



(51) International Patent Classification:

A61K 39/12 (2006.01) C12N 15/33 (2006.01)
A61K 39/02 (2006.01) A61K 39/145 (2006.01)
C07K 14/00 (2006.01) C12N 7/04 (2006.01)
C07K 14/005 (2006.01)

(21) International Application Number:

PCT/US2012/049008

(22) International Filing Date:

31 July 2012 (31.07.2012)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

61/513,695 1 August 2011 (01.08.2011) US
61/513,905 1 August 2011 (01.08.2011) US
61/527,636 26 August 2011 (26.08.2011) US

(71) Applicants (for all designated States except US): **EMORY UNIVERSITY** [US/US]; Office of Technology Transfer, 1599 Clifton Road NE, 4th Floor, Atlanta, Georgia 30322 (US). **CHILDREN'S HEALTHCARE OF ATLANTA, INC.** [US/US]; 1600 Tullie Circle NE, Atlanta, Georgia 30329 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **COMPANS, Richard W.** [US/US]; 1038 Castle Falls Drive, Atlanta, Georgia 30320 (US). **WANG, Baozhong** [CN/US]; 5055 Magnolia Gale Drive, Duluth, Georgia 30096 (US). **MOORE, Martin L.** [US/US]; 1238 Thomas Road, Decatur, Georgia 30030 (US). **QUAN, Fu Shi** [KR/KR]; Chungju National University, 61 Daehak-ro, Jeungpyeong-gun, Chungbuk, Gyeonggi-do 368-701 (KR).

(74) Agents: **MASON, James C.** et al.; Emory University, Office of Technology Transfer, 1599 Clifton Road NE, 4th Floor, Atlanta, Georgia 30322 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, 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.

[Continued on next page]

(54) Title: VLPS CONTAINING LIGANDS AND METHODS RELATED THERETO

M2e sequence: (M) SLLTEVETPIRNEWGC RC NDSSDP

Sequence used: SLLTEVETPIRNEWG S RS NDSSDP

4.M2e:

AAASLLTEVETPIRNEWGSRNSDSSDPAAGTSAAASLLTEVETPIRNE
WGRSNDSSDPAAALQAAASLLTEVETPIRNEWGSRNSDSSDPAAA
ACAAASLLTEVETPIRNEWGSRNSDSSDPAAAACKL

4. M2e

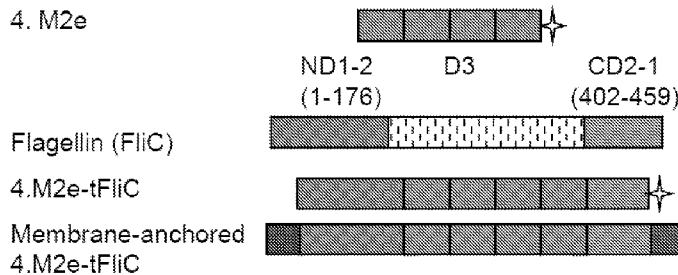


FIGURE 1

(57) Abstract: This disclosure relates to immunogenic compositions and methods of enhancing an immune response to an antigen. In certain embodiments, the disclosure relates to virus-like carries comprising a TLR5 agonist on the exterior without an antigen.



(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, 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, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

Published:

— *with international search report (Art. 21(3))*

— *with sequence listing part of description (Rule 5.2(a))*

VLPS CONTAINING LIGANDS AND METHODS RELATED THERETO

STATEMENT REGARDING FEDERALLY FUNDED RESEARCH

This invention was made with government support under Grants AI068003 and
5 UL1RR025008 awarded by the National Institutes of Health; and 1R43AI091230,
1R01AI068003, and 1R01AI087798 by the National Institute of Allergy and Infectious
Diseases. The government has certain rights in the invention.

CROSS-REFERENCE TO RELATED APPLICATIONS

10 This application claims priority to U.S. Provisional Application Number
61/513,695 filed 1st August, 2011, U.S. Provisional Application Number, 61/513,905 filed
1st of August 2011, and U.S. Provisional Application Number 61/527,636 filed 26th of
August 2011, all hereby incorporated by reference in their entirety.

15 BACKGROUND

Virus-like particle (VLP) vaccines are genetically engineered complexes of
multiple copies of protein antigens in a particulate virus-like structure. Viral proteins
presented as VLPs or recombinant vaccine are immunogenic. Methods of creating VLPs
are provided in U.S. Patent Application Publication Number 2006/02167702. See also
20 U.S. Patent Application Publication Numbers 2006/0088909; 2010/0047277;
2010/0196419; 2010/0330190; 2011/0097358; 2012/0052082, and U.S. Patent 7,763,450.

Influenza is one of the most important viral diseases in humans, with significant
medical and economic burdens. Vaccination is an effective approach for prevention of
influenza infection. Available seasonal influenza vaccines are trivalent inactivated (killed)
25 virus vaccines (TIV) or live, attenuated, trivalent influenza virus vaccine (LAIV). These
vaccines are targeted to primarily induce neutralizing antibodies directed against the viral
envelope protein HA as well as the NA of strains homologous to the virus used for
vaccination. However, influenza viruses undergo changes in their surface protein over
time, called antigenic drift, allowing them to evade the host immune system and to reduce
30 the effectiveness of immunity to prior infections. Such drifted strains can compromise
vaccine-induced immunity due to antigenic mismatch with the vaccine strain, and the
resulting seroprotection rates can vary according to the antigenic distance between the
vaccine strain and the circulating strain. In addition, unexpected occurrence of shifted

strains (resulting from the replacement of HA and less frequently NA subtypes with novel ones) may cause influenza pandemics. Major limitations of the current vaccines include the need to produce new vaccines every season, uncertainty in choice of the correct strains, long production times as well as the fact that the vaccines are produced by a slow process requiring embryonated eggs. Also, the current vaccines do not protect against future influenza pandemics. Improved vaccines are therefore needed, not only for seasonal influenza, but also for potential new influenza pandemic strains.

Because of these limitations of current vaccines, a universal vaccine that is based on relatively conserved protein domains would be a promising approach. A precondition is the accessibility to antibodies of these domains on infectious virus particles, intact infected cells, or both. The M2 protein of influenza A viruses is a tetrameric type III membrane protein, exhibiting pH-dependent proton transport activity. It is expressed at high density on the plasma membrane of infected cells, and its conserved extracellular domain (M2e) is accessible to M2e-specific antibodies. However, because only a few copies of M2 are incorporated into the envelope of influenza viruses and the small M2e is shielded by the large surface HA and NA from efficient interaction with immune effector cells, M2e is poorly immunogenic although it is highly conserved. Studies have shown that, although M2e-specific antibodies were not able to prevent infection, they restricted subsequent virus replication and reduced illness and deaths. See Treanor et al., *J Virol*, 1990, 64(3):1375-7.

The bacterial flagellar antigen flagellin is the natural ligand of Toll-like receptor (TLR) 5. Also, it can be recognized by an intracellular receptor Ipaf. It can be used as an adjuvant when co-administered with antigen in a physically associated form or mixture. As a protein adjuvant, flagellin can be genetically modified to produce different vaccine formulations. It has known that, in most isolates of *Salmonella*, two genes encode flagellar antigens. *FliC* encodes the phase I flagellin *FliC*, and *fljB* encodes the phase II flagellin *FljB*. These genes are coordinately expressed by a phase-variation mechanism. Both *FliC* and *FljB* share conserved N- and C-termini which form the flagellar filament backbone, and contain motifs recognized by cell surface TLR5 and cytoplasmic Ipaf.

A membrane-anchored form of the *Salmonella Typhimurium* phase I flagellin (*FliC*) can be co-incorporated into influenza VLPs as an adjuvant molecule. See U.S. Patent Application Publication No. 2010/0330190 and Wang et al., *J Virol*, 2008, 82(23):11813-23. The variable central region of *FliC* has been found to be unnecessary for its TLR5 binding activity. See Smith et al., *Nat Immunol*, 2003, 4(12):1247-53. Huleatt

et al. Vaccine 2008; 26(2):201-14 disclose a universal influenza vaccine candidate comprising a recombinant fusion protein linking influenza M2e to the phase II flagellin (FljB). WO/2009/079564 discloses virus-like particles and a membrane-anchored flagellin constructed having repeats of M2e. Wang et al., PLoS One., 2010, 5(11):e13972, disclose
5 that intranasal immunization with influenza VLPs incorporating membrane-anchored flagellin induces strong heterosubtypic protection.

Respiratory syncytial virus (RSV) is the leading cause of lower respiratory tract illness in infants and children worldwide. RSV has 10 genes encoding 11 proteins. The RSV fusion (F) and attachment glycoprotein (G) contain neutralizing antibody epitopes
10 and several T-cell epitopes. See Olson & Varga, Expert Rev Vaccines, 2008; 7:1239–55, Moore et al., J Virol 2009; 83:4185–94, and U.S. Patent Application Publication Number 2011/0097358.

References cited herein are not an admission of prior art.

15

SUMMARY

This disclosure relates to immunogenic compositions and methods of enhancing an immune response to an antigen. In certain embodiments, the disclosure relates to virus-like carrier comprising a TLR5 agonist on the exterior without an antigen. In certain
embodiments, the disclosure relates to methods of vaccinating a subject comprising
20 administering an antigen in combination with a virus-like carrier comprising a TLR5 agonist wherein the virus-like carrier does not contain the antigen under conditions such that antibodies and/or memory B or T cells are produced in a sufficient quantity to prevent near future infection in a healthy human subject, subject over 50, 60, or 65 years of age, or a subject under 4, 8, or 12 years of age. In certain embodiments, the antigen is a viral,
25 bacterial, fungal, or parasite derived molecule.

In certain embodiments, the disclosure relates to methods of immunizing a subject against a virus comprising administering an antigen in combination with a virus-like carrier comprising a TLR5 agonist to the subject. In certain embodiments, the TLR5 agonist is a flagellin in a membrane-anchored form, e.g., is FliC or FliC with the deletion
30 of the variable region. In certain embodiments, the antigen is not a part of the virus-like carrier but administered in combination with the virus-like carrier. In certain embodiments, the antigen is a molecule with repeating units connected by linking groups. In certain embodiments, the antigen comprises an influenza protein such as M2e or a repeating sequence of M2e, e.g., an M2e sequence repeated 2, 3, 4, 5, or 6 or more times.

Typically, the M2e cysteine amino acids, i.e., cysteine amino acid of the protein, are replaced with serine or alanine amino acids.

In certain embodiments, the antigen is an M2e polypeptide comprising SEQ ID NO: 1 or fragment thereof. In certain embodiments, the fragment is four, five, or six or
 5 more contiguous amino acids in SEQ ID NO: 1. In certain embodiments, the antigen comprises the M2e polypeptide SLLTEVETPIRNEWGSRSDSSD (SEQ ID NO: 29), SLLTEVETPIRNEWGSRSDSS (SEQ ID NO: 30), SLLTEVETPIRNEWGSRSDS (SEQ ID NO: 31), SLLTEVETPIRNEWGSRSD (SEQ ID NO: 32), SLLTEVETPIRNEWGSRSN (SEQ ID NO: 33), SLLTEVETPIRNEWGSR (SEQ ID NO: 34), SLLTEVETPIRNEWGSR (SEQ ID NO: 35), SLLTEVETPIRNEWGS (SEQ ID NO: 36), SLLTEVETPIRNEWG (SEQ ID NO: 37), SLLTEVETPIRNEW (SEQ ID NO: 38), SLLTEVETPIRNE (SEQ ID NO: 39), SLLTEVETPIRN (SEQ ID NO: 40), SLLTEVETPIR (SEQ ID NO: 41), SLLTEVETPI (SEQ ID NO: 42), SLLTEVETP (SEQ ID NO: 43), SLLTEVET (SEQ ID NO: 44), SLLTEVE (SEQ ID NO: 45), SLLTEV (SEQ ID NO: 46), SLLTE (SEQ ID NO: 47), SLLT (SEQ ID NO: 48), LLTE (SEQ ID NO: 49), LLTEV (SEQ ID NO: 50), LLTEVE (SEQ ID NO: 51), LLTEVET (SEQ ID NO: 52), LLTEVETP (SEQ ID NO: 53), LLTEVETPI (SEQ ID NO: 54), LLTEVETPIR (SEQ ID NO: 55), LLTEVETPIRN (SEQ ID NO: 56), LTEV (SEQ ID NO: 57), LTEVE (SEQ ID NO: 58), LTEVET (SEQ ID NO: 59), LTEVETP (SEQ ID NO: 60), LTEVETPI (SEQ ID NO: 61), LTEVETPIR (SEQ ID NO: 62), LTEVETPIRN (SEQ ID NO: 63), TEVE (SEQ ID NO: 64), TEVET (SEQ ID NO: 65), TEVETP (SEQ ID NO: 66), TEVETPI (SEQ ID NO: 67), TEVETPIR (SEQ ID NO: 68), TEVETPIRN (SEQ ID NO: 69), EVET (SEQ ID NO: 70), EVETP (SEQ ID NO: 71), EVETPI (SEQ ID NO: 72), EVETPIR (SEQ ID NO: 73), EVETPIRN (SEQ ID NO: 74), VETPI (SEQ ID NO: 75), VETPIR (SEQ ID NO: 76), VETPIRN (SEQ ID NO: 77), ETPI (SEQ ID NO: 78), ETPIR (SEQ ID NO: 79), ETPIRN (SEQ ID NO: 80), or TPIRN (SEQ ID NO: 81).
 10
 15
 20
 25

In certain embodiments, the antigen is a live attenuated virus or killed virus, i.e., inactivated vaccine. In certain embodiments, the flagellin is FliC or FliC wherein the variable region is absent and the virus-like carrier does not contain the antigen, i.e., a
 30 virus-like carrier consisting essential of a flagellin as an adjuvant. In certain embodiments, the disclosure relates to virus-like carries comprising flagellin sequences disclosed herein. In certain embodiments, the antigen and virus-like carrier are administered intra-nasally or intra-muscularly.

In certain embodiments, the disclosure relates to pharmaceutical compositions comprising virus-like carriers comprising a flagellin on the exterior without an antigen for uses disclosed herein. In certain embodiments, the disclosure relates to uses of virus-like carriers disclosed herein in the production of a medicament for the treatment or prevention
5 of a viral infection.

In certain embodiments, the disclosure relates to immunogenic compositions comprising an antigen and/or a virus like carrier comprising a flagellin wherein the virus-like carrier comprising a TLR5 agonist wherein the virus-like carrier does not contain the antigen. The antigen may be a viral protein, such as M2e wherein the M2e cysteine amino
10 acids are replaced with serine amino acids. The antigen is a repeating polypeptide sequence connected by linking groups. The TLR5 agonist may be a flagellin or a flagellin is FliC or FliC wherein the variable region is absent, e.g., polypeptides disclosed herein such as of SEQ ID NO: 28.

In certain embodiments, the disclosure relates to an immunogenic composition
15 comprising a virus-like carrier having an influenza virus matrix protein and a RSV protein or glycoprotein on the surface. In certain embodiments, the influenza virus matrix protein is M1. In certain embodiments, the RSV protein is the F or G protein. In certain embodiments, the immunogenic composition further comprises a virus-like carrier comprising a TLR5 agonist, e.g., flagellin. In certain embodiments, the flagellin is FliC or
20 FliC wherein the variable region is absent. In certain embodiments, the virus-like carrier comprises flagellin and the RSV protein or glycoprotein in the same virus-like carrier. In certain embodiments, the virus-like carrier comprises flagellin and does not contain the RSV protein or glycoprotein. In certain embodiment, the virus-like carrier is a virus-like particle.

In certain embodiments, the disclosure relates to methods of vaccinating a subject
25 comprising administering an virus-like carrier having influenza virus matrix protein and a RSV protein on the surface in combination with a virus-like carrier comprising a TLR5 agonist. Typically the influenza virus matrix protein is M1 and the RSV protein is the F or G protein. Typically, the TLR5 agonist is a flagellin, e.g., FliC or FliC wherein the
30 variable region is absent. In certain embodiments, the virus-like carrier comprising flagellin and the RSV protein or glycoprotein are in the same virus-like carrier. In certain embodiments, the virus-like carrier comprising flagellin does not contain the RSV protein or glycoprotein. Typically, the virus-like carrier is a virus-like particle.

In certain embodiments, the disclosure relates to immunogenic compositions comprising a virus-like carrier having influenza virus matrix protein wherein influenza virus matrix protein is M1 and a RSV protein is G protein or glycoprotein, optionally containing flagellin, on the surface in the absence of the F protein or glycoprotein.

5 An RSV-G virus-like particle produced by infecting insect cells, e.g., Sf9 or Sf21 cells, with a recombinant virus, e.g., rBVs, encoding RSV-G and M1, optionally containing a gene encoding a flagellin, and not the RSV-F gene.

In certain embodiments, the disclosure relates to methods of vaccinating a subject comprising administering an immunogenic composition disclosed herein. In certain
10 embodiments, the subject is a human.

In certain embodiments, the disclosure relates to nucleic acid sequences encoding polypeptides disclosed herein.

BRIEF DESCRIPTION OF THE FIGURES

15 Figure 1 shows the amino acid sequences and schematic diagram of constructs. The M2e sequence shown is the consensus of human influenza A virus M2e. Cysteines at sites 17 and 19 were substituted by serine amino acids. In 4.M2e, four repetitive M2e regions (the underlined sequences) are located in a tandem. Sequences in italics are flexible linkers. In the 4.M2e-tFliC fusion protein, the central immunogenic region of FliC
20 (domain 3, D3, Aa177-401) was replaced by the 4.M2e sequence. In the membrane-anchored 4.M2e-tFliC, the mellitin signal peptide (SP) was fused to the N-terminus of 4.M2e-tFliC (the N-terminal domains 1 and 2, ND1-2, in FliC) to enable its ectodomain to reach the exocytic pathway, and is removed in the mature protein by insect cell signal peptidase. The transmembrane and cytoplasmic domains (TM/CT) of A/PR8 HA were
25 attached to the C-terminus of the 4.M2e-tFliC fusion protein (the C-terminal domains 2 and 1, CD2-1, in FliC).

Figure 2 shows data on the characterization of fusion proteins and M2e VLPs. A. Diagram of M1-derived VLPs. The membrane-anchored form of 4M2e-tFliC fusion protein is inserted into the bilayer lipid of the envelope; B. EM of a VLP; C, D and E.
30 Characterization of VLPs. VLP samples were applied to SDS-PAGE followed by western blotting analysis. Lane1, 4.M2e-tFliC/M1 VLPs; lane 2, FliC/M1 VLPs; lane 3, M1 VLPs. Protein bands were detected by: C, anti-FliC; D, anti-M2e (14C2); E, anti-M1 antibodies; F. TLR5 agonist activity of flagellin in fusion proteins or VLPs. The mouse macrophage cell line RAW264.7 which expresses TLR-2 and -4 without TLR-5 was used to determine

the bioactivity of M2e-flagellin fusion protein or flagellin-containing VLPs. TLR-5 expressing RAW264.7 cells were prepared by transfection with the vector pUNO-hTLR5 expressing the human TLR-5. Data represent means \pm standard errors from triplicate repeats.

5 Figure 3 shows data on serum IgG endpoint titers (A) and M2-specific IgG-binding (B). A. To determine serum IgG titers, ELISA assay plates were coated with 100 μ l /well of synthesized M2e peptide (5 μ g/ml). Immune sera 4 weeks after the last immunization were diluted in 2 \times steps, and 100 μ l diluted samples were applied to plates for antibody-binding. Bound antibodies were detected by binding HRP-goat anti-mouse IgG antibody and color was developed with TMB substrate. The highest dilution which presented an OD450 2 \times higher than that of the negative control (naïve group) was designated as the endpoint titer. Representative data are the geometric mean (GM) \pm 95% confidence interval (CI) of M2e-specific IgG titers of six mice in each group 4 weeks post the last immunization. B. Serum IgG recognizing native M2 protein was determined using cell surface ELISA. MDCK cells were infected with A/PR8 viruses at a MOI of 1. Uninfected cells were used as control. Twelve h postinfection, cells were washed with PBS and fixed with 10% formalin. Diluted samples were applied to detect antibody binding. Data depict the OD450 (mean + SD) of infected cells subtracting the background of uninfected cells. Groups 1 to 4 represent mouse groups immunized with 4.M2e, 4.M2e-tFliC, 4.M2e-tFliC/M1 VLPs, and 4.M2e plus FliC/M1 VLPs, respectively. P<0.05 (*), P<0.01(*), P<0.001(***)

10
15
20

Figure 4 shows data on secretory IgA (A) and IgG (B) endpoint titers in immunized mouse lung lavages. Four weeks after the last immunization, lungs were collected and lavaged twice with 1 ml PBS containing 0.05% Tween 20 per lung. A. sIgA endpoint titers were determined as described for serum IgG endpoint titer in Fig. 3A but the secondary antibody used was HRP-conjugated goat anti-mouse IgA antibody. B. IgG titers were determined as described for serum IgG titers. Representative data are the GM \pm 95% CI of six mice in each group.

25

Figure 5 shows data on A/Philippines (H3N2) live virus challenge. Four weeks after the last immunization, 6 mice of each group were i.n. infected with 5 \times LD₅₀ of mouse-adapted A/Philippines viruses (250 pfu). Mouse survival (A) and body weight changes (B) were monitored and recorded for 15 days to indicate the protective efficacy of vaccines. In B, data represent means of the body-weight change (percentage of pre-challenge) of 6 mice in each group.

30

Figure 6 shows data on A/PR8 (H1N1) virus challenge. Four weeks after the last immunization, mice were i.n. infected with 5×LD50 of mouse-adapted A/PR8 (125 pfu). Mouse survival (A) and body weight changes (B) were monitored and recorded as described in Fig. 5.

5 Figure 7 shows data on lung viral load on day 4 postchallenge. Four weeks after the last immunization, three mice in each group were i.n. infected with 5LD50 of mouse-adapted PR8 (H1N1) or Philippines (H3N2) viruses. Mouse lungs were collected on day 4 postchallenge. Each lung was ground and cleared in 1 ml of DMEM. Virus titers of lung extracts were titrated using a standard plaque assay with MDCK cells. Lung viral titer was
10 expressed as pfu/lung. Data depict the geometric means ± 95% CI of three mice from each group. Groups 1 to 4 represent mouse groups i.m. or i.n. immunized with 4.M2e, 4.M2e-tFliC, 4.M2e-tFliC/M1 VLPs, and 4.M2e plus FliC/M1 VLPs, respectively.

Figure 8 shows data on characterization of virus-like particles (VLPs)- constructs of pFastBac vectors. Respiratory syncytial virus (RSV) fusion F gene (A), attachment
15 glycoprotein G gene (B), and influenza M1 genes (C) are in pFastBac vectors. Genes were amplified by PCR or RT-PCR. Sizes of F, G, and M1 in vectors were confirmed by cutting with EcoRI and XhoI, and the nucleotide sequences were confirmed by DNA sequencing. VLPs containing M1 and RSV F (D) or RSV G (E) were purified from SF9 cell culture supernatants by sucrose gradient ultracentrifugation and visualized by Western blots. The
20 20, 5, and 1 µg VLPs were loaded per lane as indicated (D, E).

Figure 9 shows virus-like particles (VLPs) containing M1 and respiratory syncytial virus (RSV) F (A) or RSV G (C) visualized and their size distribution determined (B, D) after negative staining EM (H-7500, Hitachi). Fifty-five (55%) of RSV F VLPs from 170 particles were distributed between 60 and 100 nm (B), and 66% of RSV-G VLPs from 161
25 particles were distributed between the size 40 and 100 nm (D).

Figure 10 shows an experimental schedule and respiratory syncytial virus (RSV)-A2-specific antibody responses to RSV-F or RSV-G virus-like particles (VLPs). A, Groups of mice were intramuscularly immunized twice as indicated with a 4-week interval. At 4 weeks after boost, mice were challenge infected with RSV-A2 virus, and at
30 day 4 after challenge mouse lungs were collected to determine lung virus loads. Enzyme-linked immunosorbent assay (ELISA) plates were coated with whole RSV virus. Serially diluted sera were used after prime and boost. Total immunoglobulin (Ig) G (B), isotypes IgG2a (C), IgG1 (D) responses, and the ratio of IgG2a to IgG1 (E) to RSV-F VLPs, and

total IgG (F), isotype IgG2a (G), IgG1 (H), and the ratio of IgG2a to IgG1 (I) to RSV-G VLPs were determined from mice immunized with RSV-F VLPs.

Figure 11 shows data on respiratory syncytial virus (RSV) A2-specific immunoglobulin (Ig) G, IgG2a, and IgG1 responses and the ratio of IgG2a to IgG1 in lung
5 extract samples collected at day 4 postchallenge. Serially diluted lung samples were used to determine IgG (A, C), IgG2a, and IgG1 (B, D) responses and the ratio (E) in mice immunized with RSV-F virus-like particles (VLPs) or immunized with RSV-G VLPs.

Figure 12 shows data on immunoglobulin (Ig) G, IgG1, and IgG2a responses against cell surface expressed respiratory syncytial virus (RSV)-A2 proteins. HEp-2 cells
10 in 96 well culture plates were infected with RSV A2 as described in Methods. Serially diluted mouse sera were added into wells. IgG, IgG2a, and IgG1 responses were determined from mice immunized with RSV-F virus-like particles (VLPs) (A, B) or immunized with RSV-G VLPs (D, E). Total IgG responses were also determined by enzyme-linked immunosorbent assay (ELISA) by using HEp-2 cells infected with RSV
15 A2 or uninfected controls. Sera were obtained at week 2 after prime from mice immunized with RSV-F VLPs (C) or RSV-G VLPs (F).

Figure 13 shows data on serum neutralizing activities. Complement inactivated mouse sera were tested for inhibition of respiratory syncytial virus (RSV)-A2 plaque formation. Serially diluted mouse sera at week 3 after boost were complement inactivated
20 and incubated with live RSV-A2. Virus was diluted and used at 750 PFU/well.

Figure 14 shows data on lung virus loads and body weight changes after respiratory syncytial virus (RSV)-A2 challenge. The experiment was repeated twice. A, Lung virus load. Lungs from individual mice in each group (6 mice) were collected on day 4 post-challenge, and lung virus loads (number of plaque-forming units [PFU]) in each
25 mouse were determined. The limit of virus detection is 50 PFU/mL. B, Comparison of lung virus loads between RSV-F and RSV-G virus-like particles (VLPs). The lower scale of the Y axis was used to see differences in lung virus loads between RSV-F and RSV-G VLP immunization. C, Body weight changes. Vaccinated mice (6 mice) were challenged with live RSV-A2 virus. The body weights were monitored daily in which 100% body
30 weight was seen at day 0.

DETAILED DISCUSSION

Influenza

Current influenza vaccines induce neutralizing antibodies against the HA and to a lesser extent to the NA protein, and are protective against closely matched virus strains.

5 However the rapid appearance of mutations allows the virus to evade preexisting anti-influenza immunity. The possibility of adaption of a highly pathogenic avian virus to humans also adds to the risk of the current influenza vaccine strategy.

In certain embodiments, disclosure contemplates uses of a broad protective efficacy of influenza vaccine candidates which include epitopes such as the extracellular domain of the influenza M2 protein (M2e). M2e is conserved in all A type influenza viruses. A systematic approach was used to target M2e for the development of a universal influenza vaccine. Firstly, a fusion protein (4.M2e-tFliC) was generated by replacing the variable region of FliC with multiple M2e peptides (4.M2e). Second, a membrane-anchor was genetically attached from the influenza HA to the 4.M2e-tFliC fusion protein and this membrane-anchored form was incorporated into M1-derived VLPs. VLPs are advantageous as immunogens in inducing strong immune responses because they mimic the structures of viruses which the immune system has evolved to fight.

The HA cytoplasmic domain contains signals guiding the envelope glycoprotein to assemble into M1-derived VLPs. A fusion protein with an HA membrane-anchor can be incorporated into M1-derived VLPs. M2e may to be delivered in a particulate form, and to be presented in its native external-membrane-microenvironment. This enables the use of a particulate form of FliC (FliC VLPs) as adjuvant to enhance the immune responses induced by the multiple M2e peptides. Although the use of tandem repeats increases the density of the target epitopes in a molecule, a possible concern is that the antibody responses induced may not recognize the native M2. Mozdzanowska et al., Vaccine 2003;21(19-20):2616-26, suggest that on average 10% of the total antibody responses induced by multiple M2e repeats cross-reacted with native M2 on virus-infected cell surface. However it has been discovered in the present study that in the right conditions M2e induces a high level of M2-specific immunity and complete protection against lethal doses of live virus challenges.

Because the variable region of FliC is hyperimmunogenic, an advantage of deleting or replacing of the variable region of FliC with M2e repeats avoids possible antibody-mediated neutralization of its TLR5 signaling. The specific innate TLR5

signaling activity of FliC may transform any appropriate foreign B cell determinant into a potentially strong immunogen.

Several different immunization routes have been used to deliver M2e-derived antigens for inducing protective immunity. I.n. immunization was found to be an advantageous

5 approach in inducing protective immunity compared to the other routes. I.n. immunization with 4.M2e-tFliC fusion protein or VLPs induces high systemic immune responses as well as strong mucosal immunity, and confers more effective protection to live virus challenge as demonstrated by the complete protection against PR8 or Philippines challenge, and minimal body weight losses. Also, virus replication is restricted in lungs, as revealed by
10 lower lung virus titers. I.n. immunization stimulates the nasopharyngeal-associated lymphoreticular tissue (NALT), and induces local mucosal immunity. Furthermore, the variable region-truncated flagellin has been found to be more efficient as a mucosal adjuvant as discussed above. These observations provide a basis for the finding that the specific M2e-tFliC fusion protein also contributes to enhanced mucosal immunity.

15 The most surprising discovery is that mice immunized with a mixture of 4.M2e plus FliC VLPs administered i.n. achieved the best immune responses.

Respiratory syncytial virus (RSV)

The protective efficacies of RSV vaccines produced in a viruslike particle form
20 were investigated after intramuscular vaccination in a mouse model. VLP vaccination provides effective protection against RSV infection. RSV-F or RSV-G VLPs elicited significant levels of IgG2a-dominant RSV-specific IgG antibody responses and significantly reduced lung viral replication and weight loss upon challenge.

The VLPs targeted the full-length RSV fusion F protein (RSV-F) and attachment G
25 glycoprotein (RSV-G) which possess neutralizing epitopes as well as several T-cell epitopes. Influenza M1 protein was used rather than RSV matrix (M) as a core protein in VLPs because matrix proteins are important for virion morphology and RSV is more pleomorphic than influenza virus. Also, some paramyxovirus M proteins are insufficient for VLP formation in the absence of NP and envelope glycoprotein co-expression. RSV-F
30 or RSV-G VLPs showed spherical particle shapes. The rBV-produced VLP vaccines from serum-free insect cells have advantages over VLPs produced in mammalian cells because mammalian cell-produced VLPs need to be validated to be free of viruses or oncogenic substances originating from the cells and/or serum.

It has been reported that an RSV VLPs vaccine containing RSV-G protein induces protection in a mouse model. See Murawski et al., J Virol 2010;84:1110-23. In this report, a chimeric protein was used in which the ectodomain was from the RSV G protein, but the cytoplasmic and transmembrane domains and M protein were from Newcastle disease virus (NDV). IgG subtype responses from vaccination with these VLPs were not
5 determined.

The currently disclosed experiments focused on the full length RSV-F or -G proteins in VLPs. The RSV-G VLPs induced better protection than RSV-F VLPs. RSV-F does not require other viral proteins for fusion activity and can undergo pre- to postfusion triggering upon expression. It is not intended that certain embodiments, be limited by any particular mechanism; however, it is possible that some F on the VLP surface may be in a postfusion form, potentially underrepresented on the challenge virus. Alternatively, RSV-F and/or -G may be differentially glycosylated in insect cells used to produce the VLPs, compared with mammalian cells and the underglycosylation of G may enable immune
10 focusing on protectopes (e.g., the central region of G). RSV-F VLPs will provide protection against RSV isolates of A and B subgroups, whereas protection induced by RSV-G VLPs may be more subgroup-specific. In mice and cotton rats, subgroup-heterologous protection is readily achievable with F antigen immunization, and significant but partial subgroup-heterologous protection is typically observed with RSV G antigens.
15 Within antigenic subgroups, RSV can be further classified into clades based on sequence analyses of a hypervariable carboxy-terminus region of RSV G.
20

An ELISA assay was developed to detect IgG, IgG2a, and IgG1 antibodies by using cell surface expressed RSV proteins. Since a correlation of antibody responses with protection was found using cell surface RSV-A2 proteins as binding antigens, detecting
25 antibody using this method may be more reliable and will contribute to RSV vaccine studies. RSV-F and RSV-G VLP vaccines induced very high levels of IgG2a isotype responses with very low levels of IgG1 isotype responses. This is encouraging since enhanced disease after RSV challenge is reported to be related to Th2 (IgG1) allergy-like or Th2-associated responses. It has been reported that F and G protein subunit RSV
30 vaccines were weakly immunogenic and caused enhanced pulmonary histopathology. In contrast, Venezuelan equine encephalitis virus replicon particles (VRPs), as well as RSV G-expressing Newcastle disease VLPs, were more immunogenic, effective, and did not cause enhanced RSV disease. Since RSV proteins in VLPs are presented in a repetitive,

particulate virus-like structure, they may be highly immunogenic and induce protective humoral, cellular, and mucosal immune responses.

This is believed to be the first report demonstrating and comparing protection induced by VLPs containing full-length fusion (F) or attachment (G) glycoproteins. RSV-
5 F or RSV-G VLPs successfully inhibit virus replication in the lung and protected mice from infection. RSV-F or RSV-G VLPs are promising vaccine candidates.

Terms

As used herein, “a flagellin” refers to the monomer subunit in flagella, e.g.,
10 flagellin gene product of FliC and FljB in *S. typhimurium* and FlaA in *L. pneumophila*, or variants, analogs, homologs, derivatives, fragments or combination thereof, such as a domain or polypeptide sequence in the domain. Typically, the flagellin monomer contains D0, D1, D2, and D3 domains. An alignment of the amino acid sequences from different Gram-negative species shows a high degree of similarity in the amino and carboxy
15 terminal domains. The central regions of these proteins may be quite divergent. Smith, K. D., et al, *Nature Immunol.* (2003) 4:1247-1253 disclose that TLR5 recognizes a site on the flagellin of *Salmonella typhimurium* (FliC) composed of N-terminal residues 78-129 and 135-173 and C-terminal residues 395-444. The term “a flagellin” is not intended to be limited to any particular amino acid sequence provided that it has some homology to
20 known flagellin sequences and the molecule retains the ability to stimulate innate immune responses. The innate immune responses of flagellin are known to include cytokine production in response to TLR (including TLR5) activation and activation of Caspase-1 and IL- β secretion in response to certain NLRs (including Ipaf). In certain embodiments, a flagellin is contemplated to include additional amino acids within the sequence, such as
25 in the case of fusion or chimeric proteins, provided that these proteins continue to affect an innate immune response that comprises a TLR5-mediated immune response, an Ipaf-mediated immune response or both. Also specifically contemplated are fragments, variants, analogs, homologs, or derivatives of said flagellin, and combinations thereof provided these molecules continue to affect an innate immune response that comprises a
30 TLR5-mediated immune response, an Ipaf-mediated immune response or both. A flagellin may be isolated from natural sources, by synthetic or recombinant technologies or combinations thereof.

Individual salmonella serotypes usually alternate between the production of two forms of flagellin, termed phase 1 and phase 2, each specified by separate structural genes

FliC and FljB. The amino acid sequences of phase-1 flagella protein of salmonella typhimurium (FliC) is set forth in SEQ ID NO: 12, MAQVINTNSL SLLTQNNLNK SQSALGTAIE RLSSGLRINS AKDDAAGQAI ANRFTANIKG 61 LTQASRNAND GISIAQTTEG ALNEINNNLQ RVRELAVQSA NSTNSQSDLD SIQAEITQRL 121
 5 NEIDRVSGQT QFNGVKVLAQ DNTLTIQVGA NDGETIDIDL KQINSQTLGL DTLNVQKQYK 181 VSDTAATVTG YADTTIALDN STFKASATGL GGTDQKIDGD LKFDDTTGKY YAKVTVTGGT 241 GKDGYYEVSVD KKTNGEVTLA GGATSPLTGG LPATATEDVK NVQVANADLT EAKAALTAAG 301 VTGTASVVKM SYTDNNGKTI DGGLAVKVGD DYYSATQNKD GSISINTTKY
 10 TADDGTSKTA 361 LNKLGADGK TEVVSIGGKT YAASKAEGHN FKAQPDIAEA AATTENPLQ KIDAALAQVD 421 TLRSDLGAVQ NRFNSAITNL GNTVNNLTSR RSRIEDSDYA TEVSNMSRAQ ILQQAGTSVL 481 AQANQVPQNV LSLLR.

The amino acid sequences of phase-2 flagella protein of salmonella typhimurium (FljB) is set forth in SEQ ID NO: 13, MAQVINTNSL SLLTQNNLNK SQSALGTAIE RLSSGLRINS AKDDAAGQAI ANRFTANIKG 61 LTQASRNAND GISIAQTTEG ALNEINNNLQ RVRELAVQSA NSTNSQSDLD SIQAEITQRL 121 NEIDRVSGQT QFNGVKVLAQ DNTLTIQVGA NDGETIDIDL KQINSQTLGL DSLNVQKAYD 181 VKDTAVTTKA YANNGTTLDV SGLDDAAIKA ATGGTNGTAS VTGGAVKFDA
 20 DNNKYFVTIG 241 GFTGADAAKN GDYEVNVATD GTVTLAAGAT KTTMPAGATT KTEVQELKDT PAVVSADAKN 301 ALIAGGVDAT DANGAELVKM SYTDKNGKTI EGGYALKAGD KYAAYDYDEA TGAIKAKTTS 361 YTAADGTTKT AANQLGGVDG KTEVVTIDGK TYNASKAAGH DFKAQPELAE AAKTTENPL 421 QKIDAALAQV DALRSDLGAV QNRFNSAITN
 25 LGNTVNNLSE ARSRIEDSDY ATEVSNMSRA 481 QILQQAGTSV LAQANQVPQN VLSLLR.

The amino acid sequences of F41 fragment of flagellin of salmonella typhimurium is set forth in SEQ ID NO: 14, FTANIKGLTQ ASRNANDGIS IAQTTEGALN EINNLLQRVR ELAVQSANST NSQSDLDISI 61 AEITQRLNEI DRVSGQTQFN
 30 GVKVLAQDNT LTIQVGANDG ETIDIDLKQI NSQTLGLDTL 121 NVQKQYKQVSD TAATVTGYAD TTIALDNSTF KASATGLGGT DQKIDGDLKF DDTTGKYYAK 181 VTVTGGTGKD GYYEVSVDKT NGEVTLAGGA TSPLTGGLPA TATEDVKNVQ VANADLTEAK 241 AALTAAGVTG TASVVKMSYT DNNGKTIDGG LAVKVGDDYY SATQNKDGTI SINTTKYTAD 301 DGTSKALNK LGGADGKTEV

VSIGGKTYAA SKAEGHNFKA QPDLAEEAAAT TTENPLQKID 361 AALAQVDTLR
SDLAAVQNRFS NSAITNLGNT VNNLTSAR.

The amino acid sequences of a flagellin fusion protein is set forth in SEQ ID
NO:15, MALTVNTNIA SLNTQRNLNN SSASLNTSLQ RLSTGSRINS

5 AKDDAAGLQI ANRLTSQVNG 61 LNVATKNAND GISLAQTAEG ALQQSTNILQ
RMRDLSLQSA NGSNSDSERT ALNGEVKQLQ 121 KELDRISNTT TFGGRKLLDG
SFGVASFQVG SAANEIISVG IGGGKLMIKL KFGVFFTVLL 181 SSAYAHGTPQ
NITDLCAEYH NTQIHTLNDK IFSYTESLAG KREMAITFK NGATFQVEVP 241
GSQHIDSQKK AIERMKDTLR IAYLTEAKVE KLCVWNNKTP HAIAAISMAN.

10 Polypeptide fragments of flagellin include SEQ ID NO: 16, GALNEINNNL
QVRRELAVQ SANSTNSQS DLDSIQAE ITQ; SEQ ID NO: 17,
TQFSGVKVLAQDNTLTIQVGANDGET IDIDLKQINS QTLGLDTL; SEQ ID NO: 18,
EGALNEINN NLQRVRELA VQSANSTNS QSDLDSIQAEITQRLNEIDRVNG; SEQ
ID NO: 19, MAQVINTNSL SLLTQNNLNK QSALGTAI

15 ERLSSGLRINSAKDDAAGQAIANF TANIKGLTQA SRNANDGISI AQTTEGALN
EINNNLQRVRELAVQS; SEQ ID NO: 20,
LQKIDAALAQVDTLRSDLGAVQNRFNNSAITNL; SEQ ID NO: 21,
TLRSDLGAVQNRFNNSAITNLGNTVNNLSS; and SEQ ID NO: 22, EQAAKTEN
PLQKIDAALAQVDTLRSDLGAVQNRFNNSAITNLGNTVNNLSS.

20 Combination of fragments of flagellin include SEQ ID NO: 23, Met Arg Gly Ser
His His His His His His Gly Met Ala Ser Met Thr1 Gly Gln Gln Met Gly Arg Asp Leu
Tyr Asp Asp Asp Asp Lys Asp Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu
Leu Thr Gln Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg Leu Ser
Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln Ala Ile Ala Asn Arg Phe
25 Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala
Gln Thr Thr Glu Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Thr Gln Phe Asn Gly Val Lys Val
Leu Ser Gln Asp Asn Gln Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile
30 Asp Leu Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val Asn Ser Pro Gly
Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala
Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp
Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu Gly
Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu Asp Ala Asp Tyr Ala Thr Glu

Val Ser Asn Met Ser Lys Ala Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala
 Asn Gln Val Pro Gln Asn Val Leu Ser Leu Leu Arg. This protein is also known as
 CBLB502 (AA') as provided for in U.S. Published Patent Application No. 2009/0011982,
 hereby incorporated by reference. CBLB502 is currently under clinical investigation to
 5 treat Acute Radiation Syndrome (ARS).

As used herein, an "RSV G" protein, or like terms refers to attachment an RSV
 glycoprotein G and all known variants or substantial fragments thereof. One example is
 MSKNKDQRTA KTLERTWDTL NHLLFISSCL YKLNLSVAQ ITLSILAMII
 STSLIIAAII 61 FIASANHKVT PTTAIIQDAT SSIKNTTPTY LTQNPQLGIS
 10 PSNPSEITSQ ITTILASTTP 121 GVKSTLQSTT VKTKNTTTTQ TQPSKPTTKQ
 RQNKPPSKPN NDFHFEVFNF VPCSICSNNP 181 TCWAICKRIP NKKPGKKTTP
 KPTTKPTLKT TKKDPKPQTT KSKEVPTTKP TEEPTINTTK 241 TNIITLLTS
 NTTGNPELTS QMETFHSTSS EGNPSPSQVS TTSEYPSQPS SPPNTPRQ (SEQ ID
 NO: 88). Other examples include those designated by Accession numbers P03423.1,
 15 P27022.1, CAA51765.1, AAD02944.1, CAA83874.1, AAD02941.1, CAA83870.1,
 P27021.1, AEO45938.1, CAA51761.1, CAA83871.1, AAU43727.1, AEO45918.1,
 AEO45888.1, AEO45878.1, AEO45849.1, AEC32086.1, AEQ98767.1, AEQ63333.1,
 CAA83875.1, AEO45908.1, AEO45948.1, AEO45898.1, AEO45928.1, AAC36327.1,
 ACO83296.1, AEO45829.1, AEQ66845.1, ACI03570.1, AEO45868.1, P20895.2,
 20 AAD02943.1, AAX23993.1, AEQ66853.1, AEO45839.1, AEJ87998.1, and AEJ88006.1.
 The term "RSV G" is not intended to be limited to any particular amino acid sequence
 provided that it has substantial homology to a known RSV G sequences. Alternative
 glycosylations are contemplated. In certain embodiments, a known RSV G sequence has
 2, 3, 4, 5, 6, 7, 8, or 9 amino acid substitutions or 2, 3, 4, 5, 6, 7, 8, or 9 amino acids have
 25 been deleted on the N or C terminal end of the polypeptide. In certain embodiments, a
 RSV G is contemplated to include additional amino acids within the sequence, such as in
 the case of fusion or chimeric proteins. In certain embodiments, variants may contain
 conserved amino acid substitutions or derivatives with common chemical groups such as
 protecting groups or halogens. In certain embodiments, the fragments are between 250 to
 30 200, 200 to 150, 150 to 100, 100 to 50, or 25 amino acids.

As used herein, the term "adjuvant molecule" includes bacterial surface proteins
 capable of eliciting an immune response in a host. In particular the term includes bacterial
 surface proteins capable of targeting a host Toll-like receptor (TLR) protein, such as, but
 not limited to, a bacterial flagellin protein that targets a host TLR5 protein. In particular

embodiments, the adjuvant molecule is a "membrane-anchored form" of the adjuvant molecule which indicates that the adjuvant molecule has been engineered to include a signal peptide (SP) and a membrane anchor sequence to direct the transport and membrane orientation of the protein. Thus, in embodiments, a membrane-anchored form of an adjuvant molecule is a recombinant protein including a portion of the bacterial protein (such as bacterial flagellin) fused to a SP and membrane anchor sequence.

The term "virus-like carrier" as used herein refers to a virus-like particle, a virosome, or both.

The term "virus-like particle" (VLPs) as used herein refers to a membrane-surrounded viral core structure having viral envelope proteins. In addition, adjuvant molecules can be expressed on the VLP. Further, viral core proteins are located within the membrane of the VLP. Additional components of VLPs, as known in the art, can be included within or disposed on the VLP. VLPs typically do not contain intact viral nucleic acids, and they are non-infectious.

The term "virosome" as used herein refers to a virus-like carrier that is similar to a virus-like particle, except that a virosome does not contain a viral core protein

A "truncated" viral surface envelope glycoprotein is one having less than a full length protein (e.g., a portion of the cytoplasmic domain has been removed), which retains surface antigenic determinants against which an immune response is generated, preferably a protective immune response, and it retains sufficient envelope sequence for proper membrane insertion. The skilled artisan can produce truncated virus envelope proteins using recombinant DNA technology and virus coding sequences, which are readily available to the public.

The terms "proteins," "peptides," and "polypeptides" refer to the molecules created by coupling with amino acid residues, i.e., amino acid sequences. Those sequences are written left to right in the direction from the amino to the carboxy terminus. In accordance with standard nomenclature, amino acid residue sequences are denominated by either a three letter or a single letter code as indicated as follows: Alanine (Ala, A), Arginine (Arg, R), Asparagine (Asn, N), Aspartic Acid (Asp, D), Cysteine (Cys, C), Glutamine (Gln, Q), Glutamic Acid (Glu, E), Glycine (Gly, G), Histidine (His, H), Isoleucine (Ile, I), Leucine (Leu, L), Lysine (Lys, K), Methionine (Met, M), Phenylalanine (Phe, F), Proline (Pro, P), Serine (Ser, S), Threonine (Thr, T), Tryptophan (Trp, W), Tyrosine (Tyr, Y), and Valine (Val, V).

"Variant" refers to a polypeptide or polynucleotide that differs from a reference polypeptide or polynucleotide, but retains essential properties. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide.

Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall (homologous) and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more modifications (e.g., substitutions, additions, and/or deletions). A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polypeptide may be naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally

Modifications and changes can be made in the structure of the polypeptides of this disclosure and still result in a molecule having similar characteristics as the polypeptide (e.g., a conservative amino acid substitution). For example, certain amino acids can be substituted for other amino acids in a sequence without appreciable loss of activity. Because it is the interactive capacity and nature of a polypeptide that defines that polypeptide's biological functional activity, certain amino acid sequence substitutions can be made in a polypeptide sequence and nevertheless obtain a polypeptide with like properties.

In making such changes, the hydrophobic index of amino acids can be considered. The importance of the hydrophobic amino acid index in conferring interactive biological function on a polypeptide is generally understood in the art. It is known that certain amino acids can be substituted for other amino acids having a similar hydrophobic index or score and still result in a polypeptide with similar biological activity. Each amino acid has been assigned a hydrophobic index on the basis of its hydrophobicity and charge characteristics. Those indices are isoleucine (+4.5), valine (+4.2), leucine (+3.8), phenylalanine (+2.8) cysteine/cysteine (+2.5) methionine (+1.9), alanine (+1.8), glycine (-0.4), threonine (-0.7), serine (-0.8), tryptophan (-0.9), tyrosine (-1.3), proline (-1.6), histidine (-3.2), glutamate (-3.5), glutamine (-3.5), aspartate (-3.5) asparagine (-3.5), lysine (-3.9), and arginine (-4.5).

It is believed that the relative hydrophobic character of the amino acid determines the secondary structure of the resultant polypeptide, which in turn defines the interaction of the polypeptide with other molecules, such as enzymes substrates, receptors, antibodies, antigens, and the like. It is known in the art that an amino acid can be substituted by another amino acid having a similar hydrophobic index and still obtain a functionally equivalent polypeptide. In such changes, the substitution of amino acids whose

hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred

Substitution of like amino acids can also be made on the basis of hydrophilicity, particularly where the biologically functional equivalent polypeptide or peptide thereby
5 created is intended for use in immunological embodiments. The following hydrophilicity values have been assigned to amino acid residues arginine (+3.0), lysine (+3.0), aspartate (+3.0), glutamate (+3.0), serine (+0.3), asparagine (+0.2), glutamine (+0.2), glycine (0), proline (-0.5), threonine (-0.4), 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),
10 and tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent polypeptide. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

15 As outlined above, amino acid substitutions are generally based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take one or more of the foregoing characteristics into consideration are well known to those of skill in the art and include, but are not limited to (original residue: exemplary substitution): (Ala: Gly, Ser), (Arg: Lys), (Asn: Gln, His), (Asp: Glu, Cys, Ser), (Gln: Asn), (Glu: Asp), (Gly: Ala), (His: Asn, Gln), (Ile: Leu, Val), (Leu: Ile, Val), (Lys: Arg), (Met: Leu, Tyr), (Ser: Thr), (Thr: Ser), (Tyr: Trp, Phe), and (Val: Ile, Leu). Embodiments of this disclosure thus contemplate functional or biological equivalents of a polypeptide as set forth above. In particular, embodiments of the polypeptides can include variants having
20 about 50%, 60%, 70%, 80%, 90%, and 95% sequence identity to the polypeptide of interest. The term "substantially homologous" is used herein to denote polypeptides of the present disclosure having about 50%, about 60%, about 70%, about 80%, about 90%, and preferably about 95% sequence identity to the reference sequence. Percent sequence identity is determined by conventional methods as discussed above. In general,
25 homologous polypeptides of the present disclosure are characterized as having one or
30 more amino acid substitutions, deletions, and/or additions.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences, as determined by comparing the sequences. In the art, "identity" also refers to the degree of sequence relatedness between polypeptides as determined by the match

between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including, but not limited to, those described in Computational Molecular Biology, Lesk, A. M., Ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., Ed., Academic Press, New York, 1993; 5 Computer Analysis of Sequence Data, Part I1 Griffin, A. M., and Griffin, H. G., Eds., Humana Press, New Jersey, 1994, Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., Eds., M Stockton Press, New York, 1991 ; and Carillo, H., and Lipman, D., SIAM J Applied Math., 48. 1073, (1988). Preferred methods to determine identity are designed to 10 give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. The percent identity between two sequences can be determined by using analysis software (Sequence Analysis Software Package of the Genetics Computer Group, Madison, Wis) that incorporates the Needleman & Wunsch (J MoI Biol , 48 443-453, 1970) algorithm (e.g. , NBLAST and 15 XBLAST). The default parameters are used to determine the identity for the polypeptides of the present disclosure. By way of example, a polypeptide sequence may be identical to the reference sequence, that is be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the % identity is less than 100%. Such alterations are selected from at least one amino acid 20 deletion, substitution (including conservative and non-conservative substitution), or insertion, and wherein said alterations may occur at the amino- or carboxy-terminus positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence, or in one or more contiguous groups within the reference sequence. The 25 number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in the reference polypeptide by the numerical percent of the respective percent identity (divided by 100) and then subtracting that product from said total number of amino acids in the reference polypeptide.

Conservative amino acid variants can also comprise non-naturally occurring amino 30 acid residues Non-naturally occurring amino acids include, without limitation, trans-3-methylproline, 2,4-methanoproline, cis-4-hydroxyproline, trans-4-hydroxyproline, N-methyl-glycine, allo-threonine, methylthreonine, hydroxy-ethylcysteine, hydroxyethylhomocysteine, nitro-glutamine, homoglutamine, pipecolic acid, thiazolidine carboxylic acid, dehydroprohne, 3- and 4-methylproline, 3,3-dimethylproline, tert-leucine,

norvaline, 2-azaphenyl-alanine, 3- azaphenylalanine, 4-azaphenylalanine, and 4-fluorophenylalanine. Several methods are known in the art for incorporating non-naturally occurring amino acid residues into proteins. For example, an in vitro system can be employed wherein nonsense mutations are suppressed using chemically aminoacylated suppressor tRNAs. Methods for synthesizing amino acids and aminoacylating tRNA are known in the art. Transcription and translation of plasmids containing nonsense mutations is carried out in a cell-free system comprising an E coli S30 extract and commercially available enzymes and other reagents. Proteins are purified by chromatography (Robertson, et al , J Am Chem Soc , 113 2722, 1991 , Ellman, et al , Methods Enzymol , 10 202 301 , 1991 , Chung, et al , Science, 259 806-9, 1993, and Chung, et al , Proc Natl Acad Sci USA, 90 10145-9, 1993). In a second method, translation is carried out in *Xenopus* oocytes by microinjection of mutated mRNA and chemically aminoacylated suppressor tRNAs (Turcatti, et al , J Biol Chem , 271 19991-8, 1996). Within a third method, E coli cells are cultured in the absence of a natural amino acid that is to be replaced (e g , phenylalanine) and in the presence of the desired non-naturally occurring amino acid(s) (e g , 2-azaphenylalanine 3-azaphenylalanine, 4- azaphenylalanine, or 4-fluorophenylalanine). The non-naturally occurring amino acid is incorporated into the protein in place of its natural counterpart (Koide, et al , Biochem , 33 7470-6, 1994). Naturally occurring amino acid residues can be converted to non-naturally occurring species by in vitro chemical modification. Chemical modification can be combined with site-directed mutagenesis to further expand the range of substitutions (Wynn, et al , Protein Sci , 2 395-403, 1993).

Furthermore, unless the context demands otherwise, the term peptide, polypeptide and protein are used interchangeably to refer to amino acids in which the amino acid residues are linked by covalent peptide bonds or alternatively (where post-translational processing has removed an internal segment) by covalent disulphide bonds, etc. The amino acid chains can be of any length and comprise at least two amino acids, they can include domains of proteins or full-length proteins. Unless otherwise stated the terms peptide, polypeptide, and protein also encompass various modified forms thereof, including but not limited to glycosylated forms, phosphorylated forms, etc.

By "administration" is meant introducing a composition (e g , a vaccine, adjuvant, or immunogenic composition) of the present disclosure into a subject. Any route of administration, such as oral, topical, subcutaneous, peritoneal, intra-arterial, inhalation,

vaginal rectal, nasal, introduction into the cerebrospinal fluid, or instillation into body compartments can be used.

"Immunogenic compositions" are those which result in specific antibody production or in cellular immunity when injected into a subject. Such immunogenic
5 compositions or vaccines are useful, for example, in immunizing against infection and/or damage caused by viruses.

By "immunogenic amount" is meant an amount capable of eliciting the production of antibodies directed against the virus, in the host to which the vaccine has been administered. It is preferred that the route of administration and the immunogenic
10 composition is designed to optimize the immune response on mucosal surfaces for example, using nasal administration (via an aerosol) of the immunogenic composition.

The term "pharmaceutically" or "pharmaceutically acceptable" as used herein refer to molecular entities and compositions that do not produce an adverse, allergic or other untoward reaction when administered to an animal, or a human, as appropriate.

15 The term "pharmaceutically acceptable carrier" as used herein refers to any carrier, excipient, diluents, adjuvants, or vehicles, such as preserving or antioxidant agents, fillers, disintegrating agents, wetting agents, emulsifying agents, suspending agents, solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active
20 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 as suitable therapeutic combinations. The term "subject" as used herein includes humans, mammals (e.g., cats, dogs, horses, etc.), and livestock. Typical subject
25 to which embodiments of the present disclosure may be administered will be mammals, particularly primates, especially humans. For veterinary applications, a wide variety of subjects will be suitable, e.g., livestock such as cattle, sheep, goats, cows, swine, and the like, poultry such as chickens, ducks, geese, turkeys and the like, and domesticated animals particularly pets such as dogs and cats.

30 The term "treat", "treating", and "treatment" are an approach for obtaining beneficial or desired clinical results. For purposes of embodiments of this disclosure, beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease, stabilization (e.g., not worsening) of disease, preventing spread of disease, delaying or slowing of disease progression,

amelioration or palliation of the disease state, and remission (partial or total) whether detectable or undetectable. In addition, "treat," "treating," and "treatment" can also mean prolonging survival as compared to expected survival if not receiving treatment.

5

EXPERIMENTAL

Cell lines and viruses

Spodoptera frugiperda sf9 cells were maintained as described in Wang et al., J Virol, 2008, 82(23):11813-23 hereby incorporated by reference. Madin-Darby canine kidney (MDCK, ATCC number PTA-6500) cells were cultured in Dulbecco's minimal essential medium (DMEM, Cellgro) plus 10% fetal bovine serum (FBS). Mouse-adapted influenza A/PR/8/34 (H1N1) and A/Philippines/2/82/X-79 (H3N2) viruses were prepared as described in Quan et al., J Virol 2007;81(7):3514-24, hereby incorporated by reference. The LD50 (lethal dose inducing 50% mortality) of these strains was determined by infection of mice with serial virus dilutions. RAW264.7 (ATCC number TIB-71) cells were cultured in DMEM plus 10% FBS.

15

Construction of a membrane-anchored flagellin gene

A full-length membrane-anchored flagellin encoding gene was generated by fusing encoding sequences of a signal peptide (SP) from honeybee mellitin Mellitin MKFLVNVALVFMVVYISYIY ADPINMTGS (SEQ ID NO:26) and the transmembrane (TM) and cytoplasmic tail (CT) regions from the influenza A virus PR8 hemagglutinin (HA) to the 5' and 3' termini of the flagellin gene in frame, respectively. Influenza virus HA TM is DWILWISFAISCFLLCVALLGFIMWAC (SEQ ID NO:24) and the CT is QKGNIRCNICI (SEQ ID NO:25). The substitution of the HIV Env signal peptide (SP) with that from honeybee mellitin was shown to promote higher-level expression and secretion of HIV-1 gp120 in insect cells. Substitution of the HIV TM-CT with sequences derived from the mouse mammary tumor virus (MMTV) envelope glycoprotein, influenza virus hemagglutinin, or baculovirus (BV) gp64 was found to enhance Env incorporation into VLPs.

25

The mellitin SP-encoding fragment was PCR amplified from the plasmid M-TM.CT_{MMTV} as described in Wang et al., J. Virol., 2007, 81:10869-10878, hereby incorporated by reference, by use of primers 5'-GGTTCTAGAATGAAATTCTTAGTC-3'(SEQ ID NO:2) and 5'-GTGGGATCCTTTCATGTTGATCGG-3' (SEQ ID NO:3) (XbaI and BamHI sites) and cloned into cloning vector pBluescript (-) with XbaI/BamHI

30

sites, resulting in plasmid pBluescript-SP. The *Salmonella enterica* serovar Typhimurium flagellin gene (fliC; GenBank accession no. D13689) was amplified from plasmid pEM045 pEF6 FliC stop (a kind gift from Alan Aderem, Institute of Systems Biology, Seattle, WA) by using primers 5'-GCAGGATCCATGGCACAAGTCAT-3' (SEQ ID NO:4) and 5'-CGCGAATTCACGCAGTAAAGAGAG-3' (SEQ ID NO:5) and inserted into pBluescript-SP, resulting in pBluescript-SP-FliC. HA TM-CT was amplified from plasmid pc/pS1 containing the full-length HA gene by using primers 5'-GCTAGAATTCCAGATTCTGGCGATC-3' (SEQ ID NO:6) and 5'-GCTAGGGCCCTTATCAGATGCATATTCT-3' (SEQ ID NO:7) and cloned into pBluescript-SP-FliC to produce pBluescript-SP-FliC-HA tail. The full-length membrane-anchored flagellin gene was amplified from pBluescript-SP-FliC-HA tail by using primers 5'-GCTCGTCGACATGAAATTCTTAG-3' (SEQ ID NO:8) and 5'-GCTACTCGAGTTATCAGATGCATATTC-3' (SEQ ID NO:9) and cloned into pFastBac 1 under the control of the polyhedrin promoter. The sequence of the membrane-anchored flagellin gene was verified by DNA sequencing.

Construction of genes encoding 4 repeats of M2e (4.M2e) and fusion proteins containing 4.M2e

Four DNA fragments encoding individual repeats of a consensus M2e (SLLTEVETPIRNEWGSRSDSSDP) (SEQ ID NO: 1) and flexible linker sequences (AAASLLTEVETPIRNEWGSRSDSSDPAAGTSAASLLTEVETPIRNEWGSRSDSDPAAALQAAASLLTEVETPIRNEWGSRSDSSDPAACAAASLLTEVETPIRNEWGSRSDSDPAAAACKL) (SEQ ID NO: 11) were produced by primer-extension PCR, and ligated together to generate the gene encoding 4.M2e. M2e contains two cysteine residues SLLTEVETPIRNEWGC RC NDSSDP (SEQ ID NO: 10) at sites 17 and 19. Since these cysteines could result in formation of intramolecular disulfide bonds and aggregation of particles under oxidative conditions, the two cysteine residues in M2e were replaced by two serine residues. To generate genes encoding fusion protein in which the variable region of FliC is replaced by 4.M2e, the DNA fragment encoding the variable region (AA 177-401 in FliC) was deleted from FliC gene (fliC, GenBank accession no. D13689, a gift from Dr. Alan Aderem), and replaced by the 4.M2e coding sequence by overlapping PCR. An N-terminal mellitin signal peptide (SP) and a C-terminal histidine (His) tag encoding sequences were added to the above fusion constructs in frame for protein production and purification. In addition, a membrane-anchored form of the 4.M2e-

FliC construct was generated by adding the influenza HA (A/PR8) membrane-anchor coding sequence to the 4.M2e-FliC encoding gene in frame at the C-terminus as disclosed in Wang et al., J Virol, 2008, 82(23):11813-23 hereby incorporated by reference. The integrity of constructs was confirmed by DNA sequencing.

5 DNA sequence of the truncated flagellin with an HA transmembrane/cytoplasmic domains. TGAAATTCTTAGTCAACGTTGCCCTTGTTTTATGGTCGTGTACATTT
 CTTACATCTATGCGGACCCGATCAACATGACCGGATCCATGGCACAAGTCATT
 AATACAAACAGCCTGTGCTGTTGACCCAGAATAACCTGAACAAATCCCAGTC
 CGCTCTGGGCACCGCTATCGAGCGTCTGTCTTCCGGTCTGCGTATCAACAGCG
 10 CGAAAGACGATGCGGCAGGTCAGGCGATTGCTAACCGTTTTACCGCGAACATC
 AAAGGTCTGACTCAGGCTTCCCGTAACGCTAACGACGGTATCTCCATTGCGCA
 GACCACTGAAGGCGCGCTGAACGAAATCAACAACAACCTGCAGCGTGTGCGT
 GAACTGGCGGTTTCAGTCTGCTAACAGCACCAACTCCCAGTCTGACCTCGACTC
 CATCCAGGCTGAAATCACCCAGCGCCTGAACGAAATCGACCGTGTATCCGGCC
 15 AGACTCAGTTCAACGGCGTGAAAGTCCTGGCGCAGGACAACACCCTGACCAT
 CCAGGTTGGTGCCAACGACGGTGAAACTATCGATATCGATCTGAAGCAGATCA
 ACTCTCAGACCCTGGGTCTGGATACGCTGAATGTGGGCGCGCCGGTCTACCCG
 TATGACGTGCCGGACTACGCGTCGCCATGGACAACCACCGAAAACCCGCTGC
 AGAAAATTGATGCTGCTTTGGCACAGGTTGACACGTTACGTTCTGACCTGGGT
 20 GCGGTACAGAACCGTTTTCAACTCCGCTATTACCAACCTGGGCAACACCGTAAA
 CAACCTGACTTCTGCCCGTAGCCGTATCGAAGATTCCGACTACGCGACCGAAG
 TTTCCAACATGTCTCGCGCGCAGATTCTGCAGCAGGCCGGTACCTCCGTTCTG
 GCGCAGGCGAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTGAATTCCG
 AGTGAAATTGGAATCAATGGGGATCTATCAGATTCTGGCGATCTACTCAACTG
 25 TCGCCAGTTCACTGGTGCTTTTGGTCTCCCTGGGGGCAATCAGTTTCTGGATGT
 GTTCTAATGGATCTTTGCAGTGCAGAATATGCATCTGATAA (SEQ ID NO: 27)

Protein sequence of the truncated flagellin with the HA transmembrane/
 cytoplasmic domains.

MKFLVNVALVFMVVYISYIYADPINMTGSMAQVINTNSLSLLTQNNLNKS
 30 QSALGTAIERLSSGLRINSKDDAAGQAIANRFTANIKGLTQASRNANDGISIAQTT
 EGALNEINNNLQRVRELAVQSANSTNSQSDLSIQAEITQRLNEIDRVSGQTQFNG
 VKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVGAPVYPYDVPDYAS
 PWTTTENPLQKIDAALAQVDTLRSDLGAVQNRFNSAITNLGNTVNNLTSARSRIE

DSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLREFGVKLESMGIYQIL
AIYSTVASSLVLLVSLGAISFWMCNSGLQCRICI (SEQ ID NO: 28)

Protein purification

5 The above genes were cloned into the transfer vector pFastBac-1 (Invitrogen) and used for generating recombinant baculoviruses (rBVs) using the Bac-to-Bac insect cell protein expression system (Invitrogen) according to the manufacturer's instructions. His-tagged 4.M2e and 4.M2e-tFliC were purified using nickel affinity chromatography (Qiagen) by following the manufacturer's instructions. Sf9 cell cultures that were infected
10 with rBVs expressing the above proteins were cleared by centrifugation (8000 rpm, 20 min). Proteins were purified from supernatants, dialyzed against PBS and stored at -80 °C.

Flagellin VLP production

 A recombinant BV expressing the membrane-anchored 4.M2e-tFliC was generated
15 as described above. Recombinant BVs expressing membrane-anchored FliC and M1 were described in Wang et al., J Virol, 2008, 82(23):11813-23, hereby incorporated by reference. The 4.M2e-FliC VLPs were produced by co-infection of sf9 cells with rBVs expressing the membrane-anchored 4.M2e-FliC and M1 at multiplicities of infection (MOIs) 6 and 3 respectively. The M2e content in 4.M2e-tFliC VLPs was 1.5% when
20 normalized by western blot using purified 4.M2e as a standard. FliC VLPs were produced by co-infection of sf9 cells with rBVs expressing FliC and M1 with MOIs 6 and 3. VLPs were concentrated from the supernatants of Sf9 cell culture 60 h post-infection by porous fiber filtration using the Quixstand Benchtop system (GE Healthcare, Uppsala, Sweden) followed by sucrose density gradient ultracentrifugation. VLPs were characterized by
25 protein assay, Western blot, sterility assay and electron microscopy (EM). VLPs were negatively stained for EM observation.

TLR-5-specific bioactivity assay

 The TLR5 binding activity of the above fusion protein and VLPs containing FliC
30 were evaluated using a RAW264.7 cell-based assay. Soluble FliC was used as a positive control. VLPs containing M1 only were used as a negative control. All proteins or VLPs were diluted from 10 µg/ml to 0.001 ng/ml in 10-fold steps with DMEM medium containing 10% FBS. Cell cultures were treated with these diluted protein or VLP solutions. After 24 h treatment, cell culture supernatants were collected. Levels of tumor

necrosis factor alpha (TNF- α) production stimulated by the above fusion protein of VLPs in both TLR5-positive and -negative cell cultures were determined by ELISA using a TNF- α assay kit (eBioscience, San Diego, CA) according to the manufacturer's instruction. TLR5 bioactivity was presented as the level of TNF- α production in TLR5
5 positive cells subtracting that in TLR5 negative cells.

Immunization and challenge

Groups of six inbred female BALB/c mice (from Charles River Laboratory) were immunized three times with fusion proteins or M2e VLPs at defined doses as shown in
10 Table 1 by the intramuscular (i.m.) or intranasal (i.n.) routes at 4-week intervals. Serum samples were collected at one week before prime immunization as preimmune sera. Immune sera and lung lavage samples were collected at 4 weeks after the last immunization. Blood samples were collected by retro-orbital plexus puncture. For virus challenge, mice were lightly anesthetized by inhalation of isoflurane, and 5 LD₅₀ of
15 mouse-adapted PR8 or Philippines viruses in a volume of 25 μ l PBS were administered into mouse nostrils. Mouse body weight and survival were monitored daily for 15 days. Groups of infected mice were sacrificed at day 4 postinfection to determine lung virus loads. Lung virus titers were determined.

20 Antibody responses

Serum M2e-specific IgG endpoint titers were determined by ELISA. 96-well ELISA plates (Nunc Life Technologies) were coated with 100 μ l M2e peptide (17 amino acids, 2 to 18, SLLTEVETPIRNEWGCR (SEQ ID NO: 89), synthesized at the Emory University Biochemical Core Facility) in carbonate buffer (pH 9.4, 5 μ g/ml) at 4 °C
25 overnight. The serum samples were serially diluted in twofold steps. The highest dilution which gave an OD₄₅₀ twice that of the naïve group without dilution was designated as the antibody endpoint titer. Serum M2-specific antibody levels were determined using cell surface ELISA. MDCK cells in 96-well culture plates were grown near to 90% confluency and then infected with PR8 virus at a MOI of 1 (5×10^4 pfu). After 12 h growth, the plates
30 were washed and the cells were fixed with 0.5% glutaraldehyde at 4°C for 30 min. After three washes with PBS, serial dilutions of test sera were added to the wells and incubated for 2 h in room temperature. Antibody binding to non-infected MDCK cells was

subtracted as a background. M2-specific antibody levels were presented as the value of OD₄₅₀.

For the determination of mucosal antibody levels, lung lavages of immunized mice were evaluated for IgA and IgG endpoint titers as described above for serum IgG using HRP-
5 conjugated rabbit anti-mouse IgA as the secondary antibody.

Purification of fusion proteins and production of VLPs

M2e in repetitive forms is immunogenic. A fusion protein of 4.M2e attached to the C-terminal of the typhimurium phase II flagellin fljB was found to be quantitatively
10 and qualitatively superior to M2e in inducing anti-M2 immunity. Huleatt et al., Potent immunogenicity and efficacy of a universal influenza vaccine candidate comprising a recombinant fusion protein linking influenza M2e to the TLR5 ligand flagellin. Vaccine 2008;26(2):201-14. A DNA fragment was generated encoding a consensus M2e peptide (upper panel in Fig. 1). A histidine (His)-tagged fusion protein 4.M2e-tFliC (lower panel
15 in Fig. 1) was also constructed in which the variable region of the FliC was replaced by 4.M2e, and the fusion protein was produced from sf9 cell cultures in a BV-based protein expression system. A his-tagged 4.M2e was also constructed and purified as a control.

To further improve the immunogenicity of M2e, membrane-anchored fusion protein 4.M2e-tFliC gene (lower panel Fig. 1), was constructed and incorporated into
20 influenza M1-derived VLPs as schematized in Fig. 2A. The integrity of VLPs was confirmed by electron microscopy (Fig. 2B). The incorporation of the membrane-anchored 4.M2e-tFliC in VLPs was confirmed by western blotting assays using either anti-FliC antibody (lane 1 in Fig. 2C) or anti-M2e antibody (14C2, lane 1 in Fig. 2D). FliC/M1 VLPs were produced as control. The incorporation of FliC into FliC/M1 VLPs was
25 confirmed by western blot using anti-FliC (Lane 2 in Fig. 2C) or anti-M1 antibody (Fig. 2E).

Because TLR5 is the extracellular sensor of flagellin, the ability of the soluble M2e-tFliC fusion protein, or the membrane-anchored fusion protein in VLPs, to function as a TLR5 ligand was determined. As shown in Fig. 2F, either the fusion protein or VLPs
30 containing FliC showed TLR5-specific bioactivity, inducing a mouse macrophage cell line RAW264.7 to produce TNF- α in a concentration range of 0.01ng to 1000 ng/ml. The 50% effective concentration (concentration which produces 50% of maximal activity, EC₅₀) of 4.M2e-tFliC was 5 ng, and that of the 4.M2e-tFliC VLPs was 60ng. The EC₅₀ of the

soluble flagellin was 0.8 ng/ml. Considering that the soluble FliC has a much lower molecular weight than the fusion protein or VLPs, EC₅₀ titers are within expected ranges.

The 4.M2e-tFliC fusion protein or VLPs induce high IgG responses

5 To evaluate the potential of multiple M2e-containing fusion protein or VLPs as universal influenza vaccines, mouse groups (6 mice in each group) were immunized three times at 4-week intervals with doses indicated in Table 1. The immune responses were compared by either intramuscular (i.m.) or intranasal (i.n.) immunization. The result in Fig. 3A showed that both the fusion protein and VLP groups trigger robust humoral
10 responses against M2e by either the i.m. or i.n. route compared to the 4.M2e group which showed a very low serum IgG response. The serum IgG titers in i.m. and i.n. immunizations were 6.5×10^5 and 4.0×10^5 , respectively. An interesting observation is that soluble 4.M2e protein when adjuvanted with flagellin VLPs induced higher levels of serum IgG titers (8.2×10^5 for i.m, 6.4×10^5 for i.n, geometric mean), demonstrating the
15 adjuvant effect of FliC in a particulate form.

Table 1. Mouse groups for immunization.

Group	Antigen form	Dose (μ g)	Number of immunization	Immunization route
4.M2e	Protein	10	3	i.m.
4.M2e	Protein	10	3	i.n.
4.M2e-tFliC	Fusion protein	10	3	i.m.
4.M2e-tFliC	Fusion protein	10	3	i.n.
4.M2e-tFliC	VLPs	50	3	i.m.
4.M2e-tFliC	VLPs	50	3	i.n.
4.M2e + tFliC	Mixture	10+10	3	i.m.
4.M2e + tFliC	Mixture	10+10	3	i.n.
Naïve mice				

i.m., intramuscular; i.n., intranasal.

Three immunizations were performed at 4 weeks intervals.

Although the 4.M2e-tFliC fusion protein or its membrane-anchored form in VLPs induced a high level of M2e-specific antibody responses, only antibodies capable of targeting native tetrameric M2 may confer protection. Influenza virus-infected MDCK cells express high levels of M2 on the cell membrane and can be used to determine the M2-specific antibody binding. Therefore antibodies binding to native M2 protein were evaluated by a MDCK cell-based ELISA. As shown in Fig.3B, antibodies in immune sera recognized and bound M2 expressed on MDCK cell surfaces in ELISA. Sera from the 4.M2e peptide-immunized mice showed very low binding close to background. The mixture of 4.M2e plus FliC VLPs induced highest M2-specific antibody responses.

Comparatively, the i.m. immunization induced better systemic immune responses than the i.n. route. The antibody-binding levels to M2 on cell surface in all groups showed similarity with M2e-specific IgG titers, demonstrating that the M2e-specific antibodies confer M2 recognition and are correlated with binding to the native M2.

The 4.M2e-tFliC fusion protein or VLPs induce enhanced mucosal immune responses

The respiratory tract is the dominant site of influenza virus infection and replication. Effective mucosal antibody responses can prevent the initiation of viral infection in the respiratory tract. FliC with the deletion of the variable region has been reported to be an effective mucosal adjuvant. Nempont et al., J Immunol, 2008,181(3):2036-43. The result in Fig. 4 shows that both the 4.M2e-tFliC fusion protein and VLPs induced higher titers of secretory IgA (sIgA, Fig. 4A) and IgG (Fig. 4B) in respiratory secretions after i.n. immunization. Data also demonstrate that flagellin-containing VLPs are very effective as a mucosal adjuvant when mixed with 4.M2e, inducing high titers of sIgA (3.2×10^4) and IgG (8×10^4) responses at mucosal surfaces. These data demonstrate that flagellin is effective as a mucosal adjuvant when associated with M2e antigen in fusion proteins or VLPs, or mixtures of M2e and FliC VLPs.

The breadth of protective efficacy of 4.M2e-tFliC fusion proteins or VLPs

The above results demonstrate that the immunogenicity of M2e is enhanced by insertion of 4.M2e into FliC to replace the variable region, or by assembly of the membrane-anchored 4.M2e-tFliC into VLPs. To determine whether the above vaccine

candidates confer enhanced protection to influenza virus challenge, immunized mice were challenged i.n. with 5 LD₅₀ (250 pfu) of mouse-adapted A/Philippines (H3N2) virus in which the M2e has the same sequence as the consensus used for making the fusion protein or VLPs (Fig. 1). Also, this sequence is the one most frequently found in human influenza virus strains. As shown in Fig. 5, five groups (i.n.-delivered 4.M2e-tFliC fusion protein, both i.m. and i.n.-delivered 4.M2e-tFliC VLPs, and mixtures of 4.M2e plus FliC VLPs) of immunized mice completely survived the Philippines virus challenges (Fig. 5A). Mice immunized with mixtures of 4.M2e and FliC VLPs lost less bodyweight (8 and 10% for i.n. and i.m. immunizations, respectively. Fig. 5B), revealing the best comparative protection. Mice immunized i.n. with 4.M2e-tFliC VLPs and 4.M2e-FliC fusion protein lost their 12 and 17% of bodyweight, respectively (Fig. 5B). Mice immunized i.m. with 4.M2e-tFliC fusion protein survived 67% (4 of 6 mice, Fig.5A) in the challenge with a 20-25% body weight loss (Fig.5B). Mice immunized either i.n. or i.m. with 4.M2e protein, as well as the naïve mice, reached their endpoints (Fig. 5A and B).

The protection induced by the 4.M2e-tFliC fusion protein or VLPs against A/PR8 virus challenge were further evaluated. The M2e sequence of PR8 M2 that were used in this work has one amino acid difference from the consensus, and no other human influenza virus shares this M2e sequence. Four weeks after the last immunization, mice were infected i.n. with a dose of 5 LD₅₀ (125 pfu) of mouse-adapted PR8 live virus. Intranasally-immunized mice showed complete protection against PR8 challenge (Fig. 6A). Some i.m.-immunized mice survived except for the mixture of the 4.M2e peptide plus FliC VLPs (Fig. 6A), which induced full protection by either i.n. or i.m. immunization.

A common feature of the above challenge results is that i.n. immunity is much more effective in providing protection against influenza virus infection. As shown in Fig.5, i.n and i.m.-delivered 4.M2e-tFliC fusion proteins induced 100 and 67% (4 of 6 mice) protection against Philippines virus challenges, respectively. I.n.-immunized mice with 4.M2e-tFliC VLPs survived both Philippines and PR8 challenges, but 17% (1 of 6) of i.m. immunized mice were terminated after PR8 challenge (Fig. 6A). Although mice immunized both i.m. and i.n. by the mixture of 4.M2e and FliC VLPs survived 100% in either Philippines or PR8 virus challenge, respectively, i.n.-immunized mice lost less body weight, as shown in Fig. 5B and 6B. In all the above immunized mice, i.m. immunizations induced higher titers of serum M2-specific IgG responses compared to i.n

immunizations as shown in Fig. 3, but the i.n. vaccination induced better protection, demonstrating the advantage of mucosal immunity in M2e-induced protective immunity.

Because the M2e-specific antibodies do not neutralize the infectivity of influenza viruses but instead exert their protective effect at the level of the infected cell, the effect of 4.M2e-tFliC or VLPs in decreasing the viral replication in mouse lung was further
5 evaluated. As shown in Fig.7, all surviving groups have lung virus loads lower than 1×10^4 for the PR8 challenge, or 1×10^5 for Philippines. The i.n.-immunized mice showed lower lung virus titers than i.m. groups, further demonstrating the advantage of mucosal immunization.

10

Construction of rBVs Expressing RSV F, RSV G, and Influenza M1

RSV-F and RSV-G genes from RSV strain A2 were amplified by PCR, and the influenza M1 gene was amplified by RT-PCR with primers containing restriction enzyme sites. Genes were cloned into pFastBac vectors, and insertion of RSV-F, RSV-G, and
15 influenza M1 in pFastBac expressing vectors was confirmed by cutting with enzyme sites, EcoRI and XhoI (Figure 8A–C). The nucleotide sequences of the RSV-F, RSV-G, and influenza M1 genes were found to be identical to the previously published sequences (accession numbers FJ614814 for F, AF035006 for G, FJ966085 for M1, all hereby incorporated by reference) by DNA sequencing

20 The RSV A2 F and G genes were polymerase chain reaction (PCR)-amplified using RNA from infected HEp-2 cells as described in Moore et al. A chimeric A2 strain of respiratory syncytial virus (RSV) with the fusion protein of RSV strain line 19 exhibits enhanced viral load, mucus, and airway dysfunction, J Virol, 2009, 83:4185–94, hereby incorporated by reference. The RSV-F gene was PCR-amplified from a complementary
25 DNA (cDNA) clone of A2 F by use of primers 5-AAAGAATTCACCATGGAGGAGTTGCTAATCCTCAA-3 (SEQ ID NO: 82) and 5-TTACTCGAGTTAGTTACTAAATGCAATATTATT-3 (SEQ ID NO: 83) (EcoRI and XhoI underlined) and cloned into pFastBac with EcoRI/XhoI sites, resulting in plasmid pFastBac-F. The RSV-G gene was PCR-amplified from a cDNA clone of A2 G
30 by use of primers 5-AAAGAATTCACCATGTCCAAAAACAAGGACCAAC-3 (SEQ ID NO: 84) and 5-TTACTCGAGTACTGGCGTGGTGTGTTG-3 (SEQ ID NO: 85) (EcoRI and XhoI underlined) and cloned into pFastBac with EcoRI/ XhoI sites, resulting in plasmid pFastBac-G.

For influenza M1 gene cloning, A/California/04/2009 virus was inoculated into MDCK cells and total viral RNA was extracted using an RNeasy Mini kit (Qiagen). Reverse transcription (RT) and PCR were performed on extracted viral RNA using the One- Step RT-PCR system (Invitrogen) with gene-specific oligonucleotide primers. The following primer pairs were used for M1: 5-
5 AAAGAATTCACCATGAGTCTTCTAACCGAGGT-3 (SEQ ID NO: 86) and 5-
TTACTCGAGTTACTCTAGCTCTATGTTGAC-3 (SEQ ID NO: 87) (EcoRI and XhoI underlined). Following RT-PCR, a cDNA fragment containing the M1 gene was cloned into the pFastBac vector.

10 Recombinant baculoviruses (rBVs) expressing RSV F, RSV G, or influenza M1 were generated. Transfections of DNA containing the above genes were accomplished using cellfectin II (Invitrogen) with SF9 cells as recommended by the manufacturer, followed by transformation of pFastBac containing RSV-F or RSV-G or M1 with white/blue screening. The rBVs were derived by using a Bac-to-Bac expression system
15 (Invitrogen) according to the instructions of the manufacturer.

Production of RSV VLPs

RSV-F VLPs were produced by infecting Sf9 cells with rBVs expressing RSV-F and M1. RSV-G VLPs were produced by infecting Sf9 cells with rBVs expressing RSV-G
20 and M1. Cell culture supernatants were collected on day 2 postinfection with centrifugation at 6000 rpm for 20 minutes at 4 C. VLPs were concentrated with QuixStand (GE) and purified through a 20%-30%-60% discontinuous sucrose gradient at 30 000 rpm for 1 hour. The VLP bands between 30% and 60% were collected and then diluted with phosphate-buffered saline (PBS) and pelleted at 28 000 rpm for 40 minutes at 4 C. VLPs
25 were resuspended in PBS overnight at 4 C.

The incorporation of F or G and M1 into VLPs was confirmed by western blot using anti-RSV or anti M1 polyclonal antibodies (Figure 8D and E). Both RSV-F or RSV-G VLPs showed spherical shapes with spikes on their surfaces (Figure 9A and C). RSV F VLPs had a peak in size distribution at 80–100 nm, whereas G-VLPs were similar but
30 somewhat more heterogeneous in size (Figure 9B and D). In total, 5–7.5 mg VLPs/liter of cell culture medium were obtained, and their antigenic properties were stable for 1 year at -80 C. Heat-treated VLPs lost immunogenicity and protective capacity.

Antibody Responses in Immune Serum

Serum antibody responses were determined in mice immunized with RSV-F or RSV-G VLPs as shown in Figure 10A. The levels of total IgG, IgG2a, and IgG1 antibody responses in the serum specific to RSV after prime and boost were determined. Total IgG and IgG2a responses from the mice immunized with RSV-F VLPs showed significantly higher titers after boost compared with those after prime, indicating the progressive maturation of virus-specific antibodies (Figure 10B and C). Low IgG1 responses were observed both after prime and boost (Figure 10D). In contrast, the levels of IgG2a antibody increased significantly, both after prime and boost, compared with IgG1. The levels of IgG2a were higher after boost than prime at various serum dilutions (Figure 10E). Similar patterns of total IgG, IgG2a, and IgG1 responses to RSV A2 were found in mice immunized with RSV-G VLPs. The levels of IgG and IgG2a antibody responses were lower relative to those observed with RSV-F VLPs. Antibody responses (IgG, IgG2a) were significantly higher in mice after boost compared with primary immunization (Figure 10F and G). As seen in Figure 10, IgG2a-dominant responses were found after the boost but not after prime. These results indicate that both RSV-F and RSV-G VLPs are highly immunogenic and induce IgG2a-dominant responses.

Antibody Responses in Mouse Lung

The lung is an important location for RSV replication, where disease development occurs. At day 4 after challenge, mouse lungs were harvested and total IgG, IgG1, and IgG2a antibody responses were determined. As shown in Figure 11A and C, significantly higher levels of RSV A2 specific IgG antibodies were found in mice immunized with RSV-F VLPs or RSV-G VLPs. Interestingly, IgG responses specific to RSV-G or RSV-F in immunized mice showed similarly high levels. As seen in Figure 11B and D, significantly higher IgG2a responses were elicited in mice immunized with RSV-F VLPs or RSV-G VLPs compared with IgG1. The ratios of IgG2a to IgG1 from both RSV-G VLPs and RSV-F VLPs were similar at lung extract dilutions of 10, 20, and 40 (Figure 11E). Compared with serum samples, lung extract samples showed a much higher ratio of IgG2a to IgG1 (Figure 11E and I, Figure 11E). These results indicate that both RSV-G VLPs and RSV-F VLPs elicit RSV IgG2a dominant responses in lungs.

Immune Sera Effectively Bind to RSV Infected Cells

Immune responses against cell surface proteins were determined using monolayers of HEp-2 cells infected with RSV A2 or uninfected cells. After 12 hours of incubation, the supernatants were removed and the immune sera were added to the cell surface to
5 determine IgG, IgG1 and IgG2a responses. As seen in Figure 12, sera from mice immunized with RSV-F or RSV-G VLPs from prime and boost showed significantly high levels of total IgG and IgG2a antibody responses against cell surface proteins expressed 12 hours postinfection (Figure 12A, B, D, and E). Total IgG responses against infected or uninfected cell surface proteins were determined in mice immunized with RSV-F VLPs
10 (Figure 12C) or with RSV-G VLPs (Figure 12F), showing background responses in uninfected cells. Interestingly, RSV-G VLP vaccinations showed much higher total IgG and IgG2a responses against cell surface proteins than did RSV-F VLPs. These results indicate that immune sera specifically bind to HEp-2 cell surface expressed proteins.

15 Neutralizing Antibody Responses

Neutralizing antibody is an important functional component of immune responses induced by vaccination. To determine whether immunization with RSV VLPs induces neutralizing antibodies, an in vitro plaque reduction assay was used. Serially diluted mouse sera at week 3 after boost were complement inactivated, incubated with live
20 RSVA2, and plaque assays were conducted. As shown in Figure 13, RSV-F or RSV-G VLPs showed similar plaque reduction rates. At 1:1000 serum dilutions, either RSV-G or RSV-F VLP vaccination reduced the number of plaques by 55% whereas naïve serum reduced plaques by 7%. At the 1:10 000 serum dilutions, RSV-G VLPs showed 38% plaque reduction versus 25% reduction by RSV-F VLPs and no reduction by naive sera
25 (Figure 13). Naive sera showed very high background effects at serum dilution of 1:10 or 1:100, with neutralizing titers .100. Virus neutralizing titers from immunization with RSV-F or RSV-G VLPs were .1000 when the highest serum dilution showing 50% plaque reduction was taken as the neutralizing antibody titer in comparison to the negative medium control showing no plaque reduction. These results indicate that RSV-F
30 and RSV-G VLPs vaccines can induce protective functional antibodies to RSV.

Protection Against Live RSV A2 Virus Challenge Infection

Virus load in lungs and body weight changes following challenge infection are important indicators to assess vaccine protective efficacy. Immunized mice were challenge

infected with live RSV-A2 virus (1.5×10^6 PFU/mouse) at 4 weeks after boost, and lung virus loads at day 4 postchallenge were determined. As shown in Figure 14A, significantly decreased lung virus loads were detected in mice immunized with RSV-F (11-fold) or RSV-G VLPs (600-fold) compared with naive mouse controls. The difference in lung virus loads in mice immunized with RSV-F VLPs and RSV-G VLPs also was compared (Figure 14B). Lower lung virus load was found in mice immunized with RSV-G VLPs than those in mice immunized with RSV-F VLPs (Figure 14B). These results indicate that vaccination of mice with RSV-F or RSV-G VLPs effectively can inhibit virus replication in lung. The level of body weight loss postchallenge was measured, and days 6 or 7 postinfection showed the highest body weight loss. Naive control mice showed the highest body weight loss (20%), whereas mice immunized with RSV-F VLPs or RSV-G VLPs showed 13% and 6.4% of body weight loss, respectively, at day 6, and 8% and 5% of body weight loss, respectively, at day 7 postchallenge (Figure 14C). Significant differences in body weight loss were found at day 7 between naive controls and RSV-F or RSV-G VLPs, and between RSV-F and RSV-G VLPs. The differences correlate with better lung virus clearance, which was observed with RSV-G VLPs compared with RSV-F VLPs. These results indicate that RSV-F and RSV-G VLPs both confer substantial protection of mice from RSV-induced illness.

CLAIMS

What we claim:

1. A method of vaccinating a subject comprising administering an antigen in combination with a virus-like carrier comprising a TLR5 agonist, wherein the virus-like carrier does not contain the antigen, under conditions such that antibodies to the antigen are produced.
2. The method of Claim 1, wherein the antigen is a viral, bacterial, fungal, or parasite derived molecule.
3. The method of Claim 1, wherein the antigen comprises an M2e polypeptide of SEQ ID NO 1.
4. The method of Claim 3, wherein the antigen comprises an M2e polypeptide with four or more contiguous amino acids within SEQ ID NO: 1.
5. The method of Claim 1, wherein the antigen is a repeating polypeptide sequence.
6. The method of Claim 1, wherein the TLR5 agonist is a flagellin in a membrane-anchored form.
7. The method of Claim 6, wherein the flagellin is FliC or FliC wherein the variable region is absent.
8. The method of Claim 6, wherein the virus-like carrier comprises a polypeptide of SEQ ID NO: 28.
9. The method of Claim 1, wherein the antigen and virus-like carrier are administered intranasally or intramuscularly.
10. An immunogenic composition comprising an antigen and a virus like carrier comprising a flagellin wherein the virus-like carrier comprising a TLR5 agonist wherein the virus-like carrier does not contain the antigen.

11. The composition of Claim 10, wherein the antigen is a viral protein.
12. The composition of Claim 10, wherein the antigen comprises an M2e polypeptide of SEQ ID NO 1.
13. The composition of Claim 10, wherein the antigen comprises an M2e polypeptide with multiple contiguous amino acids within SEQ ID NO: 1.
14. The composition of Claim 10, wherein the antigen is a repeating polypeptide sequence.
15. The composition of Claim 10, wherein the TLR5 agonist is a flagellin.
16. The composition of Claim 15, wherein the flagellin is FliC or FliC wherein the variable region is absent.
17. The composition of Claim 10, wherein the virus-like carrier comprises a polypeptide of SEQ ID NO: 28.
18. A nucleic acid sequence encoding a polypeptide of SEQ ID NO: 28.
19. An immunogenic composition comprising a virus-like carrier having influenza virus matrix protein wherein influenza virus matrix protein is M1 and a RSV protein is G protein or glycoprotein on the surface in the absence of the F protein or glycoprotein.
20. An RSV-G virus-like particle produced by infecting insect cells with rBVs encoding RSV-G and influenza M1 and not the RSV-F gene.
21. A method of vaccinating a subject comprising administering an immunogenic composition of Claims 19 or 20.

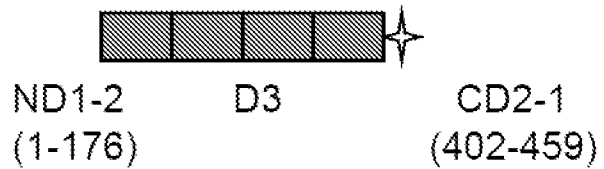
M2e sequence: (M) SLLTEVETPIRNEWGC RC NDSSDP

Sequence used: SLLTEVETPIRNEWG S RS NDSSDP

4.M2e:

AAASLLTEVETPIRNEWGSRSDSSDPAAGTSAAAASLLTEVETPIRNE
WGRSNDSSDPAAALQAAASLLTEVETPIRNEWGSRSDSSDPAAA
ACAAASLLTEVETPIRNEWGSRSDSSDPAAAACKL

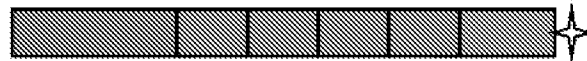
4. M2e



Flagellin (FliC)



4.M2e-tFliC



Membrane-anchored
4.M2e-tFliC



FIGURE 1

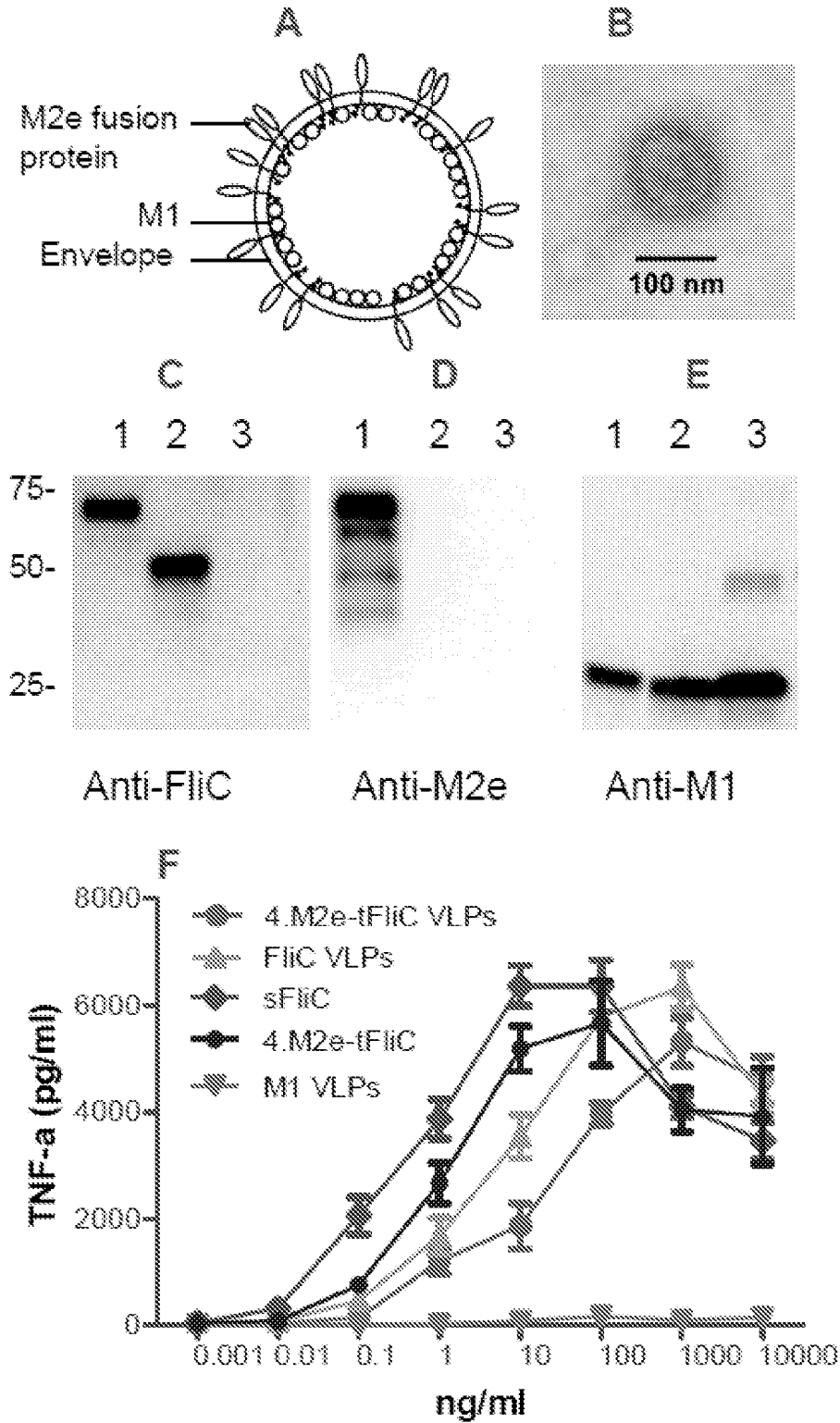


FIGURE 2

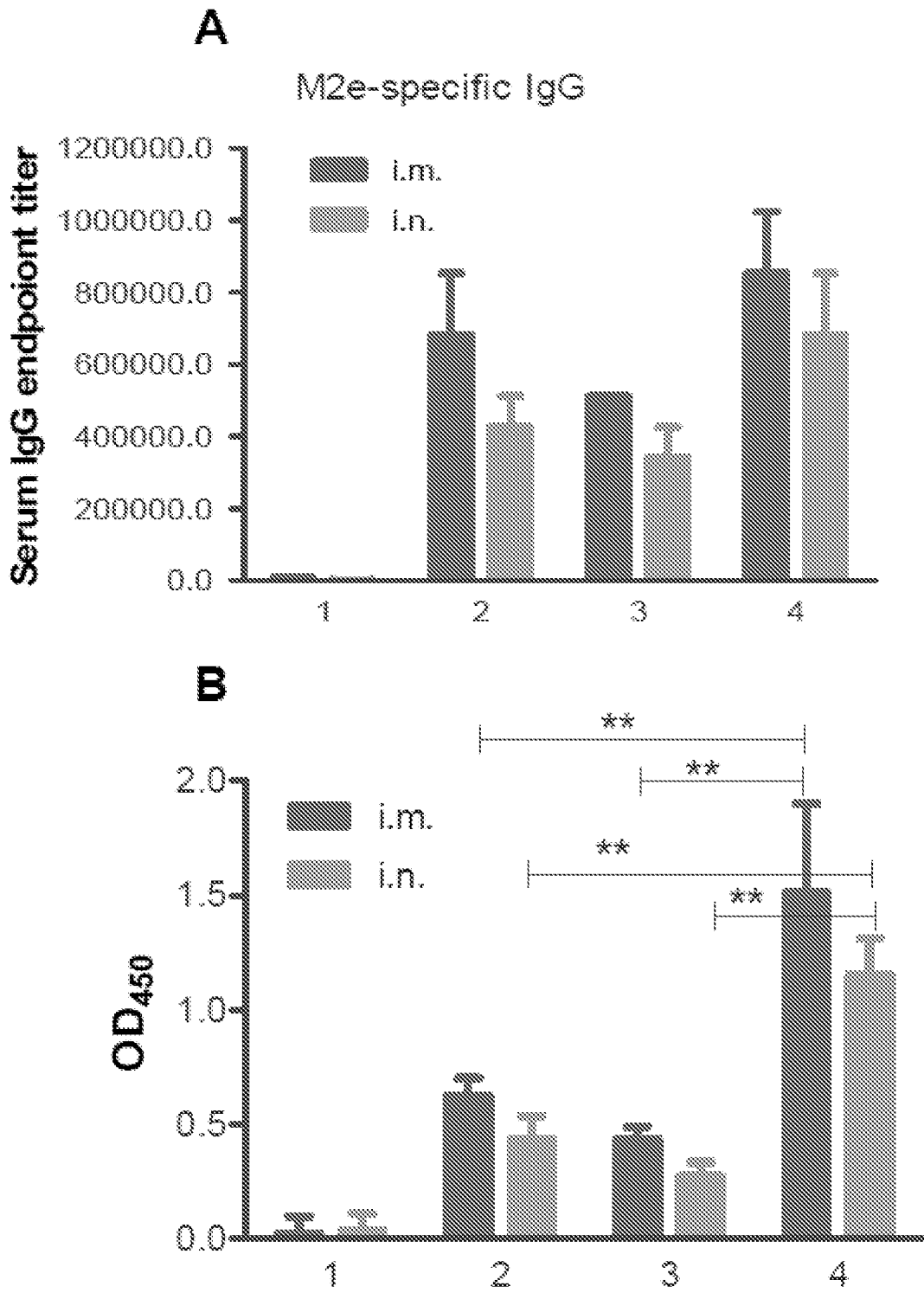


FIGURE 3

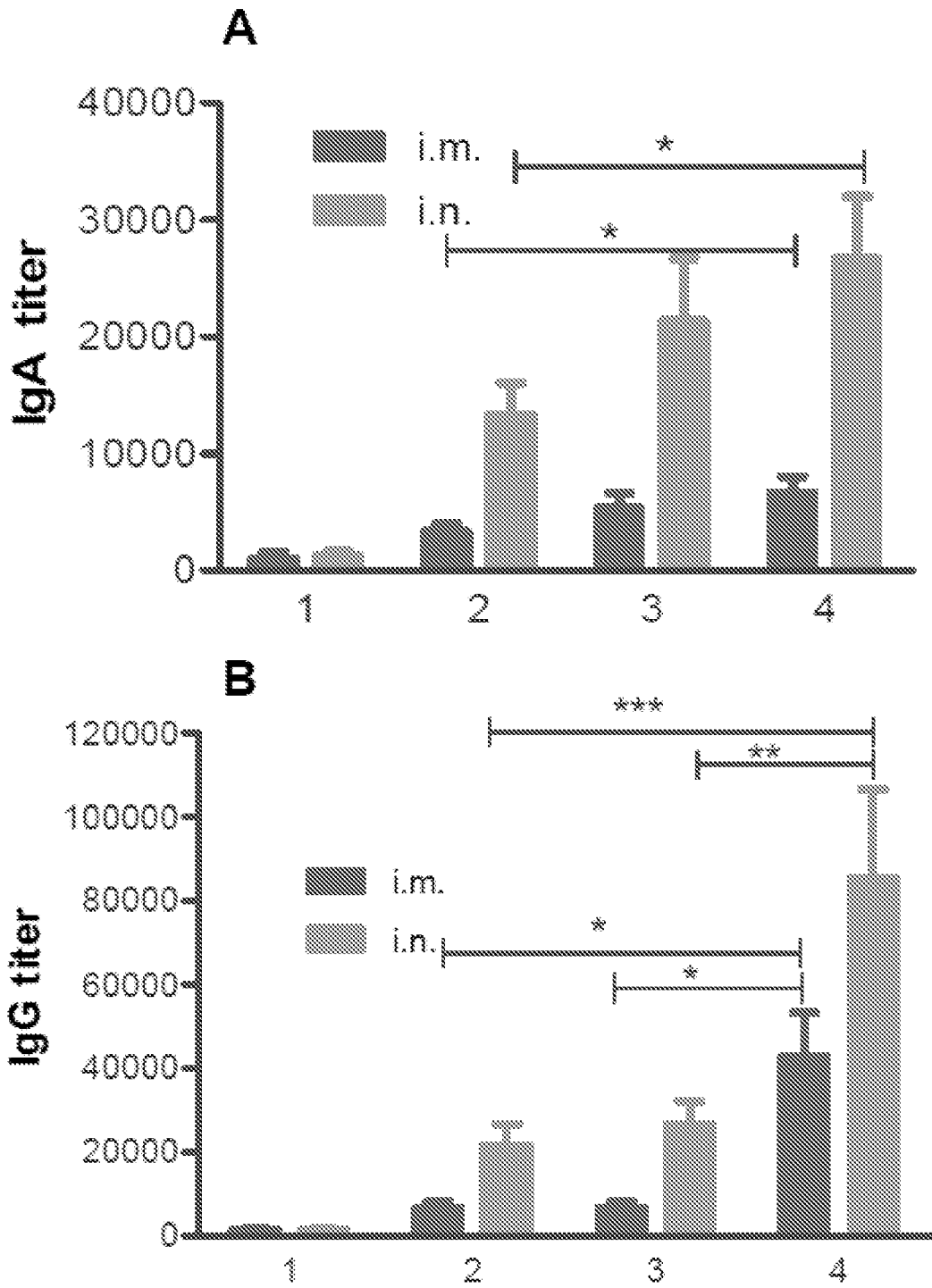


FIGURE 5

5/13

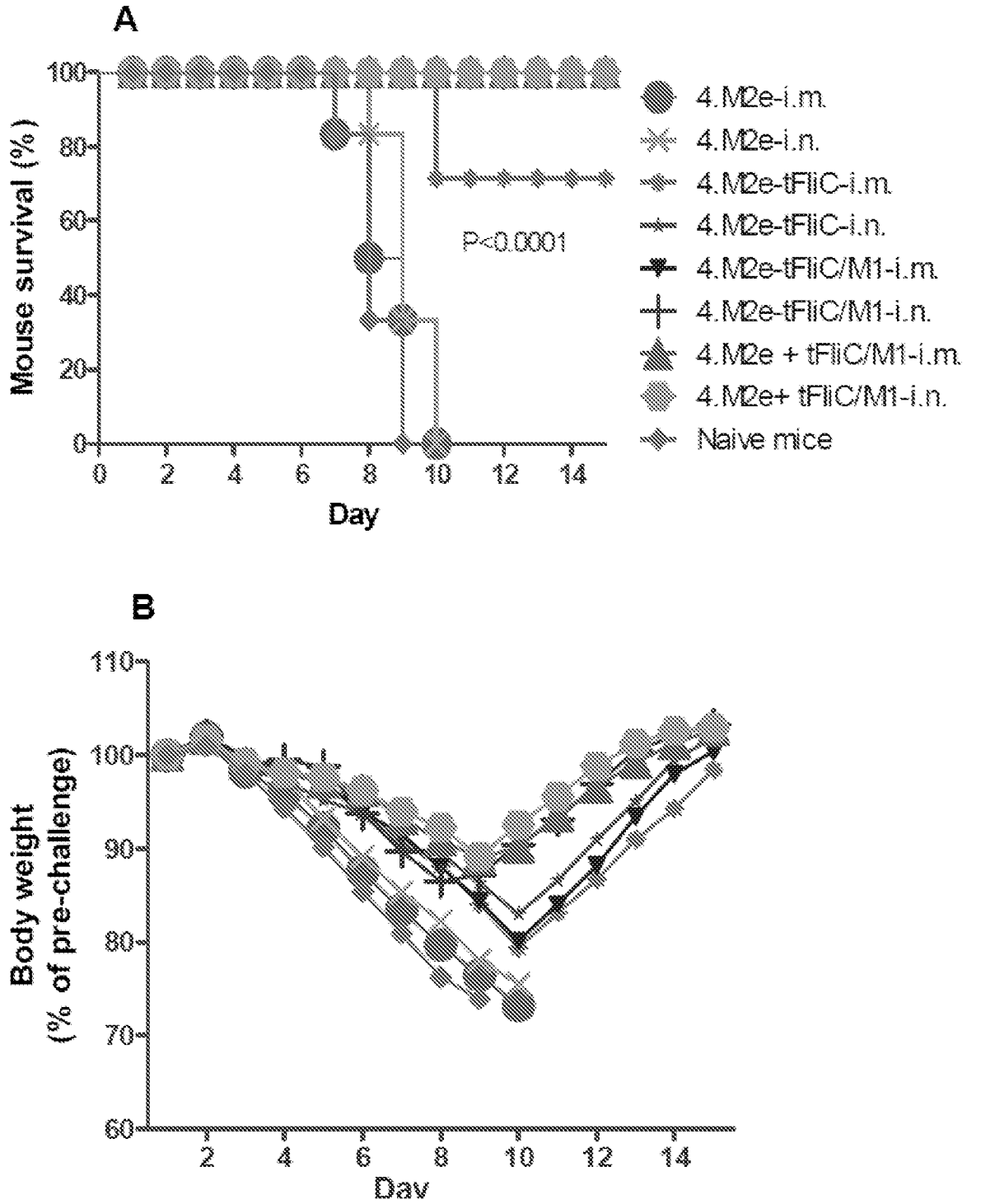


FIGURE 5

6/13

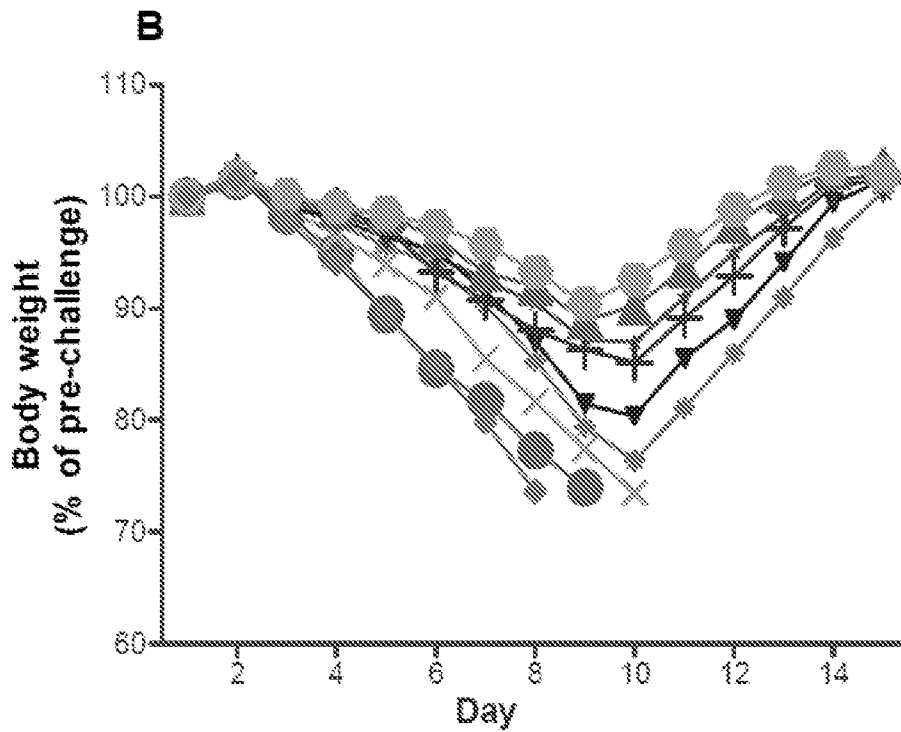
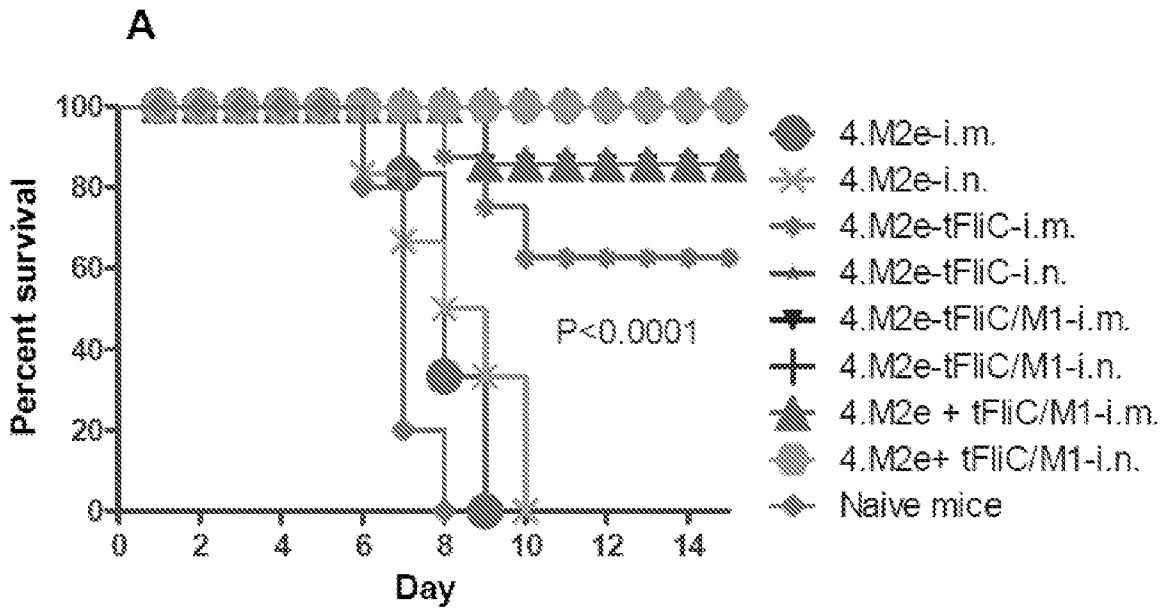


FIGURE 6

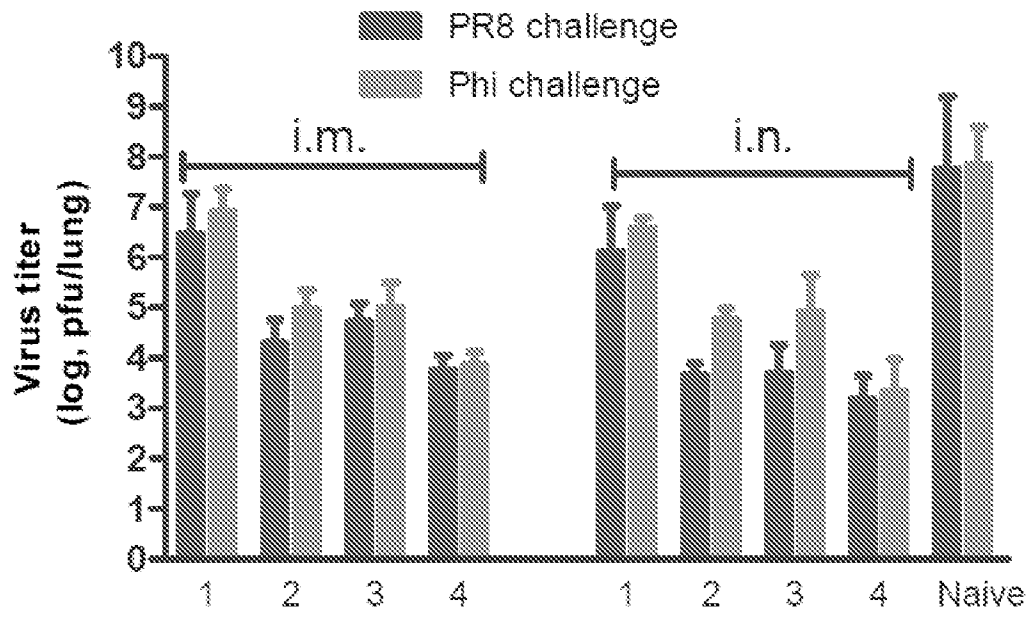


FIGURE 7

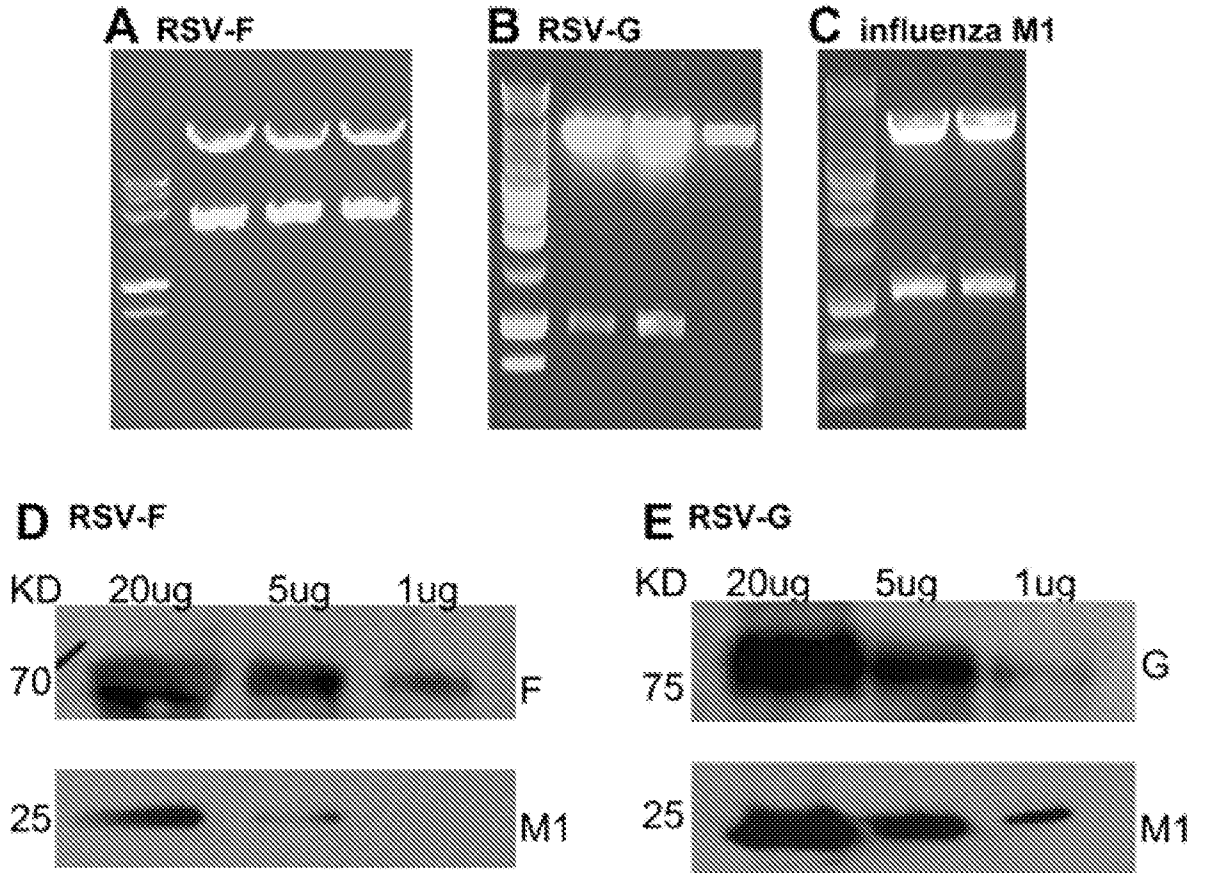


FIGURE 8

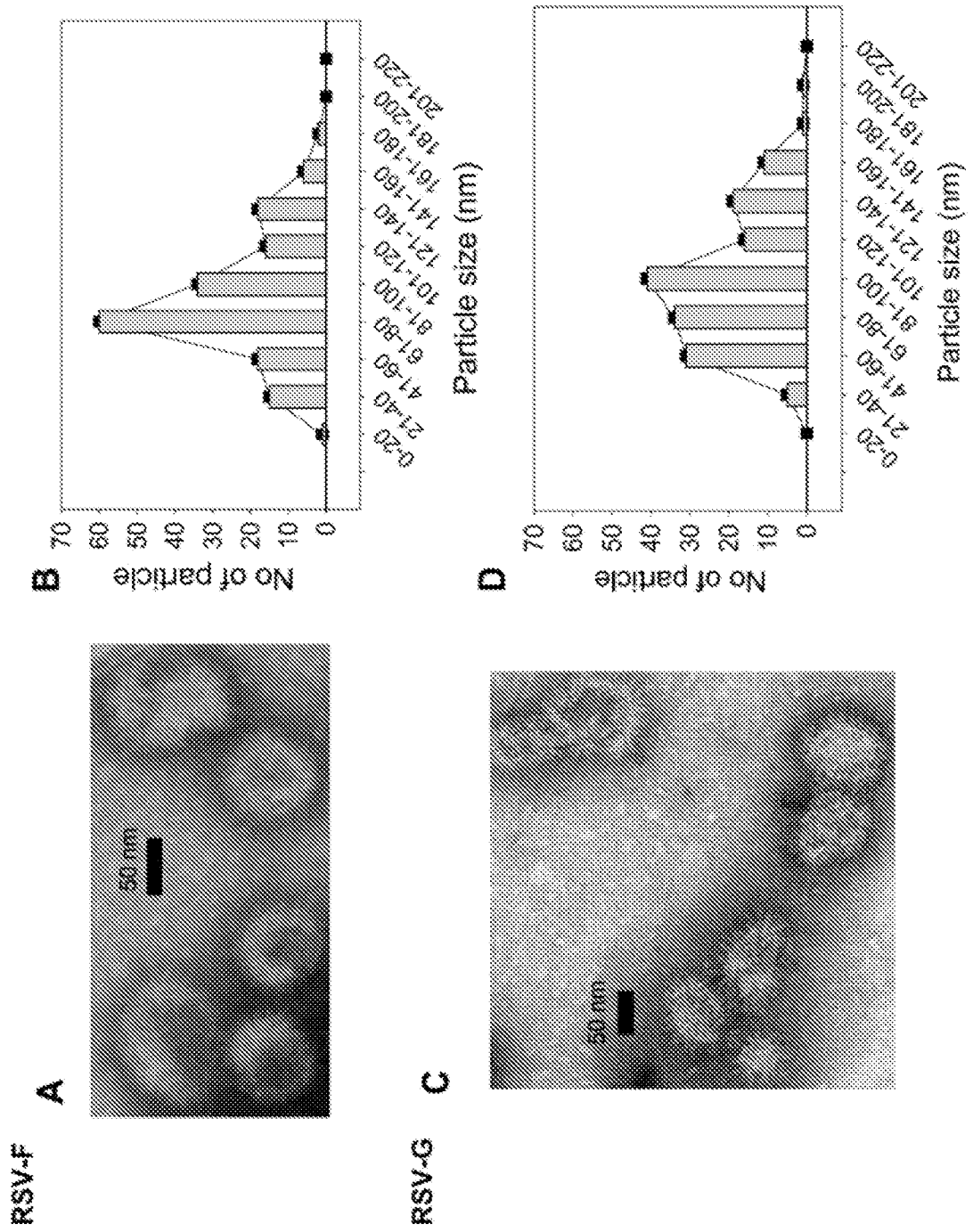


FIGURE 9

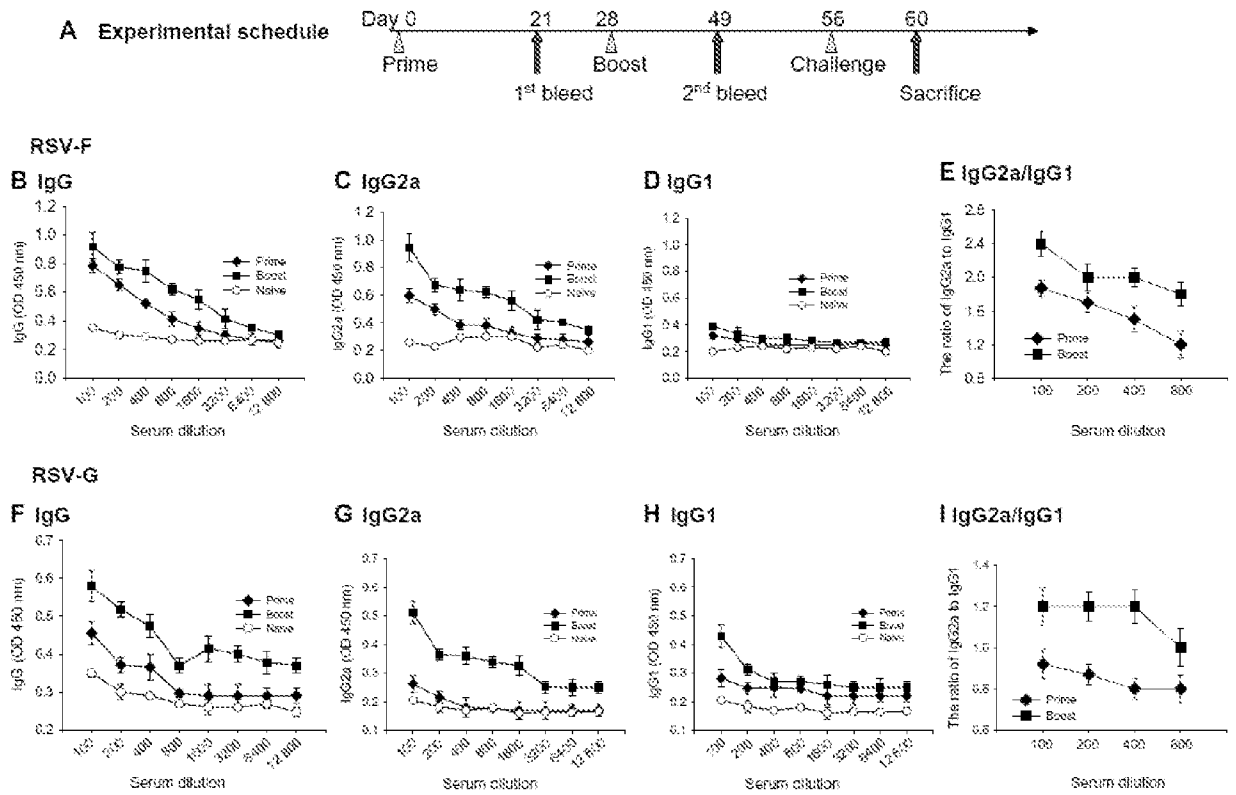


FIGURE 10

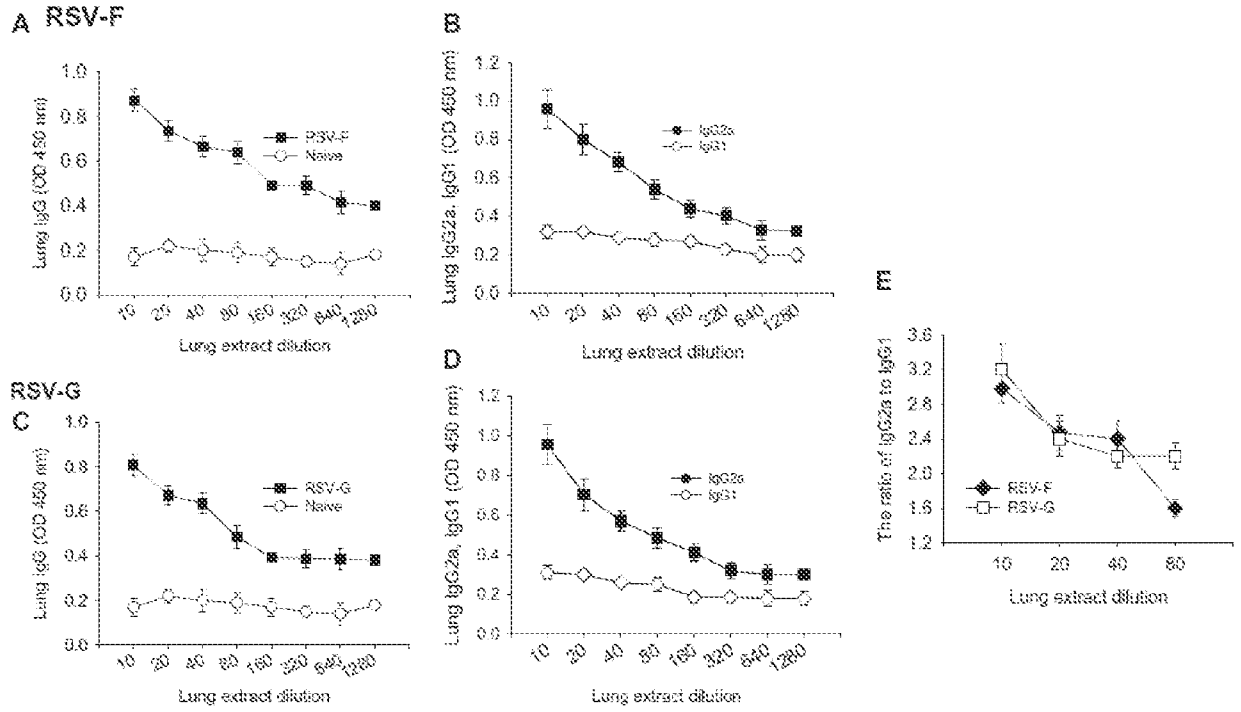


FIGURE 11

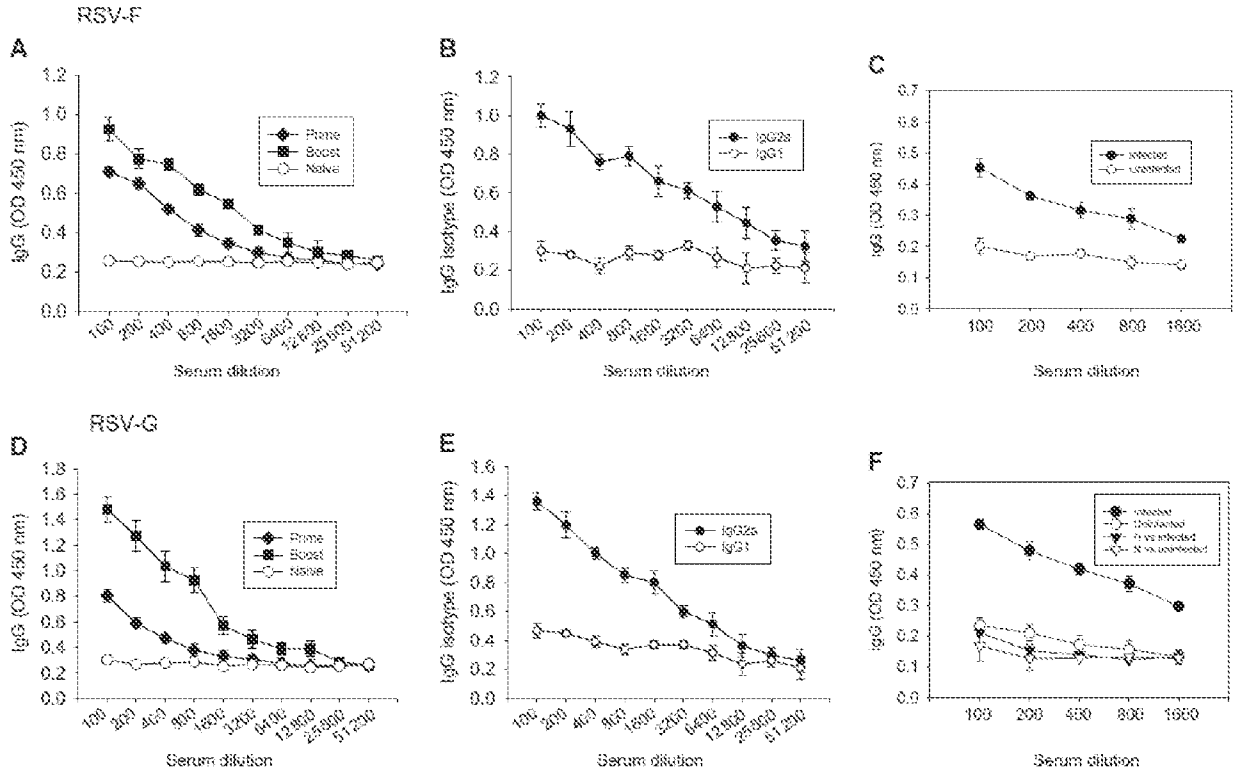


FIGURE 12

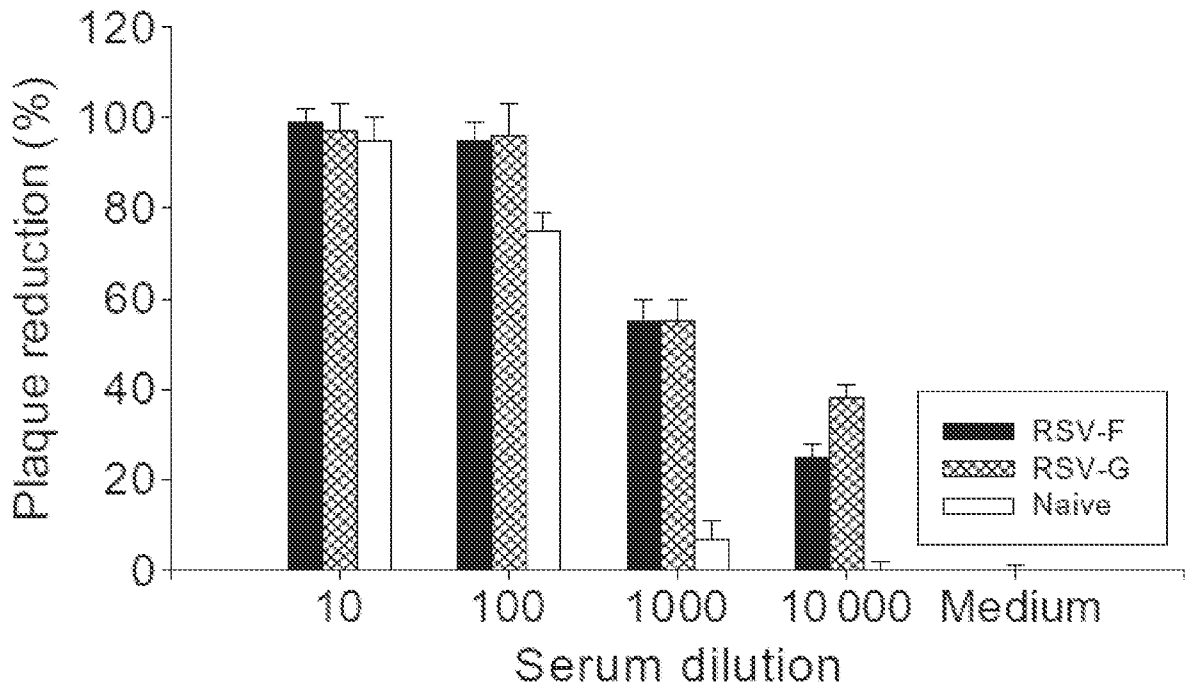


FIGURE 13

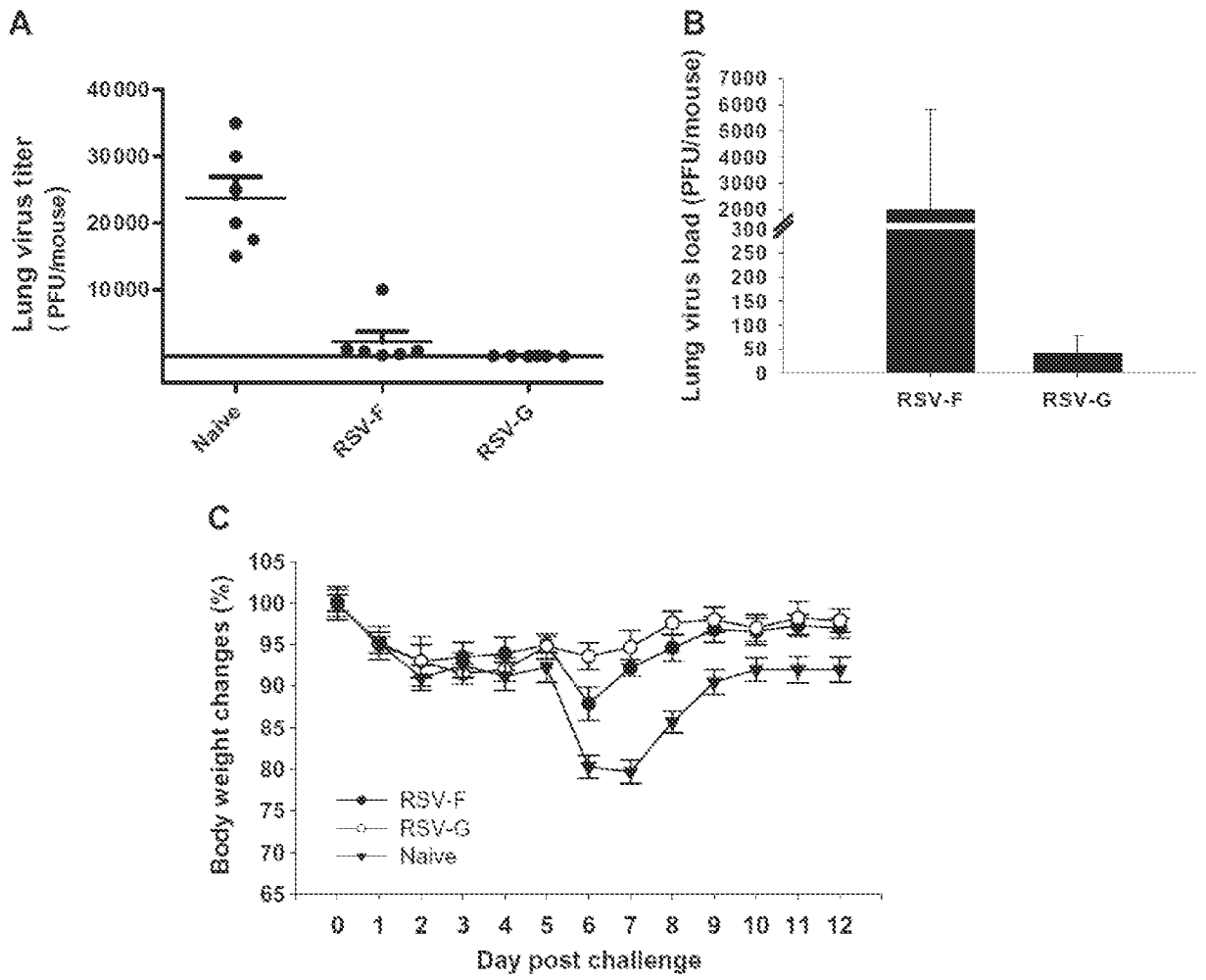


FIGURE 14

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 2012/049008

A. CLASSIFICATION OF SUBJECT MATTER		<i>A61K 39/12 (2006.01)</i> <i>A61K 39/02 (2006.01)</i> <i>C07K 14/00 (2006.01)</i> <i>C07K 14/005 (2006.01)</i> <i>C12N 15/33 (2006.01)</i> <i>A61K 39/145 (2006.01)</i> <i>C12N 7/04 (2006.01)</i>	
According to International Patent Classification (IPC) or to both national classification and IPC			
B. FIELDS SEARCHED			
Minimum documentation searched (classification system followed by classification symbols)			
A61K 39/12, 39/02, C07K 14/00, 14/005, C12N 15/33, A61K 39/145, C12N 7/04			
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched			
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)			
CIPO, DEPATISnet, DWPI, EAPATIS, EMBL, EPO-Internal, Esp@ce, Esp@cenet, Google, KIPRIS, PAJ, PabMed, RUPTO, SCIEDIRECT, SIPO, USPTO, WIPO, ВИНІТИ (VINITI)			
C. DOCUMENTS CONSIDERED TO BE RELEVANT			
Category*	Citation of document, with indication, where appropriate, of the relevant passages		Relevant to claim No.
X Y	RU 2375076 C2 (TSITOS BIOTEKHOLOGI AG) 10.12.2009, claims, p. 6, 10, 17, 28		1, 2, 6, 7, 9-11, 15, 16 3-5, 8, 12-14, 17
Y	US 2009/0162400 A1 (THOMAS J.POWELL et al.) 25.06.2009, claims, SEQ.ID.NO:47		3-5, 12-14
X Y	WO 2009/079564 A2 (EMORY UNIVERSITY) 25.06.2009, claims, fig.8		18 8, 17
Y	WO 2011/046925 A1 (TECHNOVAX, INC.) 21.04.2011, claims		19-21
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C.		<input type="checkbox"/> See patent family annex.	
* Special categories of cited documents:			
"A"	document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E"	earlier document but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family
"P"	document published prior to the international filing date but later than the priority date claimed		
Date of the actual completion of the international search		Date of mailing of the international search report	
10 October 2012 (10.10.2012)		22 November 2012 (22.11.2012)	
Name and mailing address of the ISA/ FIPS Russia, 123995, Moscow, G-59, GSP-5, Berezhkovskaya nab., 30-1		Authorized officer O. Fedonova	
Facsimile No. +7 (499) 243-33-37		Telephone No. (495)531-65-15	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 2012/049008

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

According to Rule 13 of the Regulations under the PCT the claimed inventions does not meet the requirement of unity of invention, therefore independent claims 1, 10, 18-21 form several groups of inventions, which are not so linked as to form a single general inventive concept.

The special technical feature of independent claims 1 and 10 is combination an antigen with a virus-like carrier.

The special technical feature of independent claim 18 is a nucleic acid sequence encoding a polypeptide of SEG ID NO: 28.

The special technical feature of independent claims 19-21 is a virus-like carrier having influenza virus matrix protein M1 and a protein RSV G or glycoprotein.

Consequently, in the independent claims 1, 15-17, 20, 26 - 29 the special technical feature is absent.

Hence, claims comprise 3 groups of inventions, namely:

1 group includes inventions of claims 1-17

2 group includes inventions of claim 18

3 group includes inventions of claims 19-21

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 2012/049008

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2009/0263420 A1 (UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL) 22.10.2009, claims	19-21
A	US 2011/0097358 A1 (TECHNO VAX, INC.) 28.04.2011, claims	1-21