1 genetic sequence (Genscript, Inc.) in place of the VSV G gene within the rVSV genomic cDNA. The CHIKV- E3-E2-6K-E1 sequence was amplified by PCR using the following primers:

[0227] Primer Alpha_001: GGGCCCA***CTCGAG***AACATGAGCCTGGCCATCCCCGTG (contains XhoI site and Kozak sequence) (SEQ ID NO:69)

[0228] Primer Alpha_002: 61/ (Contains NotI site and NheI site) (SEQ ID NO:70)

[0229] The resultant PCR product was digested with Xho/ NotI restriction enzymes and cloned into rVSVN4CT1 vector cDNA. This vector cDNA was then amplified and digested with XhoI/ NotI restriction enzymes and the released insert encoding CHIKV-E3-E2-6K-E1 proteins was cloned into XhoI/NotI digested pPBS-ISFV-HIV-015 (described above in Example 2). Recombinant ISFV (rISFV) encoding CHIKV-E3-E2-6K-E1 proteins was then rescued from this pDNA as described above in Example 1. The result was a rISFV-N4 G-CTΔ25(CHIKV GP)1 designated pPBS-ISF-Alpha-003 virus expressing CHIKV-GP from the first position in the rISFV genome, and where CHIKV-GP represents CHIKV-E3-E2-6K-E1.

[0230] Rescued virus was plaque purified and amplified on Vero E6 cell monolayers (ATCC CCL-81). For animal studies, virus vectors were purified from infected BHK-21(ATCC CCL-10) cell supernatants by centrifugation through a 10% sucrose cushion. Purified virus was resuspended in PBS, pH 7.0, mixed with a sucrose phosphate (SP) stabilizer (7mM K_2HPO_4, 4mM KH_2PO_4, 218mM Sucrose), snap frozen in ethanol/dry ice and stored at -80^{0}C until ready for use.

[0231] A study was performed to investigate the safety and efficacy of an immunogenic composition comprising the rISFV-N4G-CTΔ25(CHIKV GP)1 vector described above that expressed CHIKV-GP from the first position. Mice numbered 11-21 lacking the receptor for type 1 interferon (A129 mice) were immunized with 1 X 10^7 pfu of rISFV-N4G-CTΔ25(CHIKV

GP)1 in their left footpad. The right footpad was not injected in order to serve as a control. A129 mice numbered 1-10 were not immunized as further controls. All 21 mice were injected in the left footpad with a 10 μl dose of 1 X 10^4 pfu of the LaReunion isolate of CHIKV and swelling was measured. The right footpad height was also measured as an internal control. The footpad heights of the left foot were not taken on the day of injection. Previous data showed that the sizes of the left and right feet were identical.

[0232] As shown in FIG. 19, mice 11-21 immunized with rISFV-N4G-CTΔ25(CHIKV GP)1 maintained their body weights after challenge, while unimmunized mice lost weight through day 4 post-challenge.

[0233] As shown in FIG. 20, immunized mice 11-21 had minor left footpad swelling by day 3 which resolved by day 5. In contrast, unimmunized mice 1-10 had left footpad swelling which continued to increase through day 4. Both groups of mice had no right footpad swelling.

[0234] As shown in FIG. 21, immunized mice 11-21 demonstrated no viremia in the blood on days 1 or 2 [below limit of detection of 100 pfu/ml]. In contrast, unimmunized mice 1-10 had signs of viremia on day 1, which increased to almost 1 X 107 pfu/ml by day 2.

[0235] By day 3, all unimmunized mice showed signs of illness, including footpad swelling, ruffled fur and lethargy. In contrast, all immunized mice were normal in appearance and behavior. As shown in FIG. 22, by day 5, all 10 unimmunized mice succumbed to illness. In contrast, all 11 immunized mice survived with no signs of illness.

[0236] All mice immunized with rISFV-N4G-CTΔ25(CHIKV GP)1 seroconverted by day 21 as determined by plaque reduction neutralization titers (PRNT80) from sera taken on days 1, 7 and 21 post-immunization as shown in Table 14 (bolded numbers indicate a positive result):

Table 14. Neutralizing antibody response against CHIKV in mice immunized with rISFV expressing Chikungunya glycoprotein

Mouse Number	Day 1	Day 7	Day 21
11	**1/20**	**1/20**	**1/40**
12	**1/160**	**1/40**	**1/80**
13	**1/20**	**1/40**	**1/40**
14	**1/40**	**1/20**	**1/40**
15	<1/20	<1/20	**1/40**
16	<1/20	**1/20**	**1/40**
17	**1/40**	<1/20	**1/40**
18	**1/20**	**1/20**	**1/40**
19	**1/40**	**1/40**	**1/80**
20	**1/320**	**1/80**	**1/80**
21	**1/40**	**1/40**	**1/40**

2015225553 10 Feb 2020

CLAIMS

1. A recombinant replication competent Isfahan virus comprising an N protein gene encoding an N protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:2, a P protein gene encoding a P protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:3, an M protein gene encoding an M protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:4, a G protein gene encoding a G protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:5, and an L protein gene encoding an L protein having an amino acid sequence that is 90, 95, 98, or 100% identical to the amino acid sequence of SEQ ID NO:6.; and further comprising a heterologous polynucleotide sequence encoding a heterologous polypeptide.

2. The Isfahan virus of claim 1, wherein the heterologous polynucleotide sequence is flanked by a transcription start signal and a transcription stop signal.

3. The Isfahan virus of claim 1, wherein the heterologous polynucleotide encodes an immunogenic polypeptide.

4. The Isfahan virus of claim 1, wherein the heterologous polynucleotide encodes one or more antigens, preferably the antigen is a viral antigen, a bacterial antigen, a tumor-specific or cancer antigen, a parasitic antigen or an allergen.

5. The Isfahan virus of claim 5, wherein the antigen is a viral antigen.

6. The Isfahan virus of claim 6, wherein the viral antigen is from Chikungunya virus.

7. The Isfahan virus of claim 1, wherein the heterologous polynucleotide sequence is located at position 1, 2, 3, 4, 5 or 6 of the Isfahan virus genome.

8. The Isfahan virus of claim 1, wherein the N protein gene is located at position 1, 2, 3, 4, or 5 of the Isfahan virus genome.

9. The Isfahan virus of claim 1, wherein the G protein gene encodes a G protein having a carboxy-terminal truncation, preferably the G protein has a carboxy-terminal truncation of 20 to 25 amino acids.

10. The Isfahan virus of claim 1, wherein the heterologous polynucleotide sequence is located at position 5 and the N protein gene is located at position 4 of the Isfahan virus genome.

11. A host cell comprising the Isfahan virus of claim 1.

12. An immunogenic composition comprising a recombinant replication competent Isfahan virus of any one of claims 1 to 10 and a pharmaceutically acceptable diluent, excipient or carrier.

13. An immunogenic composition comprising a recombinant replication competent Isfahan virus of claim 12 for inducing an antigen-specific immune response to an antigen in a mammalian subject comprising administering the immunogenic composition of claim 12.

14. A prime-boost immunization kit for inducing an antigen-specific immune response in a mammalian subject, said kit comprising:

(a) a Isfahan composition comprising a recombinant replication competent Isfahan virus of any one of claims 1 to 10 and a pharmaceutically acceptable diluent, excipient or carrier; and

(b) a vesicular stomatitis virus composition comprising a recombinant replication competent vesicular stomatitis virus encoding an N protein gene, a P protein gene, an M protein gene, a G protein gene, an L protein gene, and a heterologous polynucleotide sequence, wherein said heterologous polynucleotide sequence (i) is flanked by a transcription start signal and a transcription stop signal, and (ii) encodes a heterologous polypeptide; and a pharmaceutically acceptable diluent, excipient or carrier,

wherein the Isfahan composition is administered prior to or after the vesicular stomatitis virus composition.

15. A recombinant replication competent Isfahan virus of claim 1 for inducing an antigen-specific immune response in a mammalian subject comprising administering the immunogenic compositions of claim 14.

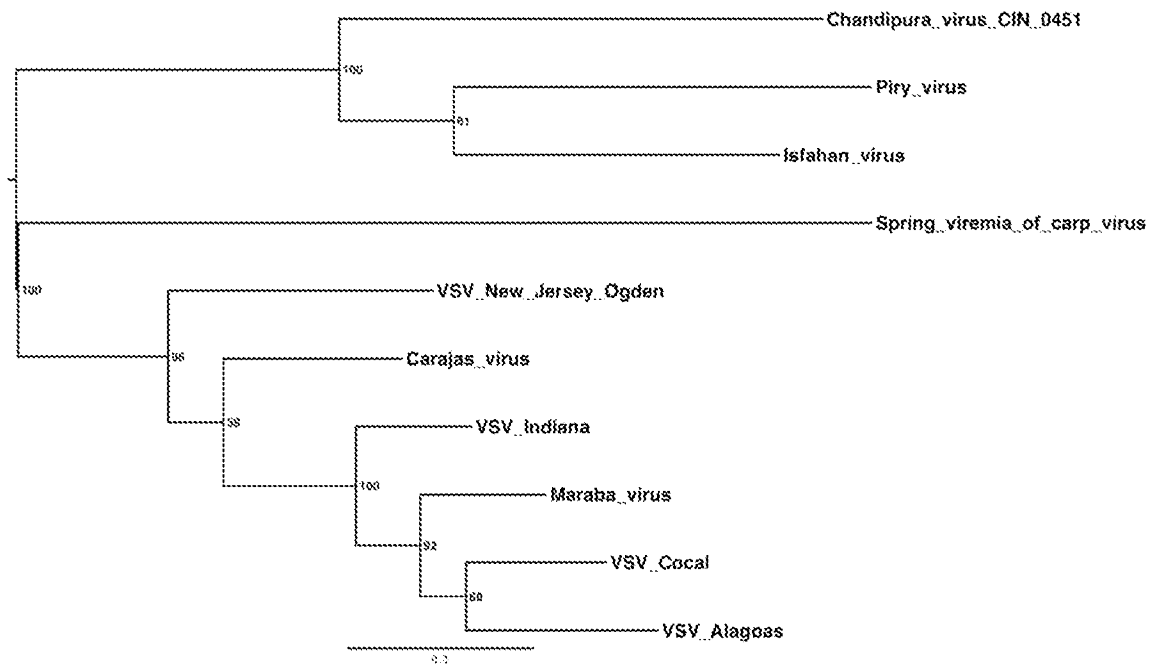


FIG. 1

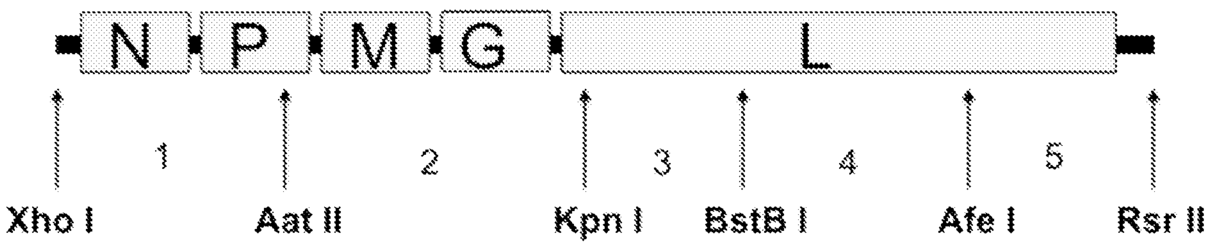


FIG. 2

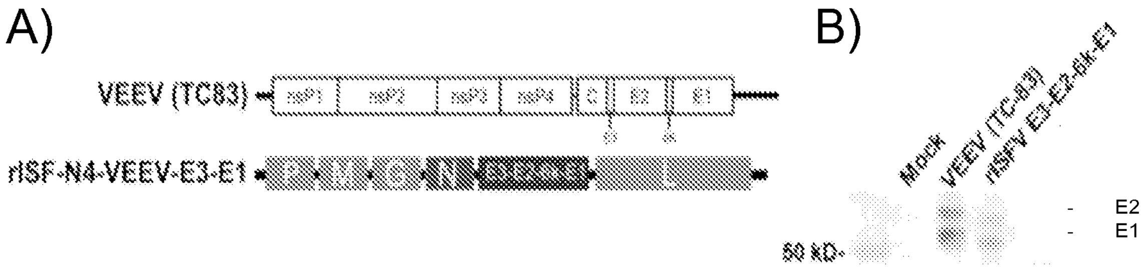


FIG. 3A-3B

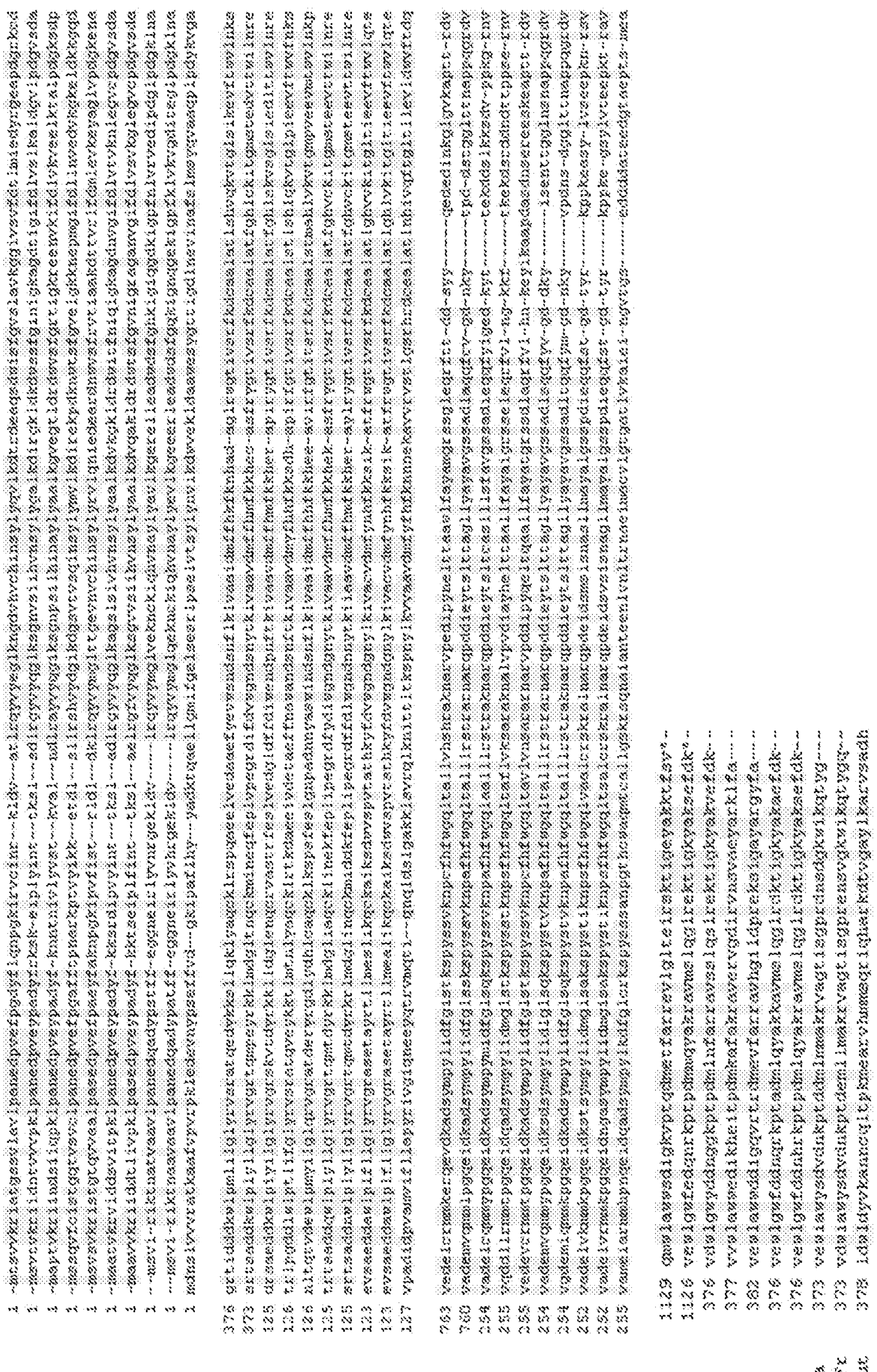


FIG. 4

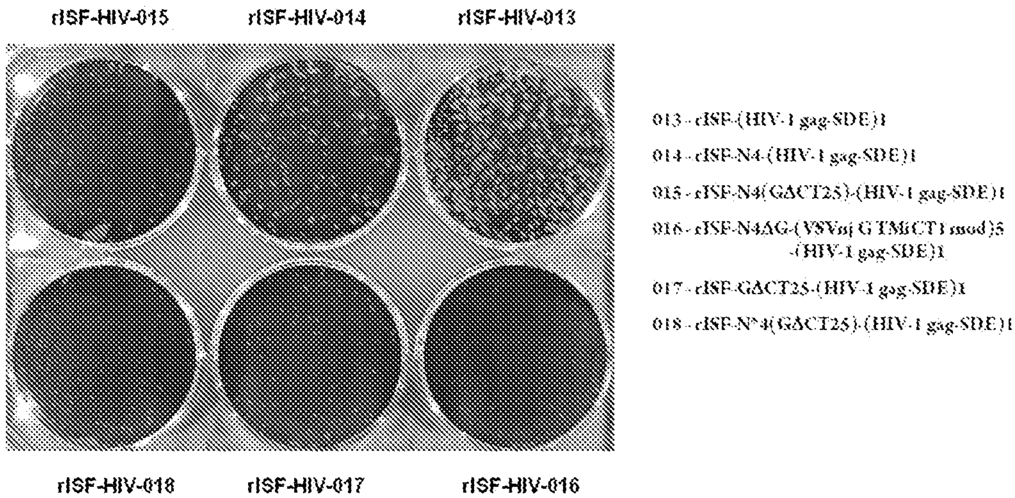

rISF-HIV-015
rISF-HIV-014
rISF-HIV-013
rISF-HIV-018
rISF-HIV-017
rISF-HIV-016
013 - rISF-(HIV-1 gag-SDE)1
014 - rISF-N4-(HIV-1 gag-SDE)1
015 - rISF-N4(GΔCT25)-(HIV-1 gag-SDE)1
016 - rISF-N4ΔG-(VSVnj G TMCT1 mod)5 -(HIV-1 gag-SDE)1
017 - rISF-GΔCT25-(HIV-1 gag-SDE)1
018 - rISF-N*4(GΔCT25)-(HIV-1 gag-SDE)1

FIG. 5

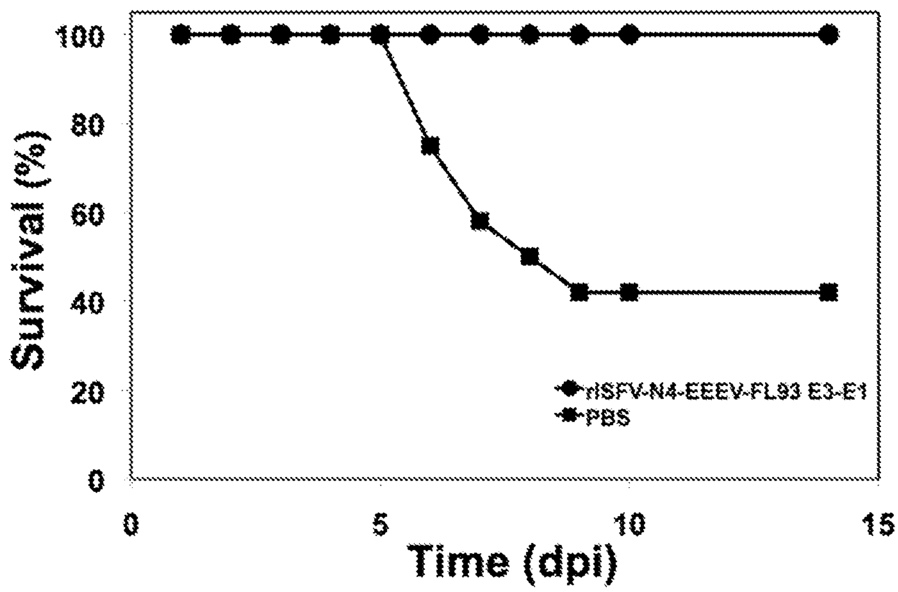

Survival (%)
0
20
40
60
80
100
0
5
10
15
Time (dpi)
rISFV-N4-EEEV-FL93 E3-E1
PBS

FIG. 6

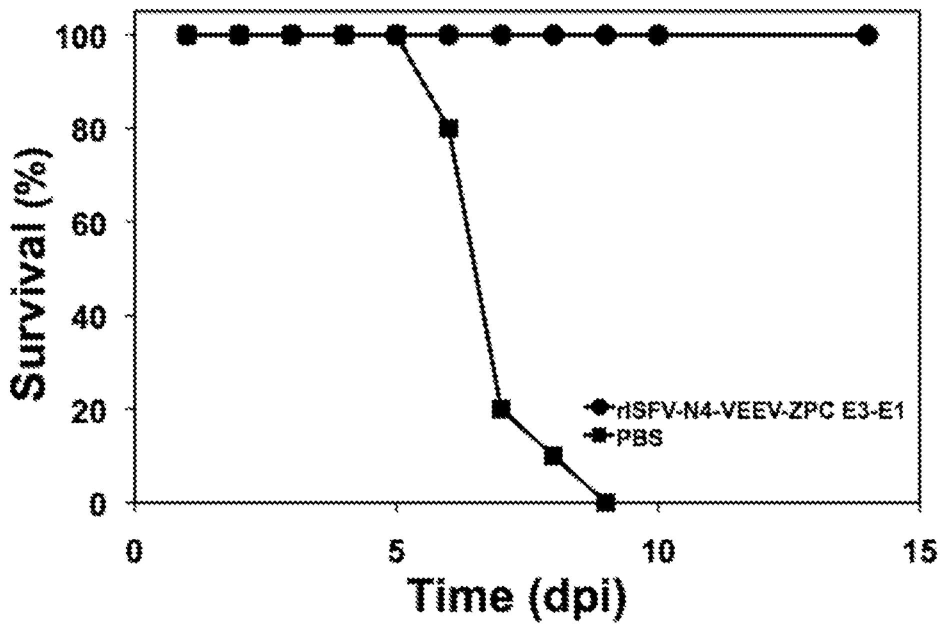

Survival (%)
100
80
60
40
20
0
0
5
10
15
Time (dpi)
rISFV-N4-VEEV-ZPC E3-E1
PBS

FIG. 7

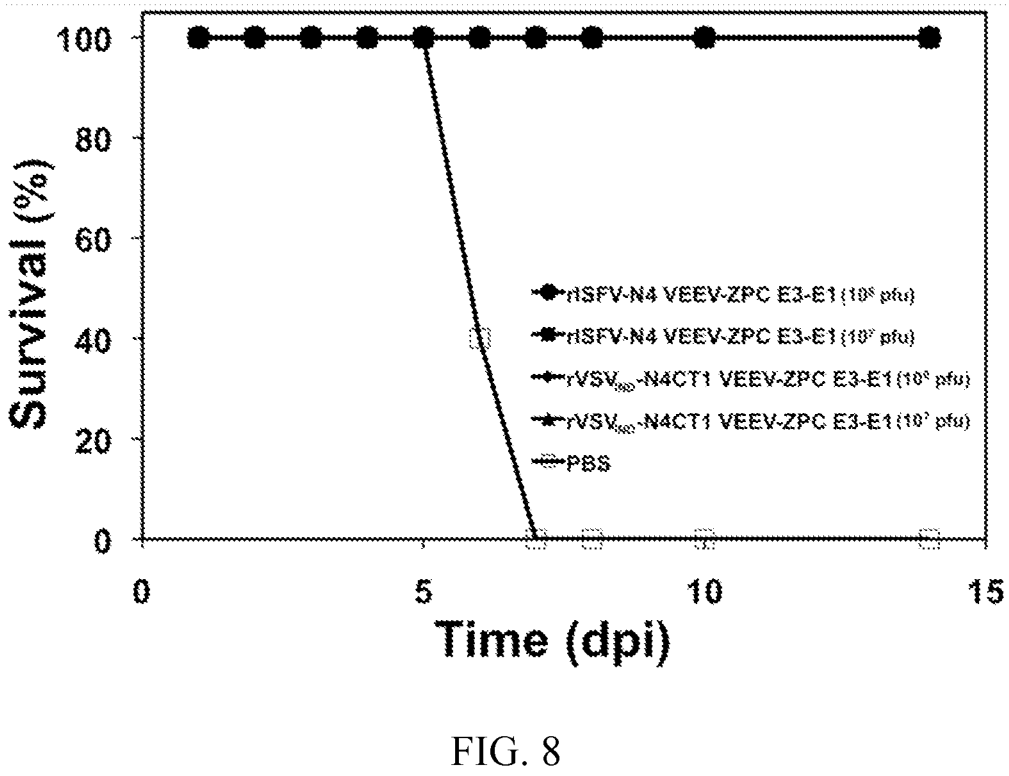
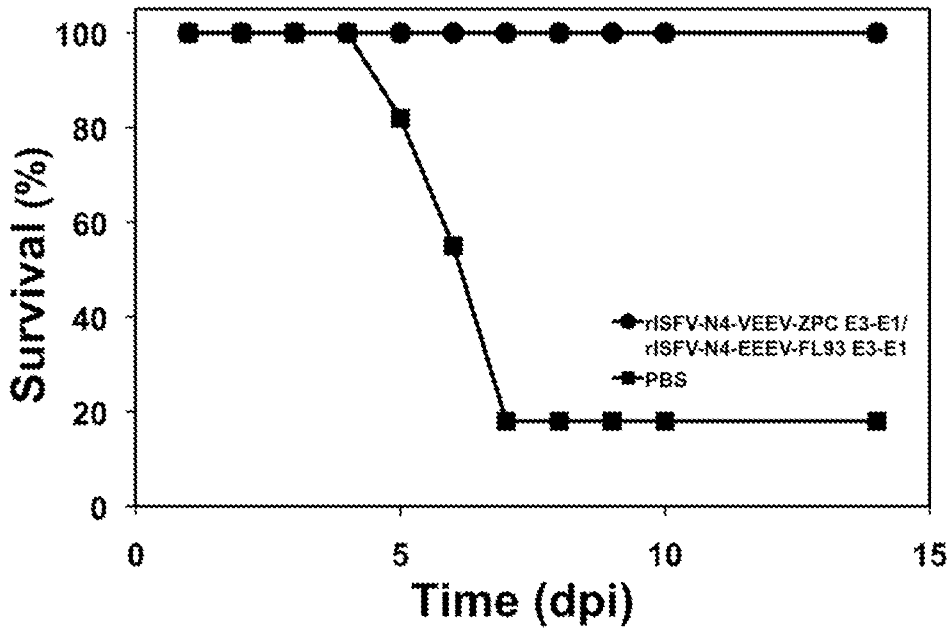
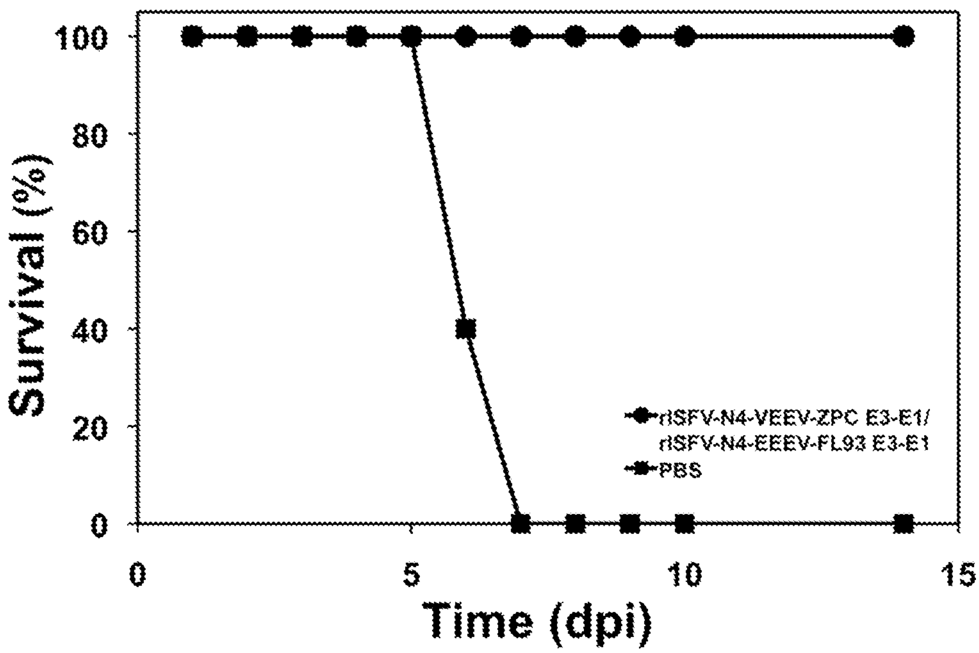

Survival (%)
100
80
60
40
20
0
0
5
10
15
Time (dpi)
rISFV-N4 VEEV-ZPC E3-E1 (10^6 pfu)
rISFV-N4 VEEV-ZPC E3-E1 (10^7 pfu)
rVSV-N4CT1 VEEV-ZPC E3-E1 (10^6 pfu)
rVSV-N4CT1 VEEV-ZPC E3-E1 (10^7 pfu)
PBS

FIG. 8



100
80
60
40
20
0
Survival (%)
0
5
10
15
Time (dpi)
rISFV-N4-VEEV-ZPC E3-E1/
rISFV-N4-EEEV-FL93 E3-E1
PBS

FIG. 9



100
80
60
40
20
0
Survival (%)
0
5
10
15
Time (dpi)
rISFV-N4-VEEV-ZPC E3-E1/
rISFV-N4-EEEV-FL93 E3-E1
PBS

FIG. 10

```
Chandipura N          ...mmtpgqeidqadsympylidmglstkspysstknp...
Piry N                ...mmtpgqeidkadsympylidfglstkspyssvknp...
Cocal N               ...mmypgqeidksdsympylidlglsqkspystvknp...
VSV Alagoas N         ...mmkpgqeidkadsympylidfglsqkspystvknp...
Spring Viraemia       ...mmkpgqeidkstsympylidmgisakspystiknp...
Vesiculo Pike Fr      ...mmkpgqeidngasympylidmgisakspystiknp...
VSVnj N               ...mmypgqeidkadsympymidfglsqkspyssvknp...
VSVi N                ...mmlpgqeidkadsympylidfglsskspyssvknp...
ISF N                 ...mmkerqevdkadsympylidfgistkspyssvknp...

ISF N*                ...mmkerqevdqsdsympymidmgistkspyssvknp...
                                  qs      m  m
```

FIG. 11

rVSVin N4CT1 (HIVgag-SDE)1 = rVSV-HIV-106

rISF-N4ΔG-(VSVnj G TMiCT1 mod)5-(HIV-1 gag-SDE)1 = rISF-HIV-016

rISF-N*4GΔCT25-(HIV-1 gag-SDE)1 = rISF-HIV-018

N*: The ISF N protein is a slightly modified form of the wild-type Isfahan protein:
A strong T cell epitope for mice has been changed (K271Q, A272S, L279M, F282M).

FIG. 12

Group #	# mice	Vaccine	Vaccine dose	Route
1	5	rVSV$_{IN}$ N4CT1 (HIVgag-SDE)1 (rVSV-HIV-106)	10^7 pfu	I.M
2	5	rISF-N4ΔG-(VSV$_{IN}$ G TMCT1 mod)5-(HIV-1 gag-SDE)1 (rISF-HIV-016)	10^7 pfu	I.M
3	5	rISF- N*4GΔCT25-(HIVgag-SDE)1 (rISF-HIV-018)	10^7 pfu	I.M

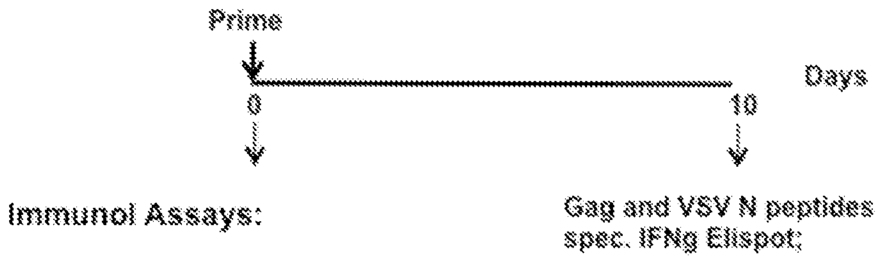
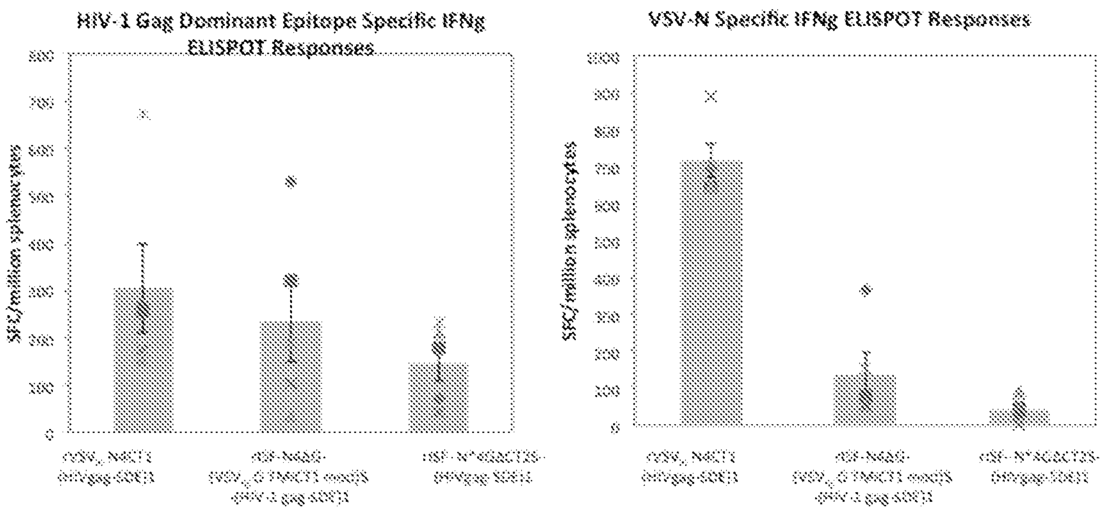


FIG. 13



Conclusion: 1) the two rISF candidates elicited similar Ag specific CMI, slightly lower than those from rVSV.
2) rISF N* mutation reduces the cross responses to rVSV N. It may benefit the prime/boost.
Further test it in Mu062b.

FIG. 14

rISF-N4GΔCT25-(HIV-1 gag-SDE)1 = rISF-HIV-015

rISF-N*4GΔCT25-(HIV-1 gag-SDE)1 = rISF-HIV-018

FIG. 15

Group #	# mice	Prime Vaccine	Vaccine dose	Boost Vaccine	Vaccine dose	Route
1	5	N/A	N/A	rVSVin N4CT1 (HIVgag-SDE)1 (rVSV-HIV-106)	10^7 pfu	I.M
2	5	rVSVnj N4CT1 (HIVgag-SDE)1 (rVSV-HIV-122)	10^7 pfu	rVSVin N4CT1 (HIVgag-SDE)1 (rVSV-HIV-106)	10^7 pfu	I.M
3	5	rISF- N*4GΔCT25-(HIVgag-SDE)1 (rISF-HIV-018)	10^7 pfu	rVSVin N4CT1 (HIVgag-SDE)1 (rVSV-HIV-106)	10^7 pfu	I.M
4	5	rVSVin N4CT1 (HIVgag-SDE)1 (rVSV-HIV-106)	10^7 pfu	rISF- N*4GΔCT25-(HIVgag-SDE)1 (rISF-HIV-018)	10^7 pfu	I.M.
5	5	rISF- N4GΔCT25-(HIVgag-SDE)1 (rISF-HIV-015)	10^7 pfu	rVSVin N4CT1 (HIVgag-SDE)1 (rVSV-HIV-106)	10^7 pfu	I.M

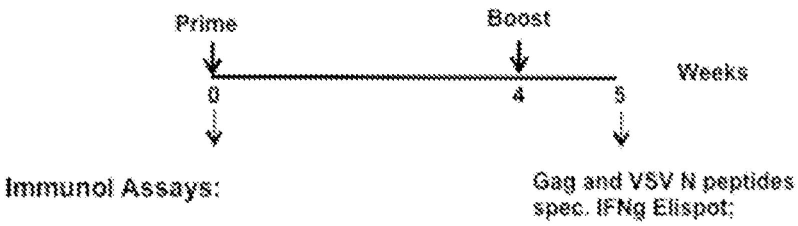


FIG. 16

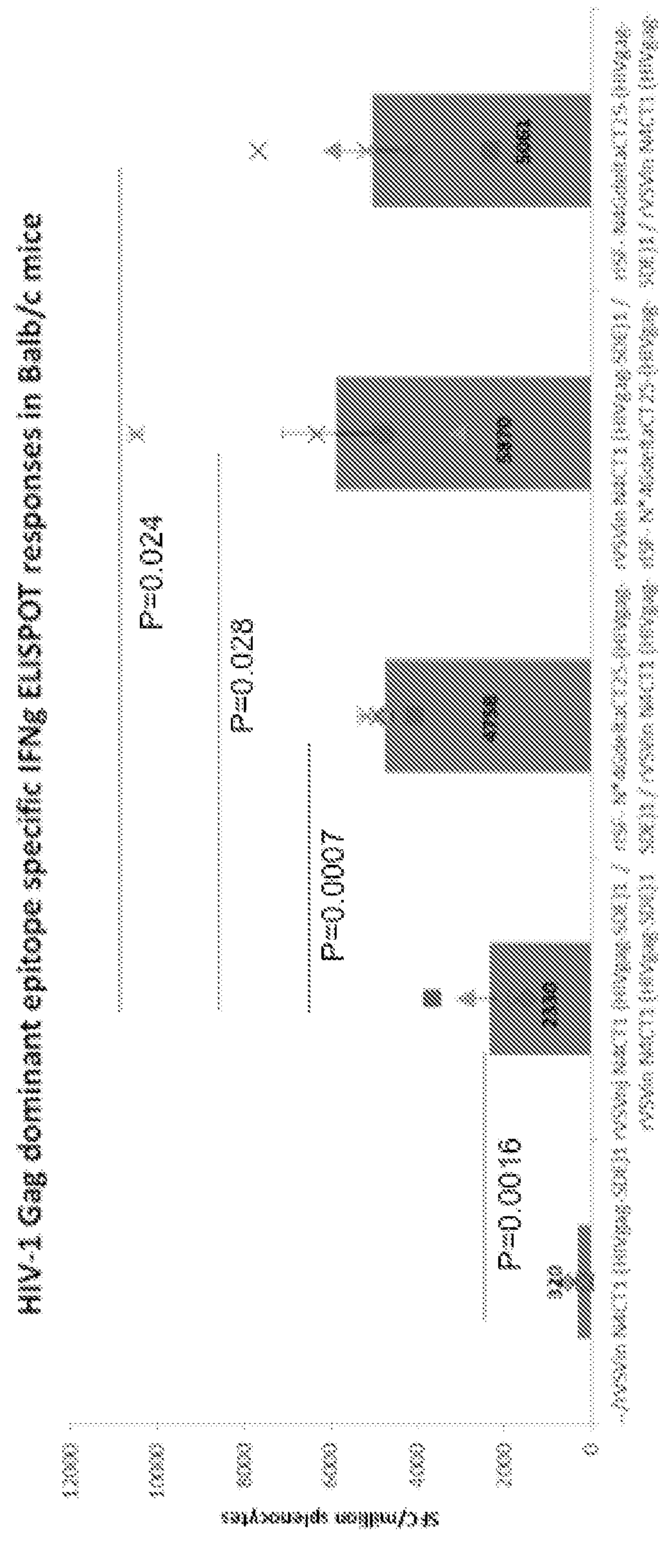

HIV-1 Gag dominant epitope specific IFNg ELISPOT responses in Balb/c mice
P=0.0016
P=0.0007
P=0.028
P=0.024

FIG. 17

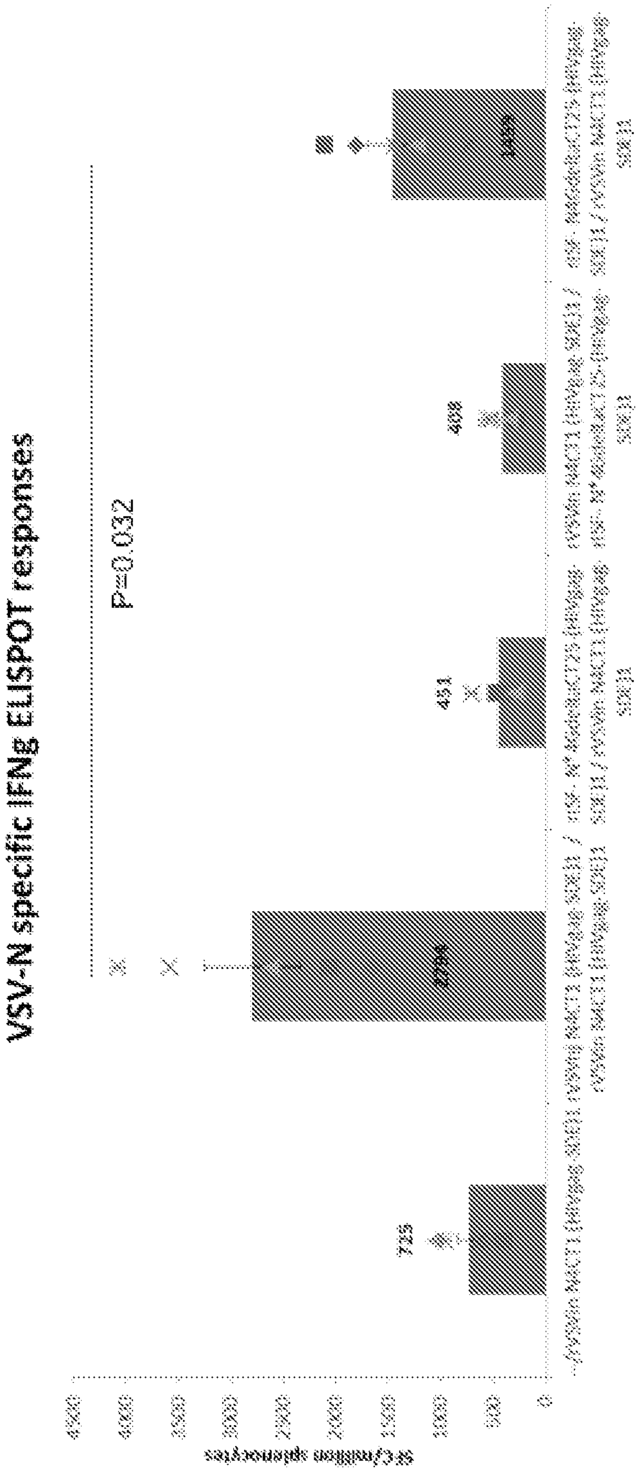

VSV-N specific IFNg ELISPOT responses
P=0.032
725
2784
451
408
1459

FIG. 18

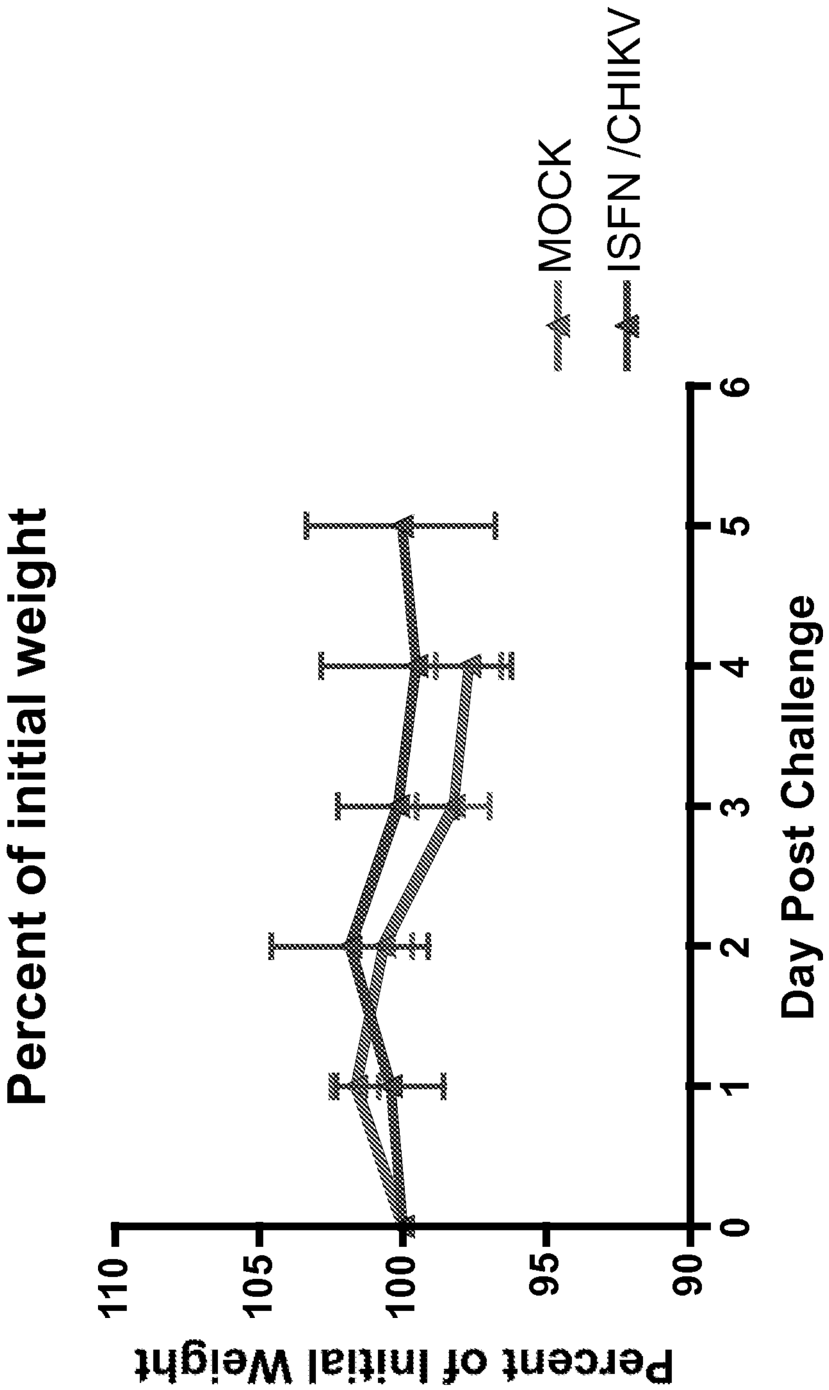

Percent of initial weight
Percent of Initial Weight
110
105
100
95
90
0
1
2
3
4
5
6
Day Post Challenge
MOCK
ISFN /CHIKV

FIG. 19

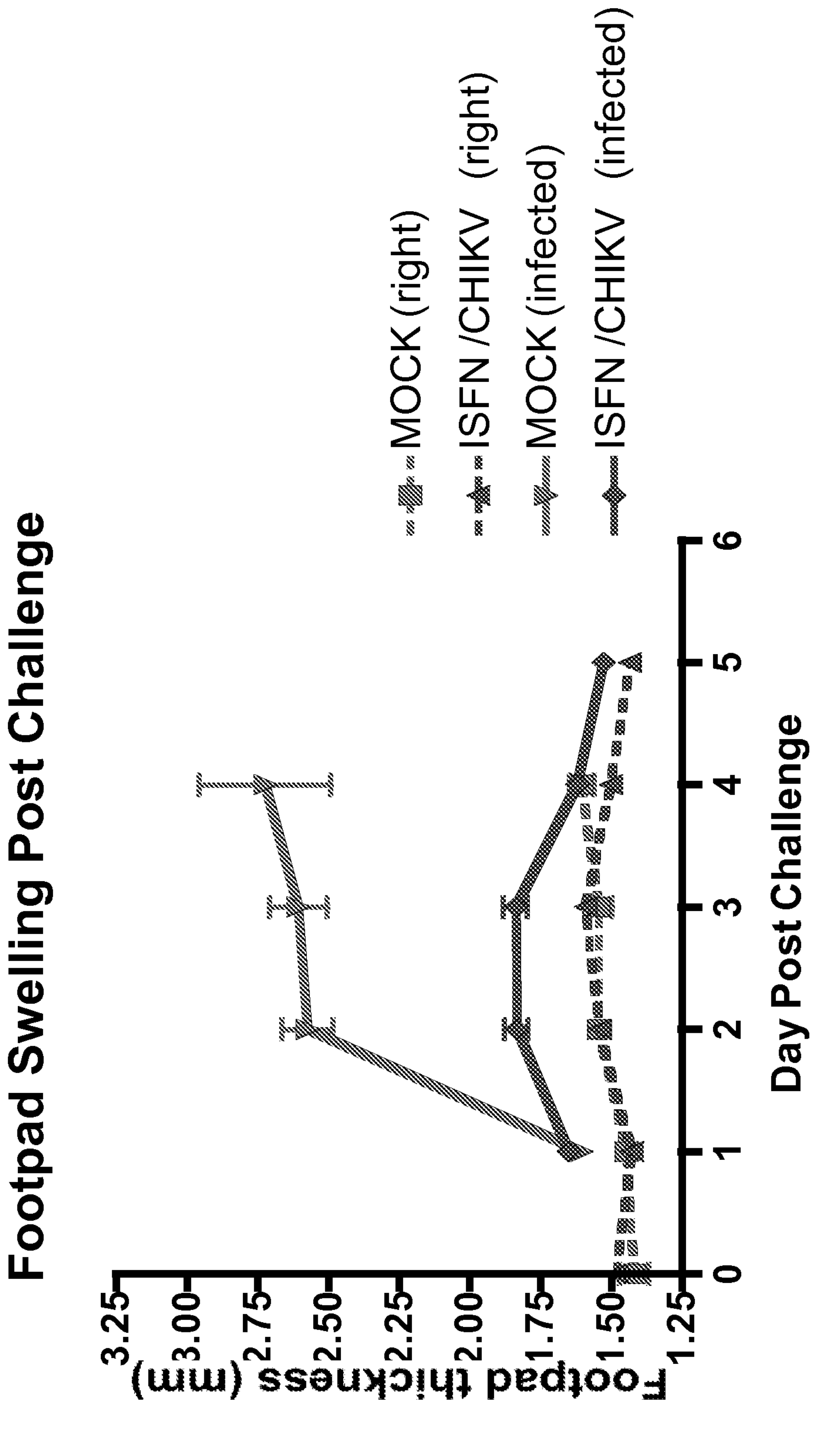

Footpad Swelling Post Challenge
Footpad thickness (mm)
3.25
3.00
2.75
2.50
2.25
2.00
1.75
1.50
1.25
0
1
2
3
4
5
6
Day Post Challenge
MOCK (right)
ISFN /CHIKV (right)
MOCK (infected)
ISFN /CHIKV (infected)

FIG. 20

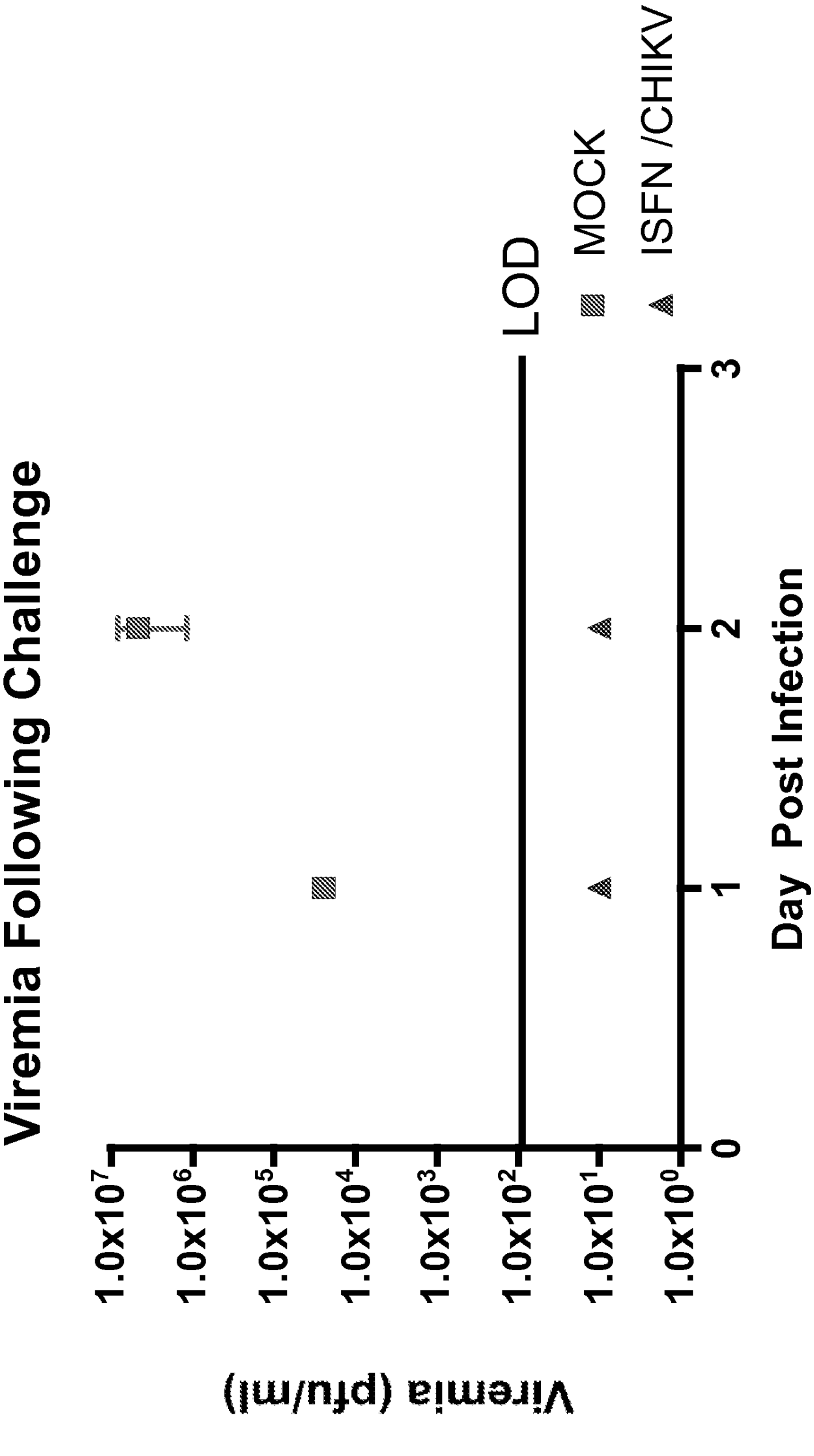

Viremia Following Challenge
Viremia (pfu/ml)
1.0x10^7
1.0x10^6
1.0x10^5
1.0x10^4
1.0x10^3
1.0x10^2
1.0x10^1
1.0x10^0
0
1
2
3
Day Post Infection
LOD
MOCK
ISFN /CHIKV

FIG. 21

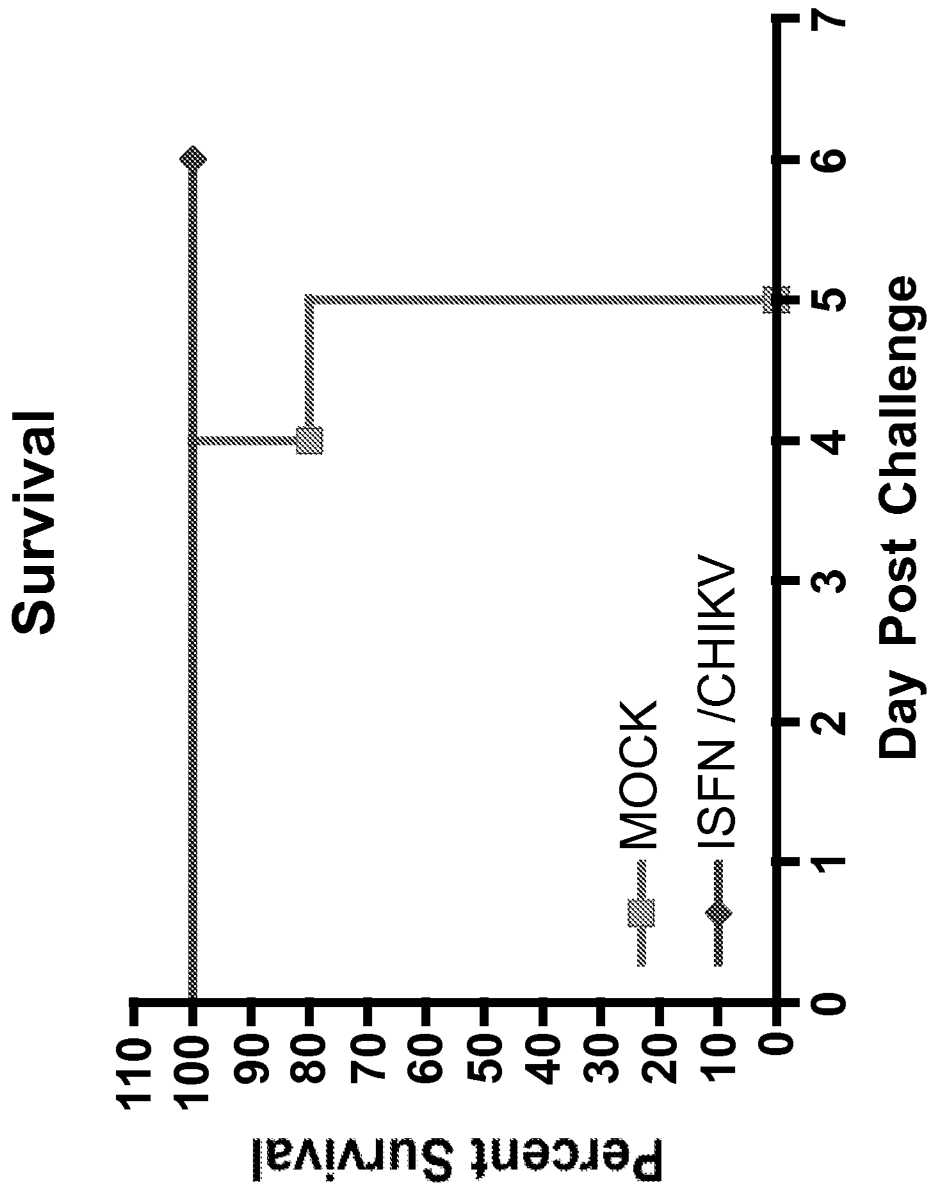

Survival
Percent Survival
110
100
90
80
70
60
50
40
30
20
10
0
0
1
2
3
4
5
6
7
Day Post Challenge
MOCK
ISFN /CHIKV

FIG. 22