NIH316.001VPC PATENT

OPTIMIZED VACCINES TO PROVIDE PROTECTION AGAINST EBOLA AND OTHER VIRUSES

Related Applications

This application claims benefit of US Provisional Application No. 60/613,883 filed September 27, 2004, US Provisional Application No. 60/677,606 filed May 03, 2005, US Provisional Application No. 60/679,767 filed May 10, 2005, US Provisional Application No. 60/701,694 filed July 22, 2005, and US Provisional Application No. 60/715,874 filed September 9, 2005, all of which are hereby incorporated by reference in their entireties.

Field of the Invention

The present invention relates generally to viral vaccines and, more particularly, to filovirus vaccines and methods of eliciting an immune response against a filovirus or a disease caused by infection with filovirus.

Background of the Invention

Ebola virus and Marburg virus make up the family *Filoviridae*. The family is divided into two genera, currently designated as "Ebola-like viruses" and "Marburg-like viruses." There are four subtypes within the "Ebola-like viruses," Zaire (type species), Sudan, Reston, and Côte d'Ivoire (Ivory Coast). A single type, Marburg virus, makes up the "Marburg-like viruses."

The glycoprotein (GP) is the sole structural protein making up the virion surface spikes that mediate virus entry into susceptible host cells through receptor binding. GP is the most studied of the filovirus proteins, not only for its importance in virus entry and pathogenesis but because it is a prime target for vaccine development. Research on filovirus GP has been facilitated through the use of recombinant DNA technology to permit biochemical and functional assays without the constraints of working with the infectious filovirus.

GP expression in cultured human endothelial and epithelial cells causes cell rounding and detachment (Yang Z.-Y. et al. 2000 *Nat Med* **6**:886-889). These effects require the presence of the mucin-like serine and threonine –rich domain of GP. The cytotoxic effects of GP on macrophage and endothelial cell function disrupt inflammatory cell function and the integrity of the vasculature. In addition, by altering the cell surface expression of adhesion proteins and immune recognition molecules, Ebola virus may

disrupt processes critical to immune activation and cytolytic-T-cell function. These phenomena likely account for the dysregulation of the inflammatory response and the vascular dysfunction characteristic of lethal Ebola virus infection, providing a rationale for focusing on GP as a target for a preventative vaccine.

Summary of the Invention

The invention is related to a nucleic acid molecule comprising a polynucleotide encoding a modified filovirus glycoprotein (GP) having at least one amino acid change located in a relatively conserved region of said GP that decreases *in vitro* cytotoxicity and retains immunogenicity when compared to *in vitro* cytotoxicity and immunogenicity of a wild type filovirus GP.

In one embodiment, the amino acid change is positioned in the N-terminal domain, excluding the conserved cysteine residues, and is located at amino acid position 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 or 300 in Ebola Zaire GP in an exemplary manner or corresponding thereto in other strains of said GP.

In another embodiment, the amino acid change is located at amino acid position 71 or 102 in Ebola Zaire GP in an exemplary manner or corresponding thereto in other strains of said GP.

In yet another embodiment, the amino acid change is E71D or G102A in Ebola Zaire GP in an exemplary manner or corresponding thereto in other strains of said GP.

In still another embodiment, the modified filovirus GP is encoded by the insert of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8, or sequence having at least 95% identity thereto.

In yet a further embodiment, the polynucleotide encoding the modified filovirus GP has a sequence taken from the insert of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8, or sequence having at least 95% identity thereto.

Other embodiments of the invention are related to modified filovirus GPs encoded by the nucleic acid molecules, plasmid DNAs comprising the nucleic acid molecules, recombinant viruses comprising the nucleic acid molecules, adenoviruses comprising the nucleic acid molecules, pharmaceutical compositions comprising the nucleic acid molecules or the modified filovirus GPs in a therapeutically effective dose, vaccine compositions comprising the nucleic acid molecules or the modified filovirus GPs in a prophylactically effective dose, antibodies that are specifically reactive with the modified filovirus GPs, and related methods of making and using the same.

Brief Description of the Drawings

Figure 1. **A)** VRC6612 (pCMV/R-Ebola GP (S/G) (G to A)/h) construct map (see human codon-optimized Ebola/Marburg plasmids in Table 2). **B)** Nucleotide sequence of VRC6612 (SEQ ID NO: 1).

Figure 2. **A)** VRC6615 (pCMV/R-Ebola GP (Z) (full length G to A)/h) construct map (see human codon-optimized Ebola/Marburg plasmids in Table 2). **B)** Nucleotide sequence of VRC6615 (SEQ ID NO: 2).

Figure 3. **A)** VRC6613 (pCMV/R-Ebola GP (S/G) (E to D)/h) construct map (see human codon-optimized Ebola/Marburg plasmids in Table 2). **B)** Nucleotide sequence of VRC6613 (SEQ ID NO: 3).

Figure 4. **A)** VRC6616 (pCMV/R-Ebola GP (Z) (full length E to D)/h) construct map (see human codon-optimized Ebola/Marburg plasmids in Table 2). **B)** Nucleotide sequence of VRC6613 (SEQ ID NO: 4).

Figure 5. **A)** VRC6712 (pCMV/R-Marburg/Angola GP/h) construct map (see human codon-optimized Ebola/Marburg plasmids in Table 2). **B)** Nucleotide sequence of VRC6712 (SEQ ID NO: 5).

Figure 6. **A)** VRC6713 (pCMV/R Marburg/Angola GP (G102A)/h) construct map (see human codon-optimized Ebola/Marburg plasmids in Table 2). **B)** Nucleotide sequence of VRC6713 (SEQ ID NO: 6).

Figure 7. **A)** pAdApt.Ebo.GP.FL.(Z).E71D (adenoviral adaptor plasmid-Ebola/Zaire GP (full length E71D)/h). **B)** Nucleotide sequence of pAdApt.Ebo.GP.FL.(Z).E71D (SEQ ID NO: 7). Upper case is the coding sequence Ebo.GP.FL.(Z).E71D, the boxed region shows the E71D mutation and restriction site sequences used for cloning are bold and underlined.

Figure 8. **A)** pAdApt.Ebo.GP.FL.(S/G).E71D (adenoviral adaptor plasmid-Ebola/(Sudan/Gulu) GP (full length E71D)/h). **B)** Nucleotide sequence of pAdApt.Ebo.GP.FL.(S/G).E71D (SEQ ID NO: 8). Upper case is the coding sequence Ebo.GP.FL.(S/G).E71D, the boxed region shows the E71D mutation and restriction site sequences used for cloning are bold and underlined.

Figure 9. Schematic representation of Ebola virus GP. The GP1 and GP2 subunits of GP are drawn to scale (residue numbers are indicated below the diagram). The positions of the signal sequence, conserved cysteine residues (S), the mucin-like region (region of O-linked glycosylation), the furin cleavage site, the fusion peptide, the coiled-coil domain, and the membrane spanning domain are indicated.

Figure 10. Elimination of GP cytopathic effects and expression of transmembrane-deleted protein. **A)** Expression of GP(ΔTM) in 293 cells. Ebola GP proteins from supernatants and cell lysates in (A) were visualized by SDS- PAGE and Western blot using a polyclonal antibody against Ebola GP. **B)** Elimination of cell rounding by GP(ΔTM). 293 cells were transfected with a plasmid encoding vector control, Ebola GP or Ebola GP(ΔTM). Cell monolayers were visualized under phase contrast using a Nikon 40X objective and photographed at 24 hours post transfection.

Figure 11. Comparative efficacy of GP and GP(ΔTM) for protection against Ebola virus challenge. **A)** Kaplan-Meier survival curve of macaques, immunized as indicated, and challenged with 1000 PFU of Ebola virus (1995 Zaire subtype) one month post immunization. The x-axis indicates weeks post-challenge. n=3 in different immunization groups except for the GP(Z)+NP (10^{12}) group, n=4, and Control, n=1. **B)** Immune responses in immunized animals. Left and middle panels: intracellular flow cytometry was performed to quantify TNF-α production from Ebola-specific $CD4^+$ or $CD8^+$ lymphocytes, respectively, from animals immunized as indicated. Immune responses were measured at 3 weeks post-immunization. Circle, diamond, square, triangle: responses for individual animals. Horizontal line: average of individual responses in the immunization group. Results represent the percent cytokine positive in the gated lymphocyte group and background stimulation (DMSO alone) has been subtracted from each sample. Right panel: ELISA titers of Ebola GP-specific antibodies in

serum of vaccinated animals collected at week 3 post-immunization. ELISA results represent endpoint dilution titers determined by optical density as described in Example 1.

Figure 12. Determination of lowest vaccine dose for immune protection against Ebola virus challenge by adenoviral vector vaccine. **A)** Kaplan-Meier survival curve of macaques: immunization and challenge were performed with the 1995 Zaire subtype Ebola virus as in Fig. 11A. **B)** Immune responses in immunized animals. Intracellular flow cytometry was performed to quantify TNF-α production from Ebola-specific CD4 (left panel) or CD8 (right panel) lymphocytes, respectively, from animals immunized as indicated. Immune responses were measured at 3 weeks post-immunization. Circle, diamond, square: responses for individual animals. Horizontal line: average of individual responses in the immunization group. Results represent the percent cytokine positive in the gated lymphocyte group and background stimulation (DMSO alone) has been subtracted from each sample (p-values obtained using unpaired Student's t-test. n. s. = not significant). **C)** Antibody responses in immunized animals. Anti-GP ELISA titers (left panel) and serum neutralizing antibody responses (right panel) were measured as described in Example 1.

Figure 13. Comparative efficacy of wild type and point mutant glycoprotein vaccines against lethal Ebola virus challenge. **A)** Kaplan-Meier survival curve of macaques: immunization and challenge were performed with the 1995 Zaire subtype Ebola virus as in Fig. 11A. **B)** Immune responses in immunized animals. Left and middle panels: intracellular flow cytometry was performed to quantify TNF-α production from Ebola-specific CD4 or CD8 lymphocytes, respectively, from animals immunized as indicated. Immune responses were measured at 3 weeks post-immunization. Circle, diamond, square: responses for individual animals. Horizontal line: average of individual responses in the immunization group. Results represent the percent cytokine positive in the gated lymphocyte group and background stimulation (DMSO alone) has been subtracted from each sample. Right panel: ELISA titers of Ebola GP-specific antibodies in serum of vaccinated animals collected at week 3 post-immunization. ELISA results represent endpoint dilution titers determined by optical density as described in Example 1.

Figure 14. Elimination of GP cytopathic effects with single point mutation. **A)** Expression of point mutants in 293 cells. Ebola GP proteins from supernatants and cell lysates in (A) were visualized by SDS- PAGE and Western blot using a polyclonal antibody against Ebola GP. **B)** Reactivity of point mutants with a conformation-dependent antibody. 293 cells were transfected with a control plasmid (Con), or plasmids expressing wild type (GP(Z)) or mutant (E71D(Z)) proteins. Eighteen hours post-transfection, cells were harvested,

stained with a GP-specific antibody and cell surface GP expression was analyzed by flow cytometry. C) Elimination of cell rounding by amino acid substitution at position 71. 293 cells were transfected with a plasmid encoding vector control, wild type Ebola glycoprotein from Zaire (GP(Z)) or Sudan-Gulu (GP(S/G)) or their respective point mutations (E71D(Z)), E71D(S/G)). Cell monolayers were visualized under phase contrast using a Nikon 40X objective and photographed at 24 hours post transfection.

Figure 15. Cellular immune responses generated in NHP immunized with GP(Z) E71D/NP.

Figure 16. Humoral immune responses generated in NHP immunized with GP(Z) E71D/NP.

Figure 17. Comparative efficacy of wild type GP vs. point mutant immunogens.

Figure 18. Elimination of GP cytopathic effects with single point mutation. Elimination of cell rounding by amino acid substitution at position 71 or 102. 293 cells were transfected with a plasmid encoding vector control, wildtype Ebola Zaire glycoprotein, WT GP, or point mutations 71E/D, 102G/A, 138V/A or a mutation in which the transmembrane domain is deleted, ΔTM. Cell monolayers were visualized under phase contrast using a Nikon 40X objective and photographed at 24 hours post transfection. Cell rounding is eliminated with mutation at residue 71 or 102, and with transmembrane deletion.

Figure 19. Single point mutation in GP and retention of reactivity with neutralizing antibodies. Reactivity of point mutants with a conformation-dependent antibody. 293 cells were transfected with a control plasmid, dashed line, or plasmids expressing wildtype Ebola GP (WT GP) or mutant (71E/D 102G/A), solid line, proteins. Eighteen hours post transfection, cells were harvested, stained with a GP-specific neutralizing antibody and cell surface GP expression was analyzed by flow cytometry.

Figure 20. Ebola Zaire GP amino acid sequence (SEQ ID NO: 9).

Table 1. Filovirus Genbank Accession Numbers

Virus	Subtype	Strain	"aa71"	"aa102"	Genbank Accession No.
Ebola	Ivory Coast	Coto d'Ivore- Tai Forest, 1994	E	G	U28006
	Reston	Reston, 1989	E	G	U23152, NC_004161, AF034645
		Philippines, 1989	E	G	U23416
		Pennsylvania	E	G	AY769362, AF522874
		Siena, 1992	E	G	U23417
		Texas, 1996			
	Sudan	Boniface, 1976	E	G	U28134
		Maleo, 1979	E	G	U23069, Q66798
		Gulu- Uganda, 2000-2001	E	G	AY729654, AY344234, AY316199
	Zaire	Mayinga- Zaire, 1976	E	G	AY142960, AF499101, AF272001, AF086833, U23187, NC_002549
		Zaire- Zaire, 1976	E	G	AY354458, U28077, U31033, P87666
		Eckron-Zaire, 1976	E	G	U81161
		Bouee-96	E	G	AY058898
		Tandala- Zaire, 1977			
		Kikwit- Zaire, 1995			
		Gabon- Zaire, 1994-1997	E	G	U77384
		Mendemba A, 2001	G	G	AY526105 (G at 71)
		Mvoula, 2003	E	G	AY526104
		Yembelengoye, 2002		G	AY526103 (partial seq, unknown at 71)
		Entsiami, 2002	G	G	AY526102 (G at 71)
		Makoukou, 2001	G	G	AY526101 (G at 71)
		Etkangaye, 2001	G	G	AY526100 (G at 71)
		Olloba	G	G	AY526099 (G at 71)
		Mendemba B, 2001	G	G	AY526098 (G at 71)
Marburg		Musoke- Kenya, 1980		G	Z12132
		Ratayczak- West Germany, 1967		G	AF005735
		Popp- West Germany, 1967		G	NC_001608, Z29337, X68493
		Voege- Yugoslavia, 1967			
Marburg (continued)		Ozolin- Zimbabwe, 1987		G	AY358025, AF005733

Virus	Subtype	Strain	"aa71"	"aa102"	Genbank Accession No.
		Ravn- Kenya, 1987		G	AF005734
		Angola, 2004-2005		G	(see Fig. 5 and SEQ ID NO: 5, human codon-optimized)
		pp3 guinea pig lethal variant		G	AY430365
		pp4 guinea pig nonlethal variant		G	AY430366

Table 2. Human Codon-Optimized Ebola/Marburg Plasmids

Construct	Construct Name/ Description	Construct Map Name	SEQ ID NO	Figure
VRC6612	pCMV/R-Ebola GP (S/G) (G to A)/h*	CMV/R-Ebola GP (S/G) (G to A)/h	1	1
VRC6615	pCMV/R-Ebola GP (Z) (full length G to A)/h	CMV/R-Ebola GP (Z) (full length G to A)/h	2	2
VRC6613	pCMV/R-Ebola GP (S/G) (E to D)/h	CMV/R-Ebola GP (S/G) (E to D)/h	3	3
VRC6616	pCMV/R-Ebola GP (Z) (full length E to D)/h	CMV/R-Ebola GP (Z) (full length E to D)/h	4	4
VRC6712	pCMV/R-Marburg/Angola GP/h	CMV/R-Marburg/Angola GP/h	5	5
VRC6713	pCMV/R Marburg/Angola GP (G102A)/h	CMV/R Marburg/Angola GP (G102A)/h	6	6
pAdApt.Ebo.GP.FL.(Z).E71D	pAdApt.Ebo.GP.FL.(Z).E71D (adenoviral adaptor plasmid-Ebola/Zaire GP (full length E71D)/h)	AdApt.Ebo.GP.FL.(Z).E71D (adenoviral adaptor plasmid-Ebola/Zaire GP (full length E71D)/h)	7	7
pAdApt.Ebo.GP.FL.(S/G).E71D	pAdApt.Ebo.GP.FL.(S/G).E71D (adenoviral adaptor plasmid-Ebola/(Sudan/Gulu) GP (full length E71D)/h)	AdApt.Ebo.GP.FL.(S/G).E71D (adenoviral adaptor plasmid-Ebola/(Sudan/Gulu) GP (full length E71D)/h)	8	8

*h = human codon-optimized

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Detailed Description of the Preferred Embodiment

In the absence of effective therapies for Ebola virus infection, the development of a vaccine becomes an important strategy to contain outbreaks. Immunization with DNA and/or replication-defective adenoviral (rAd) vectors encoding the Ebola glycoprotein (GP) and nucleoprotein (NP) has been previously shown to confer specific protective immunity in nonhuman primates (Sullivan, N. J. et al. 2000 *Nature* **408**:6O5-609; Sullivan, N. J. et al. 2003 *Nature* **424**:681-684). GP can exert cytopathic effects on transfected cells *in vitro* (Yang, Z.-Y. et al. 2000 *Nat Med* **6**:886-889) and multiple GP forms have been identified in nature, raising the question of which would be optimal for a human vaccine. To address this question, we have explored the efficacy of mutant GPs from multiple Ebola virus strains with reduced *in vitro* cytopathicity and analyzed their protective effects in the primate challenge model, with or without NP. Deletion of the GP transmembrane domain eliminated *in vitro* cytopathicity but reduced its protective efficacy by at least one order of magnitude. In contrast, single point mutations were identified that abolish *in vitro* cytopathicity but retained immunogenicity and conferred immune protection in the absence of NP. The minimal effective rAd dose was established at 10^{10} particles, two logs lower than used previously. Expression of specific GPs alone vectored by rAd are sufficient to confer protection against lethal challenge in a relevant nonhuman primate model, providing the basis for identification of a vaccine.

Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. See, *e.g.*, Singleton P and Sainsbury D., Dictionary of Microbiology and Molecular Biology 3rd ed., J. Wiley & Sons, Chichester, New York, 2001, and Fields Virology 4th ed., Knipe D.M. and Howley P.M. eds, Lippincott Williams & Wilkins, Philadelphia 2001.

Nucleic Acid Molecules

As indicated herein, nucleic acid molecules of the present invention may be in the form of RNA or in the form of DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

Nucleic acid molecules of the present invention include DNA molecules comprising an open reading frame (ORF) encoding a modified filovirus structural gene product; and DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode an ORF of a modified filovirus structural gene product. Of course, the genetic code is well known in the art. Degenerate variants optimized for human codon usage are preferred.

A filovirus structural gene product, *e.g.*, glycoprotein (GP), the sole structural protein making up the virion surface spikes that mediate virus entry into susceptible host cells through receptor binding, is modified by having at least one amino acid change that decreases *in vitro* cytotoxicity and retains immunogenicity when compared to *in vitro* cytotoxicity and immunogenicity of a wild type (*e.g.*, naturally occurring) filovirus GP. The amino acids of particular importance to the *in vitro* cytotoxicity are by no means limited to the exact position as defined for the, *e.g.*, Zaire strain of Ebola virus but are simply used in an exemplary manner to point out the preferred amino acids being at that position or corresponding to that position in other strains such as found in Sudan strain of Ebola virus or Angola strain of Marburg virus and filoviruses in general since they are highly conserved. For filoviruses other than the Ebola Zaire strain the numbering of the positions of the preferred amino acids is often different but an expert in the field of the molecular biology of filoviruses will easily identify these preferred amino acids by their position relative to the highly conserved amino acids of said glycoprotein.

The present invention is further directed to fragments of the nucleic acid molecules described herein. By a fragment of a nucleic acid molecule having the nucleotide sequence of an ORF encoding a modified filovirus structural gene product is intended fragments at least about 15 nt., and more preferably at least about 20 nt., still more preferably at least about 30 nt., and even more preferably, at least about 40 nt. in length. Of course, larger

fragments 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 nt. in length are also intended according to the present invention as are fragments corresponding to most, if not all, of the nucleotide sequence of the ORF encoding a modified filovirus structural gene product. By a fragment at least 20 nt. in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the ORF encoding a modified filovirus structural gene product.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of the filovirus structural protein. In particular, such nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing domains of a filovirus structural protein, where the domain is the N-terminal domain, the mucin-like domain, the furin cleavage site, the fusion peptide domain, the coiled-coli domain, the membrane spanning domain, and the intracellular domain, and any combination thereof, for example, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the membrane spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the coiled-coil domain and membrane-spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the fusion peptide domain, coiled-coil domain, and membrane-spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the furin cleavage site, fusion peptide domain, coiled-coil domain, and membrane-spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the mucin-like domain, furin cleavage site, fusion peptide domain, coiled-coil domain, and membrane-spanning and intracellular domain. Another example is a filovirus glycoprotein having an amino, internal, or carboxy deletion to delete the mucin-like domain, the furin cleavage site, the fusion peptide domain, the coiled-coil domain, the membrane-spanning domain, or the intracellular domain.

In another aspect, the invention provides a nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5 x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml

denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 x SSC at about 65°C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt.), and more preferably at least about 20 nt., still more preferably at least about 30 nt., and even more preferably about 30-70 nt. of the reference polynucleotide.

By a portion of a polynucleotide of "at least 20 nt. in length," for example, is intended 20 or more contiguous nucleotides from the nucleotide sequence of the reference polynucleotide. Of course, a polynucleotide which hybridizes only to a poly A sequence or a complementary stretch of T (or U) residues, would not be included in a polynucleotide of the invention used to hybridize to a portion of a nucleic acid of the invention, since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly A stretch or the complement thereof (*e.g.*, practically any double-stranded cDNA clone).

As indicated herein, nucleic acid molecules of the present invention which encode a filovirus structural gene product may include, but are not limited to those encoding the amino acid sequence of the full-length polypeptide, by itself, the coding sequence for the full-length polypeptide and additional sequences, such as those encoding a leader or secretory sequence, such as a pre-, or pro- or prepro-protein sequence, the coding sequence of the full-length polypeptide, with or without the aforementioned additional coding sequences, together with additional, non-coding sequences, including for example, but not limited to introns and non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences that play a role in transcription, mRNA processing, including splicing and polyadenylation signals, for example, ribosome binding and stability of mRNA; and additional coding sequence which codes for additional amino acids, such as those which provide additional functionalities.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of the filovirus structural gene product. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a genome of an organism. (*Genes II*, Lewin, B., ed., John Wiley & Sons, 1985 New York). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such variants include those produced by nucleotide substitutions, deletions or additions, which may involve one or more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the filovirus structural gene product or portions thereof. Also especially preferred in this regard are conservative substitutions.

Further embodiments of the invention include nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 95% identical, and more preferably at least 96%, 97%, 98% or 99% identical to a nucleotide sequence encoding a polypeptide having the amino acid sequence of a modified filovirus structural gene product or fragment thereof or a nucleotide sequence complementary thereto.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence encoding a filovirus structural gene product is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the Ebola virus structural gene product. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 95%, 96%, 97%, 98% or 99% identical to the reference nucleotide sequence can be determined conventionally using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711). Bestfit uses the local homology algorithm of Smith and Waterman 1981 *Advances in Applied Mathematics* **2**:482-489, to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for

instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

The present application is directed to nucleic acid molecules at least 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences described herein which encode a polypeptide having Ebola or Marburg polypeptide activity. By "a polypeptide having Ebola or Marburg, polypeptide activity" is intended polypeptides exhibiting Ebola or Marburg polypeptide activity in a particular biological assay. For example, GP polypeptide activity can be measured for changes in biological activity such as receptor binding activity, connection between GP1 and GP2, and contribution to the formation of the stalk structure of the virion peplomer, and modified GP polypeptide activity by decrease of *in vitro* cytotoxicity while retaining immunogenicity.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence described herein will encode a polypeptide "having Ebola or Marburg polypeptide activity". In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having Ebola or Marburg polypeptide activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (*e.g.*, replacing one aliphatic amino acid with a second aliphatic amino acid).

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al. 1990 *Science* **247**:1306-1310, wherein the authors indicate that proteins are surprisingly tolerant of amino acid substitutions.

Polypeptides and Fragments

The invention further provides a filovirus polypeptide having the amino acid sequence encoded by an open reading frame (ORF) of a modified filovirus structural gene, or a peptide or polypeptide comprising a portion thereof (*e.g.*, soluble GP).

It will be recognized in the art that some amino acid sequences of the filovirus polypeptides can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity.

Thus, the invention further includes variations of the filovirus polypeptide which show substantial filovirus polypeptide activity or which include regions of filovirus protein such as the protein portions discussed below. Such mutants include deletions, insertions, inversions, repeats, and type substitutions. As indicated, guidance concerning which amino acid changes are likely to be phenotypically silent can be found in Bowie, J.U. et al. 1990 *Science* **247**:1306-1310.

Thus, the fragment, derivative or analog of the polypeptide of the invention may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues include a substituent group, or (iii) one in which additional amino acids are fused to the mature polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the mature polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table A).

Table A. Conservative Amino Acid Substitutions

Aromatic	Phenylalanine Tryptophan Tyrosine
Ionizable: Acidic	Aspartic Acid Glutamic Acid
Ionizable: Basic	Arginine Histidine Lysine
Nonionizable Polar	Asparagine Glutamine Selenocystine Serine Threonine
Nonpolar (Hydrophobic)	Alanine Glycine Isoleucine Leucine Proline Valine
Sulfur Containing	Cysteine Methionine

Of course, the number of amino acid substitutions a skilled artisan would make depends on many factors, including those described above. Generally speaking, the number of amino acid substitutions for any given filovirus polypeptide will not be more than 50, 40, 30, 20, 10, 5 or 3.

Amino acids in the filovirus polypeptides of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham & Wells 1989 *Science* **244**:1081-1085). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as receptor binding activity, connection between GP1 and GP2, and contribution to the formation of the stalk structure of the virion peplomer, and modified GP polypeptide activity by decrease of *in vitro* cytotoxicity while retaining immunogenicity.

The polypeptides of the present invention are conveniently provided in an isolated form. By "isolated polypeptide" is intended a polypeptide removed from its native environment. Thus, a polypeptide produced and/or contained within a recombinant host cell is considered isolated for purposes of the present invention. Also intended as an "isolated polypeptide" are polypeptides that have been purified, partially or substantially,

from a recombinant host cell or a native source. For example, a recombinantly produced version of the filovirus polypeptide can be substantially purified by the one-step method described in Smith and Johnson 1988 *Gene* 67:31-40.

The polypeptides of the present invention include a polypeptide comprising a polypeptide having the amino acid sequence of a modified filovirus structural gene product or portion thereof or encoded by a nucleic acid sequence described herein; as well as polypeptides which are at least 95% identical, and more preferably at least 96%, 97%, 98%, or 99% identical to those described above and also include portions of such polypeptides with at least 30 amino acids and more preferably at least 50 amino acids.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a reference amino acid sequence of an filovirus polypeptide is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of the filovirus polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 95%, 96%, 97%, 98%, or 99% identical to a reference amino acid sequence can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

In another aspect, the invention provides portions of the polypeptides described herein with at least 30 amino acids and more preferably at least 50 amino acids. Preferred portions of the present invention include polypeptides comprising an epitope-bearing portion of a filovirus structural protein. In particular, preferred portions of the present invention include polypeptides comprising an epitope-bearing domain of a filovirus structural protein, where the domain is the N-terminal domain, the mucin-like domain, the furin cleavage site, the fusion peptide domain, the coiled-coil domain, the membrane-spanning domain, and the intracellular domain, and any combination thereof, for example, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the membrane spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the coiled-coil domain and membrane spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the fusion peptide domain, coiled-coil domain, and membrane-spanning and intracellular domain, a filovirus glycoprotein having a truncation at the carboxy terminus to delete the furin cleavage site, fusion peptide domain, coiled-coil domain, and membrane-spanning and intracellular domain, and a filovirus glycoprotein having a truncation at the carboxy terminus to delete the mucin-like domain, furin cleavage site, fusion peptide domain, coiled-coil domain, and membrane-spanning and intracellular domain. Another example is a filovirus glycoprotein having an amino, internal, or carboxy deletion to delete the mucin-like domain, the furin cleavage site, the fusion peptide domain, the coiled-coil domain, the membrane-spanning domain, or the intracellular domain.

The polypeptides of the invention may be produced by any conventional means (Houghten, R.A. 1985 *PNAS USA* **82**:5131-5135). The "Simultaneous Multiple Peptide Synthesis (SMPS)" process is described in U.S. Pat. No. 4,631,211 to Houghten et al. (1986).

The present invention also relates to vectors which include the nucleic acid molecules of the present invention, host cells which are genetically engineered with the recombinant vectors, and the production of filovirus polypeptides or fragments thereof by recombinant techniques.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus,

it may be packaged *in vitro* using an appropriate packaging cell line and then transduced into host cells.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiation at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline or ampicillin resistance genes for culturing *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60, and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pHN18A, pNH46A, available from Stratagene; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986).

The filovirus polypeptides can be recovered and purified from recombinant cell cultures by well known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

Antibodies

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for filovirus GP polypeptides or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a filovirus GP polypeptide exclusively (*i.e.*, are able to distinguish a filovirus GP polypeptide from related polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Antibodies A Laboratory Manual, Harlow et al. (Eds), Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the filovirus GP polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, a filovirus GP polypeptide of the invention from which the fragment was derived. The specific antibodies of the invention are envisioned as having utility for diagnostic purposes and passive immunization.

Use of Recombinant Virus to Induce Immune Response to Antigen

The present invention relates to generation of a CD8+ T cell immune response against an antigen and also eliciting an antibody response. More particularly, the present invention relates to "accelerated" immunization regimes in which the immune response is induced by administration of a single dose form and "prime and boost" immunization regimes in which the immune response induced by administration of a priming composition is boosted by administration of a boosting composition. The present invention, in one embodiment, is based on the inventors' experimental demonstration that effective immunization can be achieved using recombinant virus, *e.g.*, adenovirus, optionally as boosting compositions following priming with any of a variety of different types of priming compositions.

A major protective component of the immune response against a number of pathogens is mediated by T lymphocytes of the CD8+ type, also known as cytotoxic T lymphocytes (CTL). An important function of CD8+ cells is secretion of gamma interferon (IFNγ), and this provides a measure of CD8+ T cell immune response. A second component of the immune response is antibody directed to the proteins of the pathogen.

The present invention, in one embodiment, employs recombinant virus, *e.g.*, adenovirus, which, as the experiments described below show, has been found to be an effective means for inducing a CD8+ T cell immune response, optionally as a boosting composition primed by antigen using any of a variety of different priming compositions, and for eliciting an antibody response.

Replication-deficient adenovirus derived from human serotype 5 has been developed as a live viral vector by Graham and colleagues (Graham & Prevec 1995 *Mol Biotechnol* **3**:207-20; Bett et al. 1994 *PNAS USA* **91**:8802-6). Adenoviruses are non-enveloped viruses containing a linear double-stranded DNA genome of around 36 kb. Recombinant viruses can be constructed by *in vitro* recombination between an adenovirus genome plasmid and a shuttle vector containing the gene of interest together with a strong eukaryotic promoter, in a permissive cell line which allows viral replication. High viral titres can be obtained from the permissive cell line, but the resulting viruses, although capable of infecting a wide range of cell types, do not replicate in any cells other than the permissive line, and are therefore a safe antigen delivery system. Recombinant adenoviruses have been shown to elicit protective immune responses against a number of

antigens including tick-borne encephalitis virus NS1 protein (Jacobs et al. 1992 *J Virol* **66**:2086-95) and measles virus nucleoprotein (Fooks et al. 1995 *Virology* **210**:456-65).

Remarkably, the experimental work described below demonstrates that use of embodiments of the present invention allows for recombinant adenovirus expressing an antigen to induce an immune response, optionally as a boosting composition primed by a DNA vaccine. The adenovirus was found to induce an immune a CD8+ T cell and antibody response after intramuscular immunization. In prime/boost vaccination regimes the recombinant virus, *e.g.*, adenovirus, is also envisioned as being able to prime an immune response that can be boosted by a different recombinant virus or recombinantly produced antigen.

Non-human primates immunized with recombinant virus, *e.g.*, adenovirus, optionally as a boosting composition following priming with plasmid DNA were protected against challenge. Both recombinant adenovirus and plasmid DNA are vaccines that are safe for use in humans. Advantageously, the inventors found that a vaccination regime using single dose immunization, optionally prime and boost immunization, can be employed, constituting a general immunization regime suitable for inducing an immune response, *e.g.*, in humans.

The present invention in various aspects and embodiments employs a recombinant virus, *e.g.*, adenovirus, encoding an antigen for inducing an immune response to the antigen, optionally for boosting an immune response primed by previous administration of the antigen or nucleic acid encoding the antigen.

A general aspect of the present invention provides for the use of a recombinant virus, *e.g.*, adenovirus, for inducing, optionally boosting an immune response to an antigen.

One aspect of the present invention provides a method of inducing, optionally boosting an immune response to an antigen in an individual, the method including provision in the individual of a recombinant virus, *e.g.*, adenovirus, including nucleic acid encoding the antigen operably linked to regulatory sequences for production of antigen in the individual by expression from the nucleic acid, whereby an immune response to the antigen is induced or an immune response to the antigen previously primed in the individual is boosted.

An immune response to an antigen may be primed by plasmid DNA immunization, by infection with an infectious agent, or by development of a recombinantly produced antigen.

A further aspect of the invention provides a method of inducing an immune response to an antigen in an individual, the method comprising administering to the individual a single dose of composition comprising the antigen or nucleic acid encoding the antigen or a priming composition comprising the antigen or nucleic acid encoding the antigen and then administering a boosting composition which comprises a recombinant virus, *e.g.*, adenovirus, including nucleic acid encoding the antigen operably linked to regulatory sequences for production of antigen in the individual by expression from the nucleic acid.

A further aspect provides for use of a recombinant virus, *e.g.*, adenovirus, as disclosed, in the manufacture of a medicament for administration to a mammal to induce, optionally to boost an immune response to an antigen. Such a medicament is optionally for administration in single dose form or following prior administration of a priming composition comprising the antigen or nucleic acid encoding the antigen.

The inducing, boosting, or priming composition may comprise any viral vector, including adenoviral, or other than adenoviral, such as a vaccinia virus vector such as a replication-deficient strain such as modified virus Ankara (MVA) (Mayr et al. 1978 *Zentralbl Bakteriol* **167**:375-90; Sutter and Moss 1992 *PNAS USA* **89**:10847-51; Sutter et al. 1994 *Vaccine* **12**:1032-40) or NYVAC (Tartaglia et al. 1992 *Virology* **118**:217-32), an avipox vector such as fowlpox or canarypox, *e.g.*, the strain known as ALVAC (Kanapox, Paoletti et al. 1994 *Dev Biol Stand* **82**:65-9), a herpes virus vector, a vesicular stomatitis virus vector, or an alphavirus vector.

The inducing or priming composition may comprise DNA encoding the antigen, such DNA preferably being in the form of a circular plasmid that is not capable of replicating in mammalian cells. Any selectable marker should not be resistant to an antibiotic used clinically, so for example Kanamycin resistance is preferred to Ampicillin resistance. Antigen expression should be driven by a promoter which is active in mammalian cells, for instance the cytomegalovirus immediate early (CMV IE) promoter.

In particular, prime and boost embodiments of the various aspects of the present invention, administration of a priming composition is followed by boosting with a boosting composition or first and second boosting compositions, the first and second boosting compositions being the same or different from one another. Still further boosting compositions may be employed without departing from the present invention. In one embodiment, a triple immunization regime employs DNA, then adenovirus as a first

boosting composition, and then MVA as a second boosting composition, optionally followed by a further (third) boosting composition or subsequent boosting administration of one or other or both of the same or different vectors. Another option is DNA then MVA then adenovirus, optionally followed by subsequent boosting administration of one or other or both of the same or different vectors.

The antigen to be included in respective priming and boosting compositions (however many boosting compositions are employed) need not be identical, but should share epitopes. The antigen may correspond to a complete antigen in a target pathogen or cell, or a fragment thereof. Peptide epitopes or artificial strings of epitopes may be employed, more efficiently cutting out unnecessary protein sequence in the antigen and encoding sequence in the vector or vectors. One or more additional epitopes may be included, for instance epitopes which are recognized by T helper cells, especially epitopes recognized in individuals of different HLA types.

Within the recombinant virus, *e.g.*, adenovirus, regulatory sequences for expression of the encoded antigen will include a promoter. By "promoter" is meant a sequence of nucleotides from which transportation may be initiated of DNA operably linked downstream (*i.e.*, in the 3' direction on the sense strand of double-stranded DNA). "Operably linked" means joined as part of the same nucleic acid molecule, suitably positioned and oriented for transcription to be initiated from the promoter. DNA operably linked to a promoter is "under transcriptional initiation regulation" of the promoter. Other regulatory sequences including terminator fragments, polyadenylation sequences, enhancer sequences, marker genes, internal ribosome entry site (IRES) and other sequences may be included as appropriate, in accordance with the knowledge and practice of the ordinary person skilled in the art: see, for example, Molecular Cloning: a Laboratory Manual, 2nd edition, Sambrook et al. 1989 Cold Spring Harbor Laboratory Press. Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in Current Protocols in Molecular Biology, Ausubel et al. eds., John Wiley & Sons, 1994.

Suitable promoters for use in aspects and embodiments of the present invention include the cytomegalovirus immediate early (CMV IE) promoter, with or without intron A, and any other promoter that is active in mammalian cells.

Adjuvants suitable for co-administration in accordance with the present invention should be ones that are potentially safe, well tolerated and effective in people including QS-21, Detox-PC, MPL-SE, MoGM-CSF, TiterMax-G, CRL-1005, GERBU, TERamide, PSC97B, Adjumer, PG-026, GSK-1, GcMAF, B-alethine, MPC-026, Adjuvax, CpG ODN, Betafectin, Alum, and MF59 (see Kim et al., 2000 *Vaccine* **18**:597 and references therein).

Other contemplated adjuvants that may be administered include lectins, growth factors, cytokines and lymphokines such as alpha-interferon, gamma interferon, platelet derived growth factor (PDGF), granulocyte-colony stimulating factor (gCSF), granulocyte macrophage colony stimulating factor (gMCSF), tumor necrosis factor (TNF), epidermal growth factor (EGF), IL-1, IL-2, IL-4, IL-6, IL-8, IL-10, and IL-12 or encoding nucleic acids therefore.

Administration of the boosting composition is generally weeks or months after administration of the priming composition, preferably about 2-3 weeks or 4 weeks, or 8 weeks, or 16 weeks, or 20 weeks, or 24 weeks, or 28 weeks, or 32 weeks.

Preferably, administration of single dose composition, boosting composition, or priming composition is intramuscular immunization.

Intramuscular administration of adenovirus vaccines or plasmid DNA may be achieved by using a needle to inject a suspension of the virus or plasmid DNA. An alternative is the use of a needless injection device to administer a virus or plasmid DNA suspension (using, *e.g.*, Biojector™) or a freeze-dried powder containing the vaccine (*e.g.*, in accordance with techniques and products of Powderject), providing for manufacturing individually prepared doses that do not need cold storage. This would be a great advantage for a vaccine that is needed in rural areas of Africa.

Adenovirus is a virus with an excellent safety record in human immunizations. The generation of recombinant viruses can be accomplished simply, and they can be manufactured reproducibly in large quantities. Intramuscular administration of recombinant adenovirus is therefore highly suitable for prophylactic or therapeutic vaccination of humans against diseases which can be controlled by an immune response.

The individual may have a disease or disorder such that delivery of the antigen and generation of an immune response to the antigen is of benefit or has a therapeutically beneficial effect.

Most likely, administration will have prophylactic aim to generate an immune response against a pathogen or disease before infection or development of symptoms.

Diseases and disorders that may be treated or prevented in accordance with the present invention include those in which an immune response may play a protective or therapeutic role.

Components to be administered in accordance with the present invention may be formulated in pharmaceutical compositions. These compositions may comprise a pharmaceutically acceptable excipient, carrier, buffer, stabilizer or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The precise nature of the carrier or other material may depend on the route of administration, *e.g.*, intravenous, cutaneous or subcutaneous, intramucosal (*e.g.*, gut), intranasal, intramuscular, or intraperitoneal routes.

As noted, administration is preferably intradermal, subcutaneous or intramuscular.

Liquid pharmaceutical compositions generally include a liquid carrier such as water, petroleum, animal or vegetable oils, mineral oil or synthetic oil. Physiological saline solution, dextrose or other saccharide solution or glycols such as ethylene glycol, propylene glycol or polyethylene glycol may be included.

For intravenous, cutaneous or subcutaneous injection, or injection at the site of affliction, the active ingredient will be in the form of a parenterally acceptable aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of relevant skill in the art are well able to prepare suitable solutions using, for example, isotonic vehicles such as Sodium Chloride Injection, Ringer's Injection, Lactated Ringer's Injection. Preservatives, stabilizers, buffers, antioxidants and/or other additives may be included, as required.

A slow-release formulation may be employed.

Following production of adenoviral particles and optional formulation of such particles into compositions, the particles may be administered to an individual, particularly human or other primate.

Administration may be to another mammal, *e.g.*, rodent such as mouse, rat or hamster, guinea pig, rabbit, sheep, goat, pig, horse, cow, donkey, dog or cat.

Administration is preferably in a "prophylactically effective amount" or a "therapeutically effective amount" (as the case may be, although prophylaxis may be considered therapy), this being sufficient to show benefit to the individual. The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of what is being treated. Prescription of treatment, *e.g.*, decisions on dosage

etc., is within the responsibility of general practitioners and other medical doctors, or in a veterinary context a veterinarian, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of the techniques and protocols mentioned above can be found in Remington's Pharmaceutical Sciences, 16th edition, Osol, A. ed., 1980.

In one preferred regimen, DNA is administered (preferably intramuscularly) at a dose of 10 micrograms to 50 milligrams/injection, followed by adenovirus (preferably intramuscularly) at a dose of 5×10^7 - 1×10^{12} particles/injection.

The composition may, if desired, be presented in a kit, pack or dispenser, which may contain one or more unit dosage forms containing the active ingredient. The kit, for example, may comprise metal or plastic foil, such as a blister pack. The kit, pack, or dispenser may be accompanied by instructions for administration.

A composition may be administered alone or in combination with other treatments, either simultaneously or sequentially dependent upon the condition to be treated.

Delivery to a non-human mammal need not be for a therapeutic purpose, but may be for use in an experimental context, for instance in investigation of mechanisms of immune responses to an antigen of interest, *e.g.*, protection against disease or pathogens.

Specific Modifications of Ebola GP Optimize Vaccine Efficacy in Nonhuman Primates

To develop an optimal Ebola vaccine using rAd vectors, we first analyzed mutant forms of GP in which the transmembrane domain had been removed. Though we have previously reported that deletion of the mucin domain eliminates cytotoxicity (Yang, Z.-Y. et al. 2000 *Nat Med* **6**:886-889), this deletion removes nearly 200 amino acids, eliminating many potential T- and B-cell epitopes. Previous data suggested that the *in vitro* cytopathic effects of GP may be mediated at or near the cell surface and require transmembrane anchoring of the protein (Sullivan, N. J. et al. 2005 *J Virol* **79**:547-553; Takada, A. et al. 2000 *Virology* **278**:20-26; Chan, S. Y. et al. 2000 *J Gen Virol* **81**:2155-2159). An alternative approach to the elimination of the GP-induced cytopathic effects was therefore explored by removal of the 26 amino acid putative transmembrane and cytoplasmic domains.

Diminished immune protection of a mutant GP lacking a transmembrane anchor domain

GP protein was readily detected in the supernatants of cells transfected with the transmembrane-deleted vector ΔTM(Z), confirming its secretion, in contrast to supernatants from cells transfected with the wild type GP(Z) (Fig. 10A). Furthermore, synthesis of the two previously defined forms of GP, generated by post-translational processing (Volchkov, V. E. et al. 1995 *Virology* **214**:421-430; Sanchez, A. et al. 1998 *J Virol* 72:6442-6447), was readily detected at comparable levels. Deletion of the transmembrane domain eliminated GP-induced cytopathicity in transfected 293 cells in contrast to wild type GP (Fig. 10B), but total ΔTM expression was equivalent to wild type protein levels (Fig. 10A). To determine whether the ΔTM mutant of the Zaire strain could protect against infectious Ebola challenge, cynomolgus macaques were immunized with rAd vectors encoding NP and either ΔTM(Z), or GP(Z). Immunization with GP(Z) + NP protected all animals vaccinated with either 10^{11} or 10^{12} adenoviral particles and challenged with 1000 pfu of the Zaire strain of Ebola virus 28 days later (Fig. 11A). In contrast, survival frequencies decreased in animals receiving the ΔTM(Z) vaccine. In the group vaccinated with 10^{12} adenoviral particles, protective immunity was decreased by 33% and at 10^{11}, by 66%, indicating a substantial decrease in efficacy in animals vaccinated with ΔTM + NP vs GP + NP ($p < 0.05$). In a separate experiment, 10^{11} particles of ΔTM alone failed to protect against infection. Analysis of cell-mediated immune responses showed that $CD4^+$ and $CD8^+$ T-cell responses were present in the majority of animals by 3 weeks post-immunization (Fig. 11B, left and middle panels, respectively) and did not correlate with the differences in survival: antigen specific cellular responses measured by intracellular cytokine (TNF-α) secretion were indistinguishable between GP(Z)- and ΔTM(Z)-vaccinated animals. Similarly, humoral immune responses measured by anti-Ebola GP ELISA IgG titers were comparable in all vaccinated animals (Fig. 11B, right panel). Neutralizing antibody titers were low, and were absent in some surviving animals. These results suggested that deletion of the GP transmembrane domain reduces vaccine efficacy, with no readily apparent correlates of protection.

Definition of minimal protective vaccine dose for protection with a rAd vaccine encoding GP and NP

In the previous experiment, a log decrease in dose of the GP(Z) + NP vaccine was protective, in comparison to previous studies using 10^{12} rAd particles. To establish the

lowest dose of adenoviral vectors that would afford protection against Ebola infection, a dose-response analysis was performed. Animals were immunized with rAd vectors encoding GP(Z) and NP at increasing doses from 10^9 to 10^{12} particles per animal. Survival was 100% in all groups receiving a dose of 10^{10} or greater, whereas challenge infection was uniformly lethal in the 10^9 dose group (Fig. 12A). Virus isolation by plaque assay on Vero cells was negative for all surviving animals. Pre-challenge $CD4^+$ T-cell responses for TNF-α were unremarkable as reported previously for immunized cynomolgus macaques (Fig. 12B). $CD8^+$ T-cell responses were similar across vaccine dose groups, except for the higher responder immunized at 10^{12} rAd particles. Antigen-specific IgG was also generated in immunized animals, and the levels were equivalent among animals in the groups that survived Ebola virus challenge (Fig. 12C, left). However, there was a difference in more than one log ($p=0.004$) in IgG levels between survivors immunized at 10^{10} and fatalities immunized at 10^9 rAd particles, suggesting that such levels may correlate with protection for this immunization regimen. Neutralizing antibody titers against GP did not differ significantly between survivors and fatalities (Fig. 12C, right). These results indicated that the threshold for immune protection lies at about ~10^{10} rAd particles. Therefore, subsequent experiments were carried out using this dose to increase sensitivity to detect differences in antigenic strength between various immunogens.

Identification of GP point mutants with diminished *in vitro* cytotoxicity that confer effective immune protection

We sought to identify other mutants of GP that do not exhibit cytopathic effects yet retain native antigenic structures when expressed *in vitro*. Relatively conserved regions of GP were identified, and point mutations were systematically introduced. GP proteins bearing single amino acid changes were screened for decreased induction of cell rounding but wild type levels of expression and reactivity with conformation-dependent antibodies. Substitution of aspartic for glutamic acid at position 71 in Ebola GP from the Zaire or Sudan/Gulu subtypes (E71D(Z), E71D(S/G), respectively) abolished the cell rounding phenotype in transfected 293 cells but did not alter protein expression or reactivity with antibodies whose binding properties are sensitive to changes in protein conformation (Fig. 14).

The E71D mutants were evaluated for their ability to induce protective immunity alone or in combination with NP. When E71D from Zaire and Sudan-Gulu were combined with NP, survival of cynomolgus macaques immunized in these groups was diminished by

33% and 66%, respectively (Fig. 13A). In contrast, complete protection was achieved in animals immunized with E71D(Z) and E71D(S/G), as it was in animals receiving wild type GP(Z) plus NP. Ebola GP-specific responses in T-lymphocytes detected by intracellular staining of TNF-α did not show statistically significant differences in the $CD4^+$ population between different immunization groups (Fig. 13B, left panel). Similarly, individual differences in the $CD8^+$ response did not correlate with survival, though there was a trend toward diminished survival in groups with lower antigen-specific $CD8^+$ cellular responses (Fig. 13B, middle panel. Antigen-specific ELISA IgG was also stimulated in all immunized animals (Fig. 13B, right panel). The results of this experiment illustrate that NP may not be necessary for protective immunity against Ebola infection and that it may diminish protection when combined with modified GP immunogens at the lower limits of protective vaccine doses.

Ebola virus outbreaks are associated with high lethality due to the absence of treatment options or a licensed vaccine. Both DNA priming and rAd vector boosting, as well as rAd alone can confer protection to lethal challenge in an animal model that closely parallels human disease (Geisbert, T. W. et al. 2003 *Am J Pathol* **163**:2347-2370). The rAd vector vaccine conferred protection in an accelerated vaccine regimen in nonhuman primates (Sullivan, N. J. et al. 2003 *Nature* **424**:681-684). Although *in vitro* cytopathicity has been observed by over expression of Ebola GP, one of the vaccine components, we have not seen toxicity in animals vaccinated by vectors expressing Ebola GP. However, because this hypothetical complication has been raised, we sought to modify GP to eliminate *in vitro* cytopathicity yet retain antigenic properties that are necessary for protective immunity. Here, the efficacies of different forms of GP were evaluated using doses at the threshold of protection in the accelerated vaccination model. We have identified a vaccine with decreased *in vitro* cytopathicity that retained immunogenicity necessary to protect against Ebola infection.

We find that alternative forms of GP confer differential immune protection. Deletion of the GP transmembrane domain abolished cytopathic effects in transfected 293 cells, but the corresponding ΔTM(Z) vaccine was less efficacious than wild type GP(Z) in protecting nonhuman primates against infection. Though cellular and humoral immune responses were indistinguishable between groups receiving the different immunogen forms, the inherent variability in quantitating the responses in outbred macaques may obscure our ability to identify immune responses responsible for higher survival. Alternatively,

ΔTM(Z) may differ from wild type GP(Z) in antigenic qualities that are not captured by measurements of total antigen-specific IgG or intracellular cytokine responses stimulated by a broad peptide pool. For example, the transmembrane-deleted protein is secreted and likely shows conformational differences from the membrane anchored protein. Subsequent modifications of the glycoprotein to retain membrane attachment and a more native envelope structure yielded a mutant, E71D, with reduced *in vitro* cytopathicity. Recently, it has been suggested that this region of GP contributes to viral receptor binding (Manicassamy, B. et al. 2005 *J Virol* **79**:4793-4805). It is noteworthy that the envelope glycoprotein cytopathicity of other viruses such as HIV is linked to receptor binding and fusion (Cao, J. et al. 1996 *J Virol* **70**:1340-1354), raising the possibility that Ebola GP shares similar properties.

Ongoing outbreaks of both Ebola and Marburg viruses illustrate the importance of developing a filovirus vaccine for human use. This report shows that protective immunity against Ebola infection is achieved in nonhuman primates by the generation of antigen-specific immune responses to a single protein, GP, which has been modified to eliminate *in vitro* cytopathic effects. The accelerated vaccine strategy has since been repeated using vesicular stomatitis virus (VSV) vectors (Jones S. M. et al. 2005 *Nat Med*, published online June 5, 2005), validating the promise of vaccines for Ebola. However, there are concerns about the use of VSV as a human vaccine because it is replication-competent and derives from a virus that is pathogenic in animals. In contrast, the rAd vector vaccine is non-replicating, can be manufactured to high yields, and safety data exist for this platform. Immunity follows a single injection with 10^{10} rAd particles, a dose that is two orders of magnitude lower than previously reported for this single modality vaccine. Such doses of rAd vectors have proven to be well-tolerated and immunogenic for other recombinant genes *in vivo* and can be evaluated for the vectors reported here, alone or in DNA prime/rAd boost combinations. Immunization with 10^{10} rAd particles of E71D(Z) + E71D(S/G) was effective against infectious challenge with Ebola Zaire, and protection did not require NP. Elimination of NP from the vaccine and dose reductions to 10^{10} rAd particles do not diminish protection and simplify the vaccine for future development in human trials.

Example 1

Vector construction and transfections

E1/E3-deleted, replication-incompetent Ad5 vectors were generated in PER.C6® cells (Fallaux, F. J. et al. 1998 *Hum Gene Ther* **9**:1909-1917) using a pBR322-based

adaptor plasmid pAdApt together with cosmid pWE.Ad.AflIII-rITRΔE3 essentially as described elsewhere (Havenga, M. J. et al. 2001 *J Virol* **75**:3335-3342). The adaptor plasmid contained the left portion of the Ad5 genome (nucleotides 1-454), followed by transcriptional control elements and the adaptor Ad5 DNA region (nucleotides 3511-6095 in Ad5). Ebola GP encoding genes were cloned into the expression cassette in the adaptor plasmids under transcriptional control of the human full-length immediate-early CMV promoter and the SV40 polyadenylation signal. Adenoviruses containing Ebola GP, GPΔTM, and point mutations were generated by cotransfection of linearized pAdApt-Ebola GP plasmids together with the linearized cosmid pWE.Ad.AflIII-rITRΔE3 containing the right portion of the Ad5 genome to PER.C6® cells using Lipofectamine (Invitrogen). PER.C6® cells were cultured in DMEM supplemented with 10% fetal bovine serum (GIBCO) and incubated at 37°C under humified atmosphere and 10% CO_2. Homologous recombination led to the generation of rAd5-Ebola GP viruses. Adenoviral vectors in crude lysates were plaque purified using limiting dilutions and agar overlays, and Ad vector clones were analyzed for presence and expression of the transgene. Positive clones were amplified for large-scale production using PER.C6® cells in 48 triple-layer 3x175 cm^2 flasks. Viruses were purified by standard two-step CsCl gradient ultracentrifugation and subsequently desalted and formulated by three consecutive dialysis steps into TRIS-Cl pH 8.0 containing 2.5% glycerol. Purified Ad vectors were stored as single use aliquots at -80°C. Virus particle (vp) titers were determined by anion-exchange high-performance liquid chromatography based on described procedures (Shabram, P. W. et al. 1997 *Hum Gene Ther* **8**:453-465). Infectivity was assessed by TCID50 using 911 cells. Ebola GP expression was assessed by infection of A549 cells followed by analysis of culture lysates on western blot. The identity of the purified vectors was confirmed by PCR. Expression vectors p1012, pGP and pΔTM and point mutants contain a CMV enhancer promoter that have been described previously (Sullivan, N.J. et al. 2000 *Nature* **408**:605-609). The pΔTM contains a deletion from amino acid 651 to 676 and was created by digesting with BspMI/Klenow, and then fusing to TGA. The resulting plasmid also contained four extra amino acids at the C-terminus (MAAS). 293 human embryonal kidney cells were cultured in DMEM supplemented with 10% fetal bovine serum (GIBCO). Transfections to measure protein expression and cell rounding were performed in 293 cells with 2μg DNA per well of a 6-well plate using calcium phosphate (Invitrogen) according to the manufacturer's

instructions. Protein expression was evaluated by SDS-PAGE followed by Western blot with a GP-specific antibody kindly provided by A. Sanchez.

Animal study and safety

Cynomolgus macaques (*M. fascicularis*), 3-5 years old and weighing 2-3 kg, obtained from Covance, were used for immunization and challenge experiments. The monkeys, housed singly, were anesthetized with ketamine to obtain blood specimens and to administer vaccines. In conducting this research, the investigators adhered to the *Guide for the Care and Use of Laboratory Animals*, prepared by the Institute of Laboratory Animal Resources, National Research Council (National Academy Press, Washington, D.C., 1996). The facilities are fully accredited the Association for Assessment and Accreditation of Laboratory Animal Care International. They received regular enrichment according to the Guide for the Care and Use of Laboratory Animals (DHEW No. NIH 86-23). Before Ebola virus challenge and to the end of each experiment, the animals were maintained in the Maximum Containment Laboratory (BSL-4) and fed and checked daily.

Macaque immunization and challenge

Cynomolgus macaques were injected intramuscularly with a 1.0 ml equal mixture of immungens at the doses indicated. Viral challenge was performed by inoculation of animals in the left or right caudal thigh with 0.5 ml of viral stock that contained a target dose of ~1000 PFU EBOV (Zaire species) at four weeks after the initial immunization. No adverse effects of the adenovirus vaccination were observed acutely. The Ebola virus used in this study was originally obtained from a fatally infected human from the former Zaire in 1995 (Jahrling, P. B. et al. 1996 *Arch Virol Suppl* **11**:135-140). Collection of serum and blood for viral load and ELISA titers was performed as previously described (Sullivan, N.J. et al. 2000 *Nature* **408**:605-609).

Flow cytometry and antibodies

Transfected cells were collected after incubation with PBS (3 mM EDTA) and incubated with control Ig or rabbit anti-sGP/GP serum (generously provided by Dr. A. Sanchez) for 30 minutes on ice. The cells were washed twice with ice-cold PBS containing 2.5% fetal bovine serum, incubated with FITC- or PE-conjugated secondary antibodies (Jackson ImmunoResearch Laboratories and Sigma, respectively) for 30 minutes on ice, followed by washing. Analysis was conducted using a Becton Dickinson 4-color Calibur flow cytometer and FlowJo analysis software (Tree Star, Inc).

ELISA

Nunc-Immuno Maxisorp plates (Nunc, Rochester, NY) were coated with Ebola GP from 293 cell supernatants and incubated at 4°C until use. All further incubations were carried out at room temperature. Plates were then washed six times with PBS containing Tween 20. Test sera were diluted in PBS containing Tween 20 and 1% fetal calf serum and allowed to react with the Ag-coated wells for 60 minutes. After washing plates six times, goat anti-human IgG (H+L; Chemicon, Temecula, CA) conjugated to horseradish peroxidase was used as a detection antibody. Bound IgG was detected by Sigma Fast o-Phenylenediamine Dihydrochloride Tablet Sets (Sigma-Aldrich, St. Louis, MO) and the optical density was determined. A panel of normal sera was run each time the assay was performed.

Neutralizing antibody analysis

Ebola GP(Z) pseudotyped lentiviral virions were produced as previously described (Yang, 2004 *J Virol* **78**:5642-5650). Briefly, 293T cells were plated in 10-cm-diameter tissue culture dishes and transfected the next day by calcium phosphate reagent (Invitrogen) with pCMVΔR8.2, pHR'CMV-Luc and CMV/R Ebola GP(Z) plasmid DNA. Cells were transfected overnight, washed, and replenished with fresh medium. Forty-eight hours later, supernatants containing pseudotyped virus were harvested, filtered through a 0.45-μm-pore-size syringe filter, and stored in aliquots at -80°C. Neutralization assays were performed on HUVECs (Cambrex CC-2517) plated in a 24 well plate 1 day prior to infection. Virus stocks were incubated at 37°C for 1 hour in the presence of serum from immunized cynomolgus macaques. The culture media was removed from the cells and replaced with the virus/serum media in the presence of polybrene (Sigma-Aldrich, 107689) at a final concentration of 5 ug/mL. 72 hours post infection cells were lysed and assayed by Luciferase Assay System (Promega, E1501/E1531). Luciferase activity was determined using a Veritas Microplate Luminometer from Turner Biosystems.

Intracellular cytokine analysis

Peripheral blood mononuclear cells (PBMC) were isolated from cynomolgus macaque whole blood samples by separation over Ficoll. Approximately 1 x 10^6 cells were stimulated in 200 μl RPMI medium (GIBCO) for 6 hours at 37°C with anti-CD28 and -CD49d antibodies, brefeldin A, and either DMSO or a pool of 15-mer peptides spanning the Ebola GP Zaire (Mayinga strain) open reading frame. The peptides were 15-mers overlapping by 11 spanning the entire Ebola glycoprotein at a final concentration of 2

μg/ml. Cells were fixed and permeablized with FACS Lyse (Becton Dickinson) supplemented with Tween 20, and stained with a mixture of antibodies against lineage markers (CD3-PE, CD4-PerCP, CD8-FITC) and either TNF-APC. Samples were run on a FACS Calibur or FACS Aria and analyzed using the software FlowJo. Positive gating for lymphocytes using forward vs. side scatter was followed by $CD3^{+}/CD8^{-}$ and $CD3^{+/}CD4^{-}$ gating, and specific populations were further defined by anti-CD4 and anti-CD8 positivity, respectively. Cytokine positive cells were defined as a percentage within these individual lymphocyte subsets and at least 200,000 events were analyzed for each sample.

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While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention. All figures, tables, and appendices, as well as patents, applications, and publications, referred to above, are hereby incorporated by reference.

WHAT IS CLAIMED IS:

1. A nucleic acid molecule comprising a polynucleotide encoding a modified filovirus glycoprotein (GP) having at least one amino acid change located in a relatively conserved region of said GP that decreases *in vitro* cytotoxicity and retains immunogenicity when compared to *in vitro* cytotoxicity and immunogenicity of a wild type filovirus GP.

2. The nucleic acid molecule of Claim 1, wherein said amino acid change is positioned in the N-terminal domain, excluding the conserved cysteine residues, and is located at amino acid position 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 or 300 in Ebola Zaire GP in an exemplary manner or corresponding thereto in other strains of said GP.

3. The nucleic acid molecule of Claim 2, wherein said amino acid change is located at amino acid position 71 or 102 in Ebola Zaire GP in an exemplary manner or corresponding thereto in other strains of said GP.

4. The nucleic acid molecule of Claim 3, whereinsaid amino acid change is E71D or G102A in Ebola Zaire GP in an exemplary manner or corresponding thereto in other strains of said GP.

5. The nucleic acid molecule of Claim 4, wherein said modified filovirus GP is encoded by the insert of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8, or sequence having at least 95% identity thereto.

6. The nucleic acid molecule of Claim 5, wherein said polynucleotide encoding said modified filovirus GP has a sequence taken from the insert of SEQ ID NO:1, SEQ ID

NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8, or sequence having at least 95% identity thereto.

7. A modified filovirus GP encoded by the nucleic acid molecule of any of Claims 1-6.

8. A plasmid DNA comprising the nucleic acid molecule if any of Claims 1-6.

9. A recombinant virus comprising the nucleic acid molecule if any of Claims 1-6.

10. An adenovirus comprising the nucleic acid molecule if any of Claims 1-6.

11. A pharmaceutical composition comprising the nucleic acid molecule of any of Claims 1-6 or the modified filovirus GP of Claim 7 in a therapeutically effective dose.

12. A vaccine composition comprising the nucleic acid molecule of any of Claims 1-6 or the modified filovirus GP of Claim 7 in a prophylactically effective dose.

13. The composition of Claim 11 or 12 further comprising an adjuvant.

14. An antibody that is specifically reactive with the modified filovirus GP of Claim 7.

15. A method of boosting an immune response to an antigen in a primate, the method comprising provision in the primate of the modified filovirus GP of Claim 7 or the recombinant virus of Claim 8, whereby an immune response to the antigen previously primed in the primate is boosted.

16. A method of inducing an immune response to an antigen in a primate, the method comprising provision in the primate of the nucleic acid molecule of any of Claims 1-6 or the modified filovirus GP of Claim 7, whereby an immune response to the antigen in the primate is induced.

17. A method of inducing an immune response to an antigen in a primate, the method comprising provision in the primate of a priming composition comprising the nucleic acid molecule of any of Claims 1-6 or the modified filovirus GP of Claim 7 and then provision in the primate of a boosting composition comprising the antigen or a recombinant virus encoding the antigen.

18. The method of any of Claims 15-17, wherein the primate is a human.

19. A method of making the nucleic acid molecule of any of Claims 1-6 comprising preparing an adapter plasmid and achieving recombination with a virus genome to produce a recombinant virus composed of the nucleic acid molecule of any of Claims 1-6.

20. A nucleic acid molecule having SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8, or insert thereof encoding modified or wild type filovirus GP.

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