METHODS AND COMPOSITIONS FOR INDUCING PROTECTIVE IMMUNITY AGAINST FILOVIRUS INFECTION

FIELD OF THE INVENTION

This invention relates to compositions, vaccines and methods for inducing protective immunity against filovirus infection, particularly protective immunity against infection of one or more subtypes of Ebolaviruses and Marburg virus.

BACKGROUND OF THE INVENTION

Ebolaviruses, such as Zaire ebolavirus (EBOV) and Sudan ebolavirus (SUDV), and the closely related Marburg virus (MARV), are associated with outbreaks of highly lethal Ebola Hemorrhagic Fever (EHF) in humans and primates in North America, Europe, and Africa. These viruses are filoviruses that are known to infect humans and non- human primates with severe health consequences, including death. Filovirus infections have resulted in case fatality rates of up to 90% in humans. EBOV, SUDV, and MARV infections cause EHF with death often occurring within 7 to 10 days post-infection. EHF presents as an acute febrile syndrome manifested by an abrupt fever, nausea, vomiting, diarrhea, maculopapular rash, malaise, prostration, generalized signs of increased vascular permeability, coagulation abnormalities, and dysregulation of the innate immune response. Much of the disease appears to be caused by dysregulation of innate immune responses to the infection and by replication of virus in vascular endothelial cells, which induces death of host cells and destruction of the endothelial barrier. Filoviruses can be spread by small particle aerosol or by direct contact with infected blood, organs, and body fluids of human or NHP origin. Infection with a single virion is reported to be sufficient to cause Ebola hemorrhagic fever (EHF) in humans. Presently, there is no therapeutic or vaccine approved for treatment or prevention of EHF. Supportive care remains the only approved medical intervention for individuals who become infected with filoviruses.

As the cause of severe human disease, filoviruses continue to be of concern as both a source of natural infections, and also as possible agents of bioterrorism. The reservoir for filoviruses in the wild has not yet been definitively identified. Four subtypes of Ebolaviruses

have been described to cause EHF, i.e., those in the Zaire, Sudan, Bundibugyo and Ivory Coast episodes (Sanchez, A. et al. 1996 PNAS USA 93:3602–3607). These subtypes of Ebolaviruses have similar genetic organizations, e.g., negative-stranded RNA viruses containing seven linearly arrayed genes. The structural gene products include, for example, the envelope glycoprotein that exists in two alternative forms, a secreted soluble glycoprotein (ssGP) and a transmembrane glycoprotein (GP) generated by RNA editing that mediates viral entry (Sanchez, et al. 1996 PNAS USA 93:3602–3607).

It has been suggested that immunization may be useful in protecting against Ebola infection because there appears to be less nucleotide polymorphism within Ebola subtypes than among other RNA viruses (Sanchez et al. 1996 PNAS USA 93:3602–3607). Until recently, developments of preventive vaccines against filoviruses have had variable results, partly because the requirements for protective immune responses against filovirus infections are poorly understood. Additionally, the large number of filoviruses circulating within natural reservoirs complicates efforts to design a vaccine that protects against all species of filoviruses.

Currently, there are several vaccine antigen delivery platforms that demonstrated various levels of protection in non-human primates (NHPs) exposed with high infectious doses of filoviruses. Vaccine candidates are in development based on a variety of platform technologies including replication competent vectors (e.g. Vesicular Stomatitis Virus; Rabies virus; Parainfluenza Virus); replication incompetent vectors (Adenovirus, Modified Vaccinia Ankara Virus); protein subunits inclusive of Virus Like Particles expressed in bacterial cells, insect cells, mammalian cells, plant cells; DNA vaccines; and /or live and killed attenuated filovirus (Friedrich et al., 2012). The EBOV glycoprotein GP is an essential component of a vaccine that protects against exposures with the same species of EBOV. Furthermore, inclusion of the GP from EBOV and SUDV, the two most virulent species of ebolaviruses, can protect monkeys against EBOV and SUDV intramuscular exposures, as well as exposures with the distantly related Bundibugyo (BDBV), Taï Forest ebolavirus (TAFV; formerly known as Ivory Coast or Cote d'Ivoire) species. Likewise, inclusion of the GP from MARV can protect monkeys against MARV intramuscular and aerosol exposures. The development of medical countermeasures for these viruses is a high priority, in particular the development of a PAN-filovirus vaccine – that is one vaccine that protects against all pathogenic filoviruses.

Replication-defective adenovirus vectors (rAd) are powerful inducers of cellular immune responses and have therefore come to serve as useful vectors for gene-based vaccines particularly for lentiviruses and filoviruses, as well as other nonviral pathogens (Shiver, et al., (2002) Nature 415(6869): 331-5; (Hill, et al., Hum Vaccin 6(1): 78-83. ; Sullivan, et al., (2000) Nature 408(6812): 605-9; Sullivan et al., (2003) Nature 424(6949): 681-4; Sullivan, et al., (2006) PLoS Med 3(6): e177; Radosevic, et al., (2007); Santra, et al., (2009) Vaccine 27(42): 5837-45.

Adenovirus-based vaccines have several advantages as human vaccines since they can be produced to high titers under GMP conditions and have proven to be safe and immunogenic in humans (Asmuth, et al., J Infect Dis 201(1): 132-41; Kibuuka, et al., J Infect Dis 201(4): 600-7; Koup, et al., PLoS One 5(2): e9015. ; Catanzaro, et al., (2006) J Infect Dis 194(12): 1638-49; Harro, et al., (2009) Clin Vaccine Immunol 16(9): 1285-92. While most of the initial vaccine work was conducted using rAd5 due to its significant potency in eliciting broad antibody and CD8+ T cell responses, pre-existing immunity to rAd5 in humans may limit efficacy (Catanzaro, (2006); Cheng, et al., (2007) PLoS Pathog 3(2): e25.; McCoy, et al., (2007) J Virol 81(12): 6594-604.; Buchbinder, et al., (2008) Lancet 372(9653): 1881-93). This property might restrict the use of rAd5 in clinical applications for many vaccines that are currently in development including Ebolavirus (EBOV) and Marburg virus (MARV).

Replication-defective adenovirus vectors, rAd26 and rAd35, derived from adenovirus serotype 26 and serotype 35, respectively, have the ability to circumvent Ad5 pre-existing immunity. rAd26 can be grown to high titers in Ad5 E1-complementing cell lines suitable for manufacturing these vectors at a large scale and at clinical grade (Abbink, et al., 2007), and this vector has been shown to induce humoral and cell-mediated immune responses in prime-boost vaccine strategies (Abbink, et al., 2007; Liu, et al., (2009) Nature 457(7225): 87-91). rAd35 vectors grow to high titers on cell lines suitable for production of clinical-grade vaccines (Havenga, et al., (2006) J Gen Virol 87(Pt 8): 2135-43), and have been formulated for injection as well as stable inhalable powder (Jin, et al., Vaccine 28(27): 4369-75). These vectors show efficient transduction of human dendritic cells (de Gruijl, et al., (2006) J Immunol 177(4): 2208- 15; Lore, et al., (2007) J Immunol 179(3): 1721-9), and thus have the capability to mediate high level antigen delivery and presentation.

Modified Vaccinia Ankara (MVA) virus is related to Vaccinia virus, a member of the genera Orthopoxvirus in the family of Poxviridae. Poxviruses are known to be good inducers of CD8 T cell responses because of their intracytoplasmic expression. However, they are generally believed to be poor at generating CD4 MHC class II restricted T cells (see for example Haslett et al. Journal of Infectious Diseases 181 : 1264-72 (2000), page 1268). MVA has been engineered for use as a viral vector for recombinant gene expression or as recombinant vaccine.

Strains of MVA having enhanced safety profiles for the development of safer products, such as vaccines or pharmaceuticals, have been developed by Bavarian Nordic. MVA was further passaged by Bavarian Nordic and is designated MVA-BN, a representative sample of which was deposited on August 30, 2000 at the European Collection of Cell Cultures (ECACC) under Accession No. V00083008. MVA-BN is further described in WO 02/42480 (US 2003/0206926) and WO 03/048184 (US 2006/0159699), both of which are incorporated by reference herein in their entirety.

MVA-BN can attach to and enter human cells where virally-encoded genes are expressed very efficiently. MVA-BN is replication incompetent, meaning that the virus does not replicate in human cells. In human cells, viral genes are expressed, and no infectious virus is produced. MVA-BN is classified as Biosafety Level 1 organism according to the Centers for Disease Control and Prevention in the United States. Preparations of MVA-BN and derivatives have been administered to many types of animals, and to more than 2000 human subjects, including immune-deficient individuals. All vaccinations have proven to be generally safe and well tolerated. Despite its high attenuation and reduced virulence, in preclinical studies MVA-BN has been shown to elicit both humoral and cellular immune responses to vaccinia and to heterologous gene products encoded by genes cloned into the MVA genome [E. Harrer et al. (2005), Antivir. Ther. 10(2):285-300; A. Cosma et al. (2003), Vaccine 22(1):21-9; M. Di Nicola et al. (2003), Hum. Gene Ther. 14(14):1347-1360; M. Di Nicola et al. (2004), Clin. Cancer Res., 10(16):5381-5390].

There is an unmet need for improved vaccines that elicit immune responses against filoviruses, particularly, protective immunity against the more deadly Ebolaviruses and Marburg viruses.

BRIEF SUMMARY OF THE INVENTION

It is discovered in the present invention that various prime-boost combinations of replication incompetent vectors generate effective immune protection against filovirus infection.

Accordingly, one general aspect of the present invention relates to a combination vaccine comprising:

(i) a first composition comprising an immunologically effective amount of an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a first filovirus subtype or a substantially similar antigenic protein, together with a pharmaceutically acceptable carrier; and

(ii) a second composition comprising an immunologically effective amount of an MVA vector comprising a nucleic acid encoding antigenic proteins of at least two filovirus subtypes or substantially similar antigenic proteins, together with a pharmaceutically acceptable carrier;

wherein one of the compositions is a priming composition and the other composition is a boosting composition.

Another general aspect of the present invention relates to the use of:
a first composition comprising an immunologically effective amount of an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a first filovirus subtype or a substantially similar antigenic protein; and a second composition comprising an immunologically effective amount of an MVA vector comprising a nucleic acid encoding an antigenic protein of at least two filovirus subtypes or substantially similar antigenic proteins; for generating a protective immune response against at least one of the filovirus subtypes; wherein the first and second compositions are used for priming or for boosting said immune response.

In certain embodiments, the first composition (i) further comprises an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a second filovirus subtype. In other embodiments the first composition (i) further comprises an adenovirus vector

comprising a nucleic acid encoding an antigenic protein of a third filovirus subtype.

The filovirus subtypes according to the present invention can be any filovirus subtype.

In a preferred embodiment, the first, second, and third filovirus subtypes are selected from the group of Zaire, Sudan, Reston, Bundibugyo, Taï Forest and Marburg. The antigenic proteins can be any protein from any filovirus comprising an antigenic determinant. In a preferred embodiment the antigenic proteins are glycoproteins or nucleoproteins. The antigenic proteins encoded by the adenovirus vectors or MVA vectors comprised in the first and second solution according to the present invention can be any antigenic protein from any filovirus. In a preferred embodiment, the antigenic proteins of the first, second, and third filovirus type are selected from the group of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5. In a preferred embodiment, the first, second, and third filovirus subtype are not the same.

In another embodiment, the adenovirus vector in the first composition (i) comprises a nucleic acid encoding an antigenic protein having a sequence selected from the group of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5. In a preferred embodiment, the composition (i) further comprises an adenovirus comprising a nucleic acid encoding an antigenic protein having a different sequence selected from the group of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5. Preferably, the composition (i) further comprises an adenovirus comprising a nucleic acid encoding an antigenic protein having yet a different sequence selected from the group of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5.

In a preferred embodiment, the adenovirus vector in the first composition (i) comprises a nucleic acid encoding an antigenic protein with SEQ ID NO:1. In a preferred embodiment, the composition (i) further comprises an adenovirus comprising a nucleic acid encoding an antigenic protein with SEQ ID NO:2. Preferably, the composition (i) further comprises an adenovirus comprising a nucleic acid encoding an antigenic protein with SEQ ID NO:3.

In yet another preferred embodiment, the MVA vector in composition (ii) comprises a nucleic acid encoding antigenic proteins of at least four filovirus subtypes. Preferably said MVA vector comprises a nucleic acid encoding antigenic proteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

It is contemplated that the methods, vaccines, and compositions described herein can be embodied in a kit. For example, in one embodiment, the present invention can include a kit comprising:

(i) a first composition comprising an immunologically effective amount of an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a first filovirus subtype or a substantially similar antigenic protein, together with a pharmaceutically acceptable carrier; and

(ii) a second composition comprising an immunologically effective amount of an MVA vector comprising a nucleic acid encoding antigenic proteins of at least two filovirus subtypes or substantially similar antigenic proteins, together with a pharmaceutically acceptable carrier;

wherein one of the compositions is a priming composition and the other composition is a boosting composition.

Therefore in a preferred embodiment, the present invention relates to a combination vaccine, a kit or a use wherein the adenovirus vector in composition (i) comprises a nucleic acid encoding an antigenic protein with SEQ ID NO: 1; and wherein the MVA vector in composition comprises a nucleic acid encoding antigenic proteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

In yet another preferred embodiment, the present invention relates to a combination vaccine, a kit or a use wherein the first composition comprises an adenovirus comprising a nucleic acid encoding a first antigenic protein with SEQ ID NO: 1, an adenovirus comprising a nucleic acid encoding a second antigenic protein with SEQ ID NO: 2, and an adenovirus comprising a nucleic acid encoding a third antigenic protein with SEQ ID NO: 3; and wherein the MVA vector in composition (ii) comprises a nucleic acid encoding antigenic proteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

In a preferred embodiment, the adenovirus vectors comprised in the combination vaccine, kit of the present invention, or the adenovirus vectors used for generating a protective immune response against at least one of the filovirus subtypes are rAd26 or rAd35 vectors. In

a preferred embodiment of this use, the boosting composition is administered 1-12 weeks after the priming composition.

One additional general aspect of the present invention relates to a method of inducing an immune response against a filovirus in a subject, the method comprising:

a. administering to the subject a first composition comprising an immunologically effective amount of an adenovirus vector comprising a nucleic acid encoding an antigenic glycoprotein of a first filovirus subtype or a substantially similar antigenic protein; and
b. administering to the subject a second composition comprising an immunologically effective amount of an MVA vector comprising a nucleic acid encoding antigenic proteins of at least two strains of filovirus or substantially similar antigenic proteins;

wherein steps (a) and (b) are conducted in either order.

In certain embodiments, the first composition further comprises an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a second filovirus subtype. In other embodiments the first composition further comprises an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a third filovirus subtype.

In another embodiment, the adenovirus vector in the first composition comprises a nucleic acid encoding an antigenic protein with SEQ ID NO:1. In a preferred embodiment, the composition further comprises an adenovirus comprising a nucleic acid encoding an antigenic protein with SEQ ID NO:2. Preferably, the composition further comprises an adenovirus comprising a nucleic acid encoding an antigenic protein with SEQ ID NO:3.

In an even more preferred embodiment, the MVA vector in the second composition comprises a nucleic acid encoding antigenic proteins of at least four filovirus subtypes.

Preferably said MVA vector comprises a nucleic acid encoding antigenic proteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

Therefore in a preferred embodiment, the present invention relates to method of inducing an immune response against a filovirus in a subject, wherein the adenovirus vector in

the first composition comprises a nucleic acid encoding an antigenic protein with SEQ ID NO: 1; and wherein the MVA vector in the second composition comprises a nucleic acid encoding antigenic proteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

In yet another preferred embodiment, the present invention relates to a method of inducing an immune response against a filovirus in a subject, wherein the first composition comprises an adenovirus comprising a nucleic acid encoding a first antigenic protein with SEQ ID NO: 1, an adenovirus comprising a nucleic acid encoding a second antigenic protein with SEQ ID NO: 2, and an adenovirus comprising a nucleic acid encoding a third antigenic protein with SEQ ID NO: 3; and wherein the MVA vector in the second composition comprises a nucleic acid encoding antigenic proteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

In a preferred embodiment, the adenovirus vectors used in the method of the present invention are rAd26 or rAd35 vectors. In another preferred embodiment of the present invention, step (b) of the method is conducted 1-12 weeks after step (a).

In another preferred embodiment, the priming vaccination, i.e. step (a) is conducted at week 0, followed by a boosting vaccination, i.e. step (b) at week 1-10, more preferably at week 6-10 and even more preferably at week 8. In another preferred embodiment, the priming vaccination, i.e. step (a) is conducted at week 0, followed by a boosting vaccination, i.e. step (b) at week 1-4, preferably at week 1, 2 or 4.

In another preferred embodiment, the priming vaccination, i.e. step (b) is conducted at week 0, followed by a boosting vaccination, i.e. step (a) at week 1-10, more preferably at week 6-10 and even more preferably at week 8. In another preferred embodiment, the priming vaccination, i.e. step (b) is conducted at week 0, followed by a boosting vaccination, i.e. step (a) at week 1-4, preferably at week 1, 2 or 4.

In a preferred embodiment of the present invention, the method comprises a priming vaccination with an immunologically effective amount of one or more rAd26 vectors expressing one or more filovirus antigenic proteins, followed by a boosting vaccination with an immunologically effective amount of one or more vectors different from rAd26, preferably MVA vectors expressing the one or more filovirus glycoproteins or substantially similar

glycoproteins.

In preferred embodiments of the present invention, the one or more filoviruses are Ebolaviruses or Marburgviruses. The Ebolavirus may be of any species, for example, Zaire ebolavirus (EBOV) and Sudan ebolavirus (SUDV), Reston, Bundibugyo, Taï Forest. The Marburg virus (MARV) may be of any species. Exemplary amino acid sequences of suitable filovirus antigenic proteins are shown in SEQ ID NO: 1 to SEQ ID NO: 5.

BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing summary, as well as the following detailed description of the invention, will be better understood when read in conjunction with the appended drawings. It should be understood that the invention is not limited to the precise embodiments shown in the drawings.

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

In the drawings:

Figure 1 summarizes the grouping in an animal study;

Figure 2 illustrates the experimental design of the study;

Figure 3 shows the outcome of challenge with the challenge strain Ebola Zaire Kikwit 1995;

Figure 4 shows the Ebola Zaire glycoprotein specific humoral immune response (assessed by ELISA) observed from the animal study: very high antibody titers were obtained independently of the vaccination regimes (ND = time-point not analyzed);

Figure 5 shows the Sudan Gulu glycoprotein specific humoral immune response (assessed by ELISA) observed from the animal study: very high antibody titers were obtained independently of the vaccination regimes (ND = time-point not analyzed);

Figure 6 shows the Marburg Angola glycoprotein specific humoral immune response (assessed by ELISA) observed from the animal study: very high antibody titers were obtained independently of the vaccination regimes (ND = time-point not analyzed); and

Figure 7 shows the specific cellular immune response to ZEBOV, SEBOV and

MARVA GP analyzed by an IFN-γ ELISPOT;

Figure 8 shows the specific immune response to ZEBOV GP analyzed by an anti-EBOV GP ELISA, wherein at day 50, a higher humoral immune response post boost immunization is observed in subjects immunized with MVA as a prime and Ad26 as a boost than with the reverse order of vaccines;

Figure 9 shows the specific T cell response to ZEBOV GP in humans analyzed by ELISpot assay;

Figure 10 shows the specific CD8+ cellular immune response to ZEBOV GP in humans analyzed by ICS assay;

Figure 11 shows the functionality of the EBOV GP-specific CD8+ T cell responses in humans by ICS assay when using a 28 days prime boost interval;

Figure 12 shows the functionality of the EBOV GP-specific CD8+ T cell responses in humans by ICS assay when using a 56 days prime boost interval;

Figure 13 shows the specific CD4+ cellular immune response to ZEBOV GP in humans analyzed by ICS assay;

Figure 14 shows the functionality of the EBOV GP-specific CD4+ T cell responses in humans by ICS assay when using a 28 days prime boost interval;

Figure 15 shows the functionality of the EBOV GP-specific CD4+ T cell responses in humans by ICS assay when using a 56 days prime boost interval;

Figure 16 shows the immune response induced by a prime immunization with Ad26.ZEBOV followed by a MVA-BN-Filo boost 14 days later assessed by ELISA (A), ELIspot (B), and ICS (C and D);

Figure 17 shows the specific immune response to ZEBOV GP analyzed by an anti-EBOV GP ELISA;

Figure 18 shows the specific T cell response to ZEBOV GP in humans analyzed by ELISpot assay;

Figure 19 shows the strong and balanced CD4+ (A) and CD8+ (B) cellular immune response specific to ZEBOV GP in humans analyzed by ICS assay and the functionality of the EBOV GP-specific CD8+ (C) and CD4+ (D) T cell responses in humans by ICS assay when using MVA as a prime and Ad26 as a boost 14 days later.

Figure 20 shows EBOV Mayinga GP-binding Antibodies Elicited by Vaccination with Ad26.ZEBOV/ MVA-BN-Filo and MVA-BN-Filo/Ad26.ZEBOV Regimens Determined by GP ELISA. Vaccination regimens are indicated below x-axis. High IM and standard IM refer to dose and route of MVA BN Filo. Horizontal dotted line indicates LOD.

DETAILED DESCRIPTION OF THE INVENTION

Various publications, articles and patents are cited or described in the background and throughout the specification; each of these references is herein incorporated by reference in its entirety. Discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is for the purpose of providing context for the present invention. Such discussion is not an admission that any or all of these matters form part of the prior art with respect to any inventions disclosed or claimed.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention pertains. Otherwise, certain terms used herein have the meanings as set forth in the specification. All patents, published patent applications and publications cited herein are incorporated by reference as if set forth fully herein. It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise.

Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term "comprising" can be substituted with the term "containing" or "including" or sometimes

when used herein with the term "having". Any of the aforementioned terms (comprising, containing, including, having), whenever used herein in the context of an aspect or embodiment of the present invention may be substituted with the term "consisting of", though less preferred.

When used herein "consisting of" excludes any element, step, or ingredient not specified in the claim element. When used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

As used herein, the conjunctive term "and/or" between multiple recited elements is understood as encompassing both individual and combined options. For instance, where two elements are conjoined by "and/or", a first option refers to the applicability of the first element without the second. A second option refers to the applicability of the second element without the first. A third option refers to the applicability of the first and second elements together. Any one of these options is understood to fall within the meaning, and therefore satisfy the requirement of the term "and/or" as used herein. Concurrent applicability of more than one of the options is also understood to fall within the meaning, and therefore satisfy the requirement of the term "and/or."

As used herein, "subject" means any animal, preferably a mammal, most preferably a human, to whom will be or has been treated by a method according to an embodiment of the invention. The term "mammal" as used herein, encompasses any mammal. Examples of mammals include, but are not limited to, cows, horses, sheep, pigs, cats, dogs, mice, rats, rabbits, guinea pigs, monkeys, humans, etc., more preferably a human.

As used herein, the term "protective immunity" or "protective immune response" means that the vaccinated subject is able to control an infection with the pathogenic agent against which the vaccination was done. Usually, the subject having developed a "protective immune response" develops only mild to moderate clinical symptoms or no symptoms at all. Usually, a subject having a "protective immune response" or "protective immunity" against a certain agent will not die as a result of the infection with said agent.

An "adenovirus capsid protein" refers to a protein on the capsid of an adenovirus (e.g., Ad 26 or Ad 35) that is involved in determining the serotype and/or tropism of a particular adenovirus. Adenoviral capsid proteins typically include the fiber, penton and/or hexon

proteins. As used herein a “Ad26 capsid protein” or a “Ad35 capsid protein” may be, for example, a chimeric capsid protein that includes at least a part of an Ad26 or Ad35 capsid protein. In certain embodiments, the capsid protein is an entire capsid protein of Ad26 or of Ad35. In certain embodiments, the hexon, penton and fiber are of Ad26 or of Ad35.

The terms “adjuvant” and "immune stimulant" are used interchangeably herein, and are defined as one or more substances that cause stimulation of the immune system. In this context, an adjuvant is used to enhance an immune response to the adenovirus and/or MVA vectors of the invention.

The term “corresponding to”, when applied to positions of amino acid residues in sequences, means corresponding positions in a plurality of sequences when the sequences are optimally aligned.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, (e.g., glycoproteins of filovirus and polynucleotides that encode them) refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat’l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (see generally, Current Protocols in Molecular Biology,

F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1995 Supplement) (Ausubel)).

Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1990) J. Mol. Biol. 215: 403-410 and Altschuel et al. (1977) Nucleic Acids Res. 25: 3389- 3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased.

Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, Proc. Nat'l. Acad. Sci. USA 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an

indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

A further indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions, as described below.

The term "substantially similar" in the context of the filovirus antigenic proteins of the invention indicates that a polypeptide comprises a sequence with at least 90%, preferably at least 95% sequence identity to the reference sequence over a comparison window of 10-20 amino acids. Percentage of sequence identity is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

It is discovered in the present invention that heterologous prime-boost combinations, in particular, Ad26 priming followed by MVA boosting and vice versa, are surprisingly effective in generating protective immune responses against one or more subtypes of Filoviruses.

Filovirus antigenic proteins

The Ebola viruses, and the genetically-related Marburg virus, are filoviruses associated with outbreaks of highly lethal hemorrhagic fever in humans and primates in North America, Europe, and Africa (Peters, C.J. et al. in: Fields Virology, eds. Fields, B.N. et al. 1161-1176, Philadelphia, Lippincott-Raven, 1996; Peters, C.J. et al. 1994 Semin Virol 5:147-154). Although several subtypes have been defined, the genetic organization of these viruses is similar, each containing seven linearly arrayed genes. Among the viral proteins, the envelope glycoprotein exists in two alternative forms, a 50-70 kilodalton (kDa) secreted protein (sGP) and a 130 kDa transmembrane glycoprotein (GP) generated by RNA editing that mediates viral entry (Peters, C.J. et al. in: Fields Virology, eds. Fields, B.N. et al. 1161-1176, Philadelphia, Lippincott-Raven, 1996; Sanchez, A. et al. 1996 PNAS USA 93:3602-3607). Other structural gene products include the nucleoprotein (NP), matrix proteins VP24 and VP40, presumed nonstructural proteins VP30 and VP35, and the viral polymerase (reviewed in Peters, C.J. et al. in: Fields Virology, eds. Fields, B.N. et al. 1161-1176, Philadelphia, Lippincott-Raven, 1996).

The nucleic acid molecules comprised in the adenovirus and MVA vectors may encode structural gene products of any filovirus species, such as subtypes of Zaire (type species, also referred to herein as ZEBOV), Sudan (also referred to herein as SEBOV), Reston, Bundibugyo, and Ivory Coast. There is a single species of Marburg virus (also referred to herein as MARV).

The adenoviral vectors and MVA vectors of the invention can be used to express antigenic proteins which are proteins comprising an antigenic determinant of a wide variety of filovirus antigens. In a typical and preferred embodiment, the vectors of the invention include nucleic acid encoding the transmembrane form of the viral glycoprotein (GP). In other embodiments, the vectors of the invention may encode the secreted form of the viral glycoprotein (ssGP), or the viral nucleoprotein (NP).

One of skill will recognize that the nucleic acid molecules encoding the filovirus antigenic protein may be modified, e.g., the nucleic acid molecules set forth herein may be mutated, as long as the modified expressed protein elicits an immune response against a pathogen or disease. Thus, as used herein, the term "antigenic protein" or "filovirus protein"

refers to a protein that comprises at least one antigenic determinant of a filovirus protein described above. The term encompasses filovirus glycoproteins (i.e., gene products of a filovirus) or filovirus nucleoprotein as well as recombinant proteins that comprise one or more filovirus glycoprotein determinants. The term antigenic proteins also encompasses antigenic proteins that are substantially similar.

In some embodiments, the protein may be mutated so that it is less toxic to cells (see e.g., WO/2006/037038) or can be expressed with increased or decreased level in the cells. The present invention also includes vaccines comprising a combination of nucleic acid molecules. For example, and without limitation, nucleic acid molecules encoding GP, ssGP and NP of the Zaire, Sudan, Marburg and Ivory Coast/Taï forest Ebola strains may be combined in any combination, in one vaccine composition.

Adenoviruses

An adenovirus according to the invention belongs to the family of the Adenoviridae and preferably is one that belongs to the genus Mastadenovirus. It can be a human adenovirus, but also an adenovirus that infects other species, including but not limited to a bovine adenovirus (e.g. bovine adenovirus 3, BAdV3), a canine adenovirus (e.g. CAdV2), a porcine adenovirus (e.g. PAdV3 or 5), or a simian adenovirus (which includes a monkey adenovirus and an ape adenovirus, such as a chimpanzee adenovirus or a gorilla adenovirus). Preferably, the adenovirus is a human adenovirus (HAdV, or AdHu; in the present invention a human adenovirus is meant if referred to Ad without indication of species, e.g. the brief notation "Ad5" means the same as HAdV5, which is human adenovirus serotype 5), or a simian adenovirus such as chimpanzee or gorilla adenovirus (ChAd, AdCh, or SAdV).

Most advanced studies have been performed using human adenoviruses, and human adenoviruses are preferred according to certain aspects of the invention. In certain preferred embodiments, the recombinant adenovirus according to the invention is based upon a human adenovirus. In preferred embodiments, the recombinant adenovirus is based upon a human adenovirus serotype 5, 11, 26, 34, 35, 48, 49 or 50. According to a particularly preferred embodiment of the invention, an adenovirus is a human adenovirus of one of the serotypes 26 or 35.

An advantage of these serotypes is a low seroprevalence and/or low pre-existing neutralizing antibody titers in the human population. Preparation of rAd26 vectors is described, for example, in WO 2007/104792 and in Abbink et al., (2007) Virol 81(9): 4654-63, both of which are incorporated by reference herein in their entirety. Exemplary genome sequences of Ad26 are found in GenBank Accession EF 153474 and in SEQ ID NO:1 of WO 2007/104792. Preparation of rAd35 vectors is described, for example, in US Patent No. 7,270,811, in WO 00/70071, and in Vogels et al., (2003) J Virol 77(15): 8263-71, all of which are incorporated by reference herein in their entirety. Exemplary genome sequences of Ad35 are found in GenBank Accession AC_000019 and in Fig. 6 of WO 00/70071.

Simian adenoviruses generally also have a low seroprevalence and/or low pre-existing neutralizing antibody titers in the human population, and a significant amount of work has been reported using chimpanzee adenovirus vectors (e.g. US6083716; WO 2005/071093; WO 2010/086189; WO 2010085984; Farina et al, 2001, J Virol 75: 11603-13; Cohen et al, 2002, J Gen Virol 83: 151-55; Kobinger et al, 2006, Virology 346: 394-401; Tatsis et al., 2007, Molecular Therapy 15: 608-17; see also review by Bangari and Mittal, 2006, Vaccine 24: 849-62; and review by Lasaro and Ertl, 2009, Mol Ther 17: 1333-39). Hence, in other preferred embodiments, the recombinant adenovirus according to the invention is based upon a simian adenovirus, e.g. a chimpanzee adenovirus. In certain embodiments, the recombinant adenovirus is based upon simian adenovirus type 1, 7, 8, 21, 22, 23, 24, 25, 26, 27.1, 28.1, 29, 30, 31.1, 32, 33, 34, 35.1, 36, 37.2, 39, 40.1, 41.1, 42.1, 43, 44, 45, 46, 48, 49, 50 or SA7P.

Adenoviral Vectors rAd26 and rAd35

In a preferred embodiment according to the present invention the adenoviral vectors comprise capsid proteins from two rare serotypes: Ad26 and Ad35. In the typical embodiment, the vector is an rAd26 or rAd35 virus.

Thus, the vectors that can be used in the invention comprise an Ad26 or Ad35 capsid protein (e.g., a fiber, penton or hexon protein). One of skill will recognize that it is not necessary that an entire Ad26 or Ad35 capsid protein be used in the vectors of the invention. Thus, chimeric capsid proteins that include at least a part of an Ad26 or Ad35 capsid protein can be used in the vectors of the invention. The vectors of the invention may also comprise

capsid proteins in which the fiber, penton, and hexon proteins are each derived from a different serotype, so long as at least one capsid protein is derived from Ad26 or Ad35. In preferred embodiments, the fiber, penton and hexon proteins are each derived from Ad26 or each from Ad35.

One of skill will recognize that elements derived from multiple serotypes can be combined in a single recombinant adenovirus vector. Thus, a chimeric adenovirus that combines desirable properties from different serotypes can be produced. Thus, in some embodiments, a chimeric adenovirus of the invention could combine the absence of pre-existing immunity of the Ad26 and Ad35 serotypes with characteristics such as temperature stability, assembly, anchoring, production yield, redirected or improved infection, stability of the DNA in the target cell, and the like.

In certain embodiments the recombinant adenovirus vector useful in the invention is derived mainly or entirely from Ad35 or from Ad26 (i.e., the vector is rAd35 or rAd26). In some embodiments, the adenovirus is replication deficient, e.g. because it contains a deletion in the E1 region of the genome. For the adenoviruses of the invention, being derived from Ad26 or Ad35, it is typical to exchange the E4-orf6 coding sequence of the adenovirus with the E4-orf6 of an adenovirus of human subgroup C such as Ad5. This allows propagation of such adenoviruses in well-known complementing cell lines that express the E1 genes of Ad5, such as for example 293 cells, PER.C6 cells, and the like (see, e.g. Havenga et al, 2006, J Gen Virol 87: 2135-43; WO 03/104467). In certain embodiments, the adenovirus is a human adenovirus of serotype 35, with a deletion in the E1 region into which the nucleic acid encoding the antigen has been cloned, and with an E4 orf6 region of Ad5. In certain embodiments, the adenovirus is a human adenovirus of serotype 26, with a deletion in the E1 region into which the nucleic acid encoding the antigen has been cloned, and with an E4 orf6 region of Ad5. For the Ad35 adenovirus, it is typical to retain the 3' end of the E1B 55K open reading frame in the adenovirus, for instance the 166 bp directly upstream of the pIX open reading frame or a fragment comprising this such as a 243 bp fragment directly upstream of the pIX start codon, marked at the 5' end by a Bsu36I restriction site, since this increases the stability of the adenovirus because the promoter of the pIX gene is partly residing in this area (see, e.g. Havenga et al, 2006, supra; WO 2004/001032).

The preparation of recombinant adenoviral vectors is well known in the art.

Preparation of rAd26 vectors is described, for example, in WO 2007/104792 and in Abbink et al., (2007) Virol 81(9): 4654-63. Exemplary genome sequences of Ad26 are found in GenBank Accession EF 153474 and in SEQ ID NO:1 of WO 2007/104792. Preparation of rAd35 vectors is described, for example, in US Patent No. 7,270,811 and in Vogels et al., (2003) J Virol 77(15): 8263-71. An exemplary genome sequence of Ad35 is found in GenBank Accession AC_000019.

In an embodiment of the present invention, the vectors useful for the present invention include those described in WO2012/082918, the disclosure of which is incorporated herein by reference in its entirety.

Typically, a vector useful in the invention is produced using a nucleic acid comprising the entire recombinant adenoviral genome (e.g., a plasmid, cosmid, or baculovirus vector). Thus, the invention also provides isolated nucleic acid molecules that encode the adenoviral vectors of the invention. The nucleic acid molecules of the 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.

The adenovirus vectors useful the invention are typically replication defective. In these embodiments, the virus is rendered replication-defective by deletion or inactivation of regions critical to replication of the virus, such as the E1 region. The regions can be substantially deleted or inactivated by, for example, inserting the gene of interest (usually linked to a promoter). In some embodiments, the vectors of the invention may contain deletions in other regions, such as the E2, E3 or E4 regions or insertions of heterologous genes linked to a promoter. For E2- and/or E4-mutated adenoviruses, generally E2- and/or E4-complementing cell lines are used to generate recombinant adenoviruses. Mutations in the E3 region of the adenovirus need not be complemented by the cell line, since E3 is not required for replication.

A packaging cell line is typically used to produce sufficient amount of adenovirus vectors of the invention. A packaging cell is a cell that comprises those genes that have been deleted or inactivated in a replication-defective vector, thus allowing the virus to replicate in the cell. Suitable cell lines include, for example, PER.C6, 911, 293, and E1 A549.

As noted above, a wide variety of filovirus glycoproteins can be expressed in the

vectors. If required, the heterologous gene encoding the filovirus glycoproteins can be codon-optimized to ensure proper expression in the treated host (e.g., human). Codon-optimization is a technology widely applied in the art. Typically, the heterologous gene is cloned into the E1 and/or the E3 region of the adenoviral genome.

The heterologous filovirus gene may be under the control of (i.e., operably linked to) an adenovirus-derived promoter (e.g., the Major Late Promoter) or may be under the control of a heterologous promoter. Examples of suitable heterologous promoters include the CMV promoter and the RSV promoter. Preferably, the promoter is located upstream of the heterologous gene of interest within an expression cassette.

As noted above, the adenovirus vectors useful for the invention can comprise a wide variety of filovirus glycoproteins known to those of skill in the art.

In a preferred embodiment of the present invention, the rAd vector(s) comprises one or more GPs selected from the group consisting of GPs of Zaire ebolavirus (EBOV), GPs of Sudan ebolavirus (SUDV), GPs of Marburg virus (MARV), and GPs substantially similar thereto.

MVA vectors

MVA vectors useful for the present invention utilize attenuated virus derived from Modified Vaccinia Ankara virus which is characterized by the loss of their capabilities to reproductively replicate in human cell lines. The MVA vectors express a wide variety of filovirus glycoproteins as well as other structural filovirus proteins, such as VP40 and nucleoprotein (NP).

In one aspect, the present invention provides a recombinant modified vaccinia virus Ankara (MVA) comprising a nucleotide sequence encoding an antigenic determinant of a filovirus glycoprotein (GP), in particular an envelope glycoprotein. In another aspect, the present invention provides a recombinant MVA vector comprising a heterologous nucleotide sequence encoding an antigenic determinant of a filovirus glycoprotein, in particular an envelope glycoprotein, and a heterologous nucleotide sequence encoding an antigenic determinant of a further filovirus protein.

MVA has been generated by more than 570 serial passages on chicken embryo

fibroblasts of the dermal vaccinia strain Ankara [Chorioallantois vaccinia virus Ankara virus, CVA; for review see Mayr et al. (1975), Infection 3, 6-14] that was maintained in the Vaccination Institute, Ankara, Turkey for many years and used as the basis for vaccination of humans. However, due to the often severe post-vaccination complications associated with vaccinia viruses, there were several attempts to generate a more attenuated, safer smallpox vaccine.

During the period of 1960 to 1974, Prof. Anton Mayr succeeded in attenuating CVA by over 570 continuous passages in CEF cells [Mayr et al. (1975)]. It was shown in a variety of animal models that the resulting MVA was avirulent [Mayr, A. & Danner, K. (1978), Dev. Biol. Stand. 41: 225-234]. As part of the early development of MVA as a pre-smallpox vaccine, there were clinical trials using MVA-517 in combination with Lister Elstree [Stickl (1974), Prev. Med. 3: 97-101; Stickl and Hochstein-Mintzel (1971), Munch. Med. Wochenschr. 113: 1149-1153] in subjects at risk for adverse reactions from vaccinia. In 1976, MVA derived from MVA-571 seed stock (corresponding to the 571st passage) was registered in Germany as the primer vaccine in a two-stage parenteral smallpox vaccination program. Subsequently, MVA-572 was used in approximately 120,000 Caucasian individuals, the majority children between 1 and 3 years of age, with no reported severe side effects, even though many of the subjects were among the population with high risk of complications associated with vaccinia (Mayr et al. (1978), Zentralbl. Bacteriol. (B) 167:375-390). MVA-572 was deposited at the European Collection of Animal Cell Cultures as ECACC V94012707.

As a result of the passaging used to attenuate MVA, there are a number of different strains or isolates, depending on the number of passages conducted in CEF cells. For example, MVA-572 was used in a small dose as a pre-vaccine in Germany during the smallpox eradication program, and MVA-575 was extensively used as a veterinary vaccine. MVA as well as MVA- BN lacks approximately 15% (31 kb from six regions) of the genome compared with ancestral CVA virus. The deletions affect a number of virulence and host range genes, as well as the gene for Type A inclusion bodies. MVA-575 was deposited on December 7, 2000, at the European Collection of Animal Cell Cultures (ECACC) under Accession No. V00120707. The attenuated CVA-virus MVA (Modified Vaccinia Virus Ankara) was obtained by serial propagation (more than 570 passages) of the CVA on primary chicken embryo

fibroblasts.

Even though Mayr et al. demonstrated during the 1970s that MVA is highly attenuated and avirulent in humans and mammals, certain investigators have reported that MVA is not fully attenuated in mammalian and human cell lines since residual replication might occur in these cells [Blanchard et al. (1998), J. Gen. Virol. 79:1159-1167; Carroll & Moss (1997), Virology 238:198-211; U.S. Patent No. 5,185,146; Ambrosini et al. (1999), J. Neurosci. Res. 55: 569]. It is assumed that the results reported in these publications have been obtained with various known strains of MVA, since the viruses used essentially differ in their properties, particularly in their growth behavior in various cell lines. Such residual replication is undesirable for various reasons, including safety concerns in connection with use in humans.

Strains of MVA having enhanced safety profiles for the development of safer products, such as vaccines or pharmaceuticals, have been developed by Bavarian Nordic. MVA was further passaged by Bavarian Nordic and is designated MVA-BN, a representative sample of which was deposited on August 30, 2000 at the European Collection of Cell Cultures (ECACC) under Accession No. V00083008. MVA-BN is further described in WO 02/42480 (US 2003/0206926) and WO 03/048184 (US 2006/0159699), both of which are incorporated by reference herein in their entirety.

MVA-BN can attach to and enter human cells where virally-encoded genes are expressed very efficiently. MVA-BN is strongly adapted to primary chicken embryo fibroblast (CEF) cells and does not replicate in human cells. In human cells, viral genes are expressed, and no infectious virus is produced. MVA-BN is classified as Biosafety Level 1 organism according to the Centers for Disease Control and Prevention in the United States. Preparations of MVA-BN and derivatives have been administered to many types of animals, and to more than 2000 human subjects, including immune-deficient individuals. All vaccinations have proven to be generally safe and well tolerated. Despite its high attenuation and reduced virulence, in preclinical studies MVA-BN has been shown to elicit both humoral and cellular immune responses to vaccinia and to heterologous gene products encoded by genes cloned into the MVA genome [E. Harrer et al. (2005), Antivir. Ther. 10(2):285-300; A. Cosma et al. (2003), Vaccine 22(1):21-9; M. Di Nicola et al. (2003), Hum. Gene Ther. 14(14):1347-1360; M. Di Nicola et al. (2004), Clin. Cancer Res., 10(16):5381-5390].

"Derivatives" or "variants" of MVA refer to viruses exhibiting essentially the same replication characteristics as MVA as described herein, but exhibiting differences in one or more parts of their genomes. MVA-BN as well as a derivative or variant of MVA-BN fails to reproductively replicate in vivo in humans and mice, even in severely immune suppressed mice. More specifically, MVA-BN or a derivative or variant of MVA-BN has preferably also the capability of reproductive replication in chicken embryo fibroblasts (CEF), but no capability of reproductive replication in the human keratinocyte cell line HaCat [Boukamp et al (1988), J. Cell Biol. 106: 761-771], the human bone osteosarcoma cell line 143B (ECACC Deposit No. 91112502), the human embryo kidney cell line 293 (ECACC Deposit No. 85120602), and the human cervix adenocarcinoma cell line HeLa (ATCC Deposit No. CCL-2). Additionally, a derivative or variant of MVA-BN has a virus amplification ratio at least two fold less, more preferably three-fold less than MVA-575 in Hela cells and HaCaT cell lines. Tests and assay for these properties of MVA variants are described in WO 02/42480 (US 2003/0206926) and WO 03/048184 (US 2006/0159699).

The term "not capable of reproductive replication" or "no capability of reproductive replication" is, for example, described in WO 02/42480, which also teaches how to obtain MVA having the desired properties as mentioned above. The term applies to a virus that has a virus amplification ratio at 4 days after infection of less than 1 using the assays described in WO 02/42480 or in U.S. Patent No. 6,761,893, both of which are incorporated by reference herein in their entirety.

The term "fails to reproductively replicate" refers to a virus that has a virus amplification ratio at 4 days after infection of less than 1. Assays described in WO 02/42480 or in U.S. Patent No. 6,761,893 are applicable for the determination of the virus amplification ratio.

The amplification or replication of a virus is normally expressed as the ratio of virus produced from an infected cell (output) to the amount originally used to infect the cell in the first place (input) referred to as the "amplification ratio". An amplification ratio of "1" defines an amplification status where the amount of virus produced from the infected cells is the same as the amount initially used to infect the cells, meaning that the infected cells are permissive for virus infection and reproduction. In contrast, an amplification ratio of less than 1, i.e., a

decrease in output compared to the input level, indicates a lack of reproductive replication and therefore attenuation of the virus.

The advantages of MVA-based vaccine include their safety profile as well as availability for large scale vaccine production. Preclinical tests have revealed that MVA-BN demonstrates superior attenuation and efficacy compared to other MVA strains (WO 02/42480). An additional property of MVA-BN strains is the ability to induce substantially the same level of immunity in vaccinia virus prime/vaccinia virus boost regimes when compared to DNA- prime/vaccinia virus boost regimes.

The recombinant MVA-BN viruses, the most preferred embodiment herein, are considered to be safe because of their distinct replication deficiency in mammalian cells and their well-established avirulence. Furthermore, in addition to its efficacy, the feasibility of industrial scale manufacturing can be beneficial. Additionally, MVA-based vaccines can deliver multiple heterologous antigens and allow for simultaneous induction of humoral and cellular immunity.

MVA vectors useful for the present invention can be prepared using methods known in the art, such as those described in WO/2002/042480 and WO/2002/24224, the relevant disclosures of which are incorporated herein by references.

In another aspect, replication deficient MVA viral strains may also be suitable such as strain MVA-572, MVA-575 or any similarly attenuated MVA strain. Also suitable may be a mutant MVA, such as the deleted chorioallantois vaccinia virus Ankara (dCVA). A dCVA comprises del I, del II, del III, del IV, del V, and del VI deletion sites of the MVA genome. The sites are particularly useful for the insertion of multiple heterologous sequences. The dCVA can reproductively replicate (with an amplification ratio of greater than 10) in a human cell line (such as human 293, 143B, and MRC-5 cell lines), which then enable the optimization by further mutation useful for a virus-based vaccination strategy (see WO 2011/092029).

In a preferred embodiment of the present invention, the MVA vector(s) comprise a nucleic acid that encode one or more antigenic proteins selected from the group consisting of GPs of Zaire ebolavirus (EBOV), GPs of Sudan ebolavirus (SUDV), GPs of Marburg virus (MARV), the NP of Taï Forest virus and GPs or NPs substantially similar thereto.

The filovirus protein may be inserted into one or more intergenic regions (IGR) of the

MVA. In certain embodiments, the IGR is selected from IGR07/08, IGR 44/45, IGR 64/65, IGR 88/89, IGR 136/137, and IGR 148/149. In certain embodiments, less than 5, 4, 3, or 2 IGRs of the recombinant MVA comprise heterologous nucleotide sequences encoding antigenic determinants of a filovirus envelope glycoprotein and/or a further filovirus protein. The heterologous nucleotide sequences may, additionally or alternatively, be inserted into one or more of the naturally occurring deletion sites, in particular into the main deletion sites I, II, III, IV, V, or VI of the MVA genome. In certain embodiments, less than 5, 4, 3, or 2 of the naturally occurring deletion sites of the recombinant MVA comprise heterologous nucleotide sequences encoding antigenic determinants of a filovirus envelope glycoprotein and/or a further filovirus protein.

The number of insertion sites of MVA comprising heterologous nucleotide sequences encoding antigenic determinants of a filovirus protein can be 1, 2, 3, 4, 5, 6, 7, or more. In certain embodiments, the heterologous nucleotide sequences are inserted into 4, 3, 2, or fewer insertion sites. Preferably, two insertion sites are used. In certain embodiments, three insertion sites are used. Preferably, the recombinant MVA comprises at least 2, 3, 4, 5, 6, or 7 genes inserted into 2 or 3 insertion sites.

The recombinant MVA viruses provided herein can be generated by routine methods known in the art. Methods to obtain recombinant poxviruses or to insert exogenous coding sequences into a poxviral genome are well known to the person skilled in the art. For example, methods for standard molecular biology techniques such as cloning of DNA, DNA and RNA isolation, Western blot analysis, RT-PCR and PCR amplification techniques are described in Molecular Cloning, A laboratory Manual (2nd Ed.) [J. Sambrook et al., Cold Spring Harbor Laboratory Press (1989)], and techniques for the handling and manipulation of viruses are described in Virology Methods Manual [B.W.J. Mahy et al. (eds.), Academic Press (1996)]. Similarly, techniques and know-how for the handling, manipulation and genetic engineering of MVA are described in Molecular Virology: A Practical Approach [A.J. Davison & R.M. Elliott (Eds.), The Practical Approach Series, IRL Press at Oxford University Press, Oxford, UK (1993)(see, e.g., Chapter 9: Expression of genes by Vaccinia virus vectors)] and Current Protocols in Molecular Biology [John Wiley & Son, Inc. (1998)(see, e.g., Chapter 16, Section IV: Expression of proteins in mammalian cells using vaccinia viral vector)].

For the generation of the various recombinant MVAs disclosed herein, different methods may be applicable. The DNA sequence to be inserted into the virus can be placed into an E. coli plasmid construct into which DNA homologous to a section of DNA of the MVA has been inserted. Separately, the DNA sequence to be inserted can be ligated to a promoter. The promoter-gene linkage can be positioned in the plasmid construct so that the promoter-gene linkage is flanked on both ends by DNA homologous to a DNA sequence flanking a region of MVA DNA containing a non-essential locus. The resulting plasmid construct can be amplified by propagation within E. coli bacteria and isolated. The isolated plasmid containing the DNA gene sequence to be inserted can be transfected into a cell culture, e.g., of chicken embryo fibroblasts (CEFs), at the same time the culture is infected with MVA. Recombination between homologous MVA DNA in the plasmid and the viral genome, respectively, can generate an MVA modified by the presence of foreign DNA sequences.

According to a preferred embodiment, a cell of a suitable cell culture as, e.g., CEF cells, can be infected with a poxvirus. The infected cell can be, subsequently, transfected with a first plasmid vector comprising a foreign or heterologous gene or genes, preferably under the transcriptional control of a poxvirus expression control element. As explained above, the plasmid vector also comprises sequences capable of directing the insertion of the exogenous sequence into a selected part of the poxviral genome. Optionally, the plasmid vector also contains a cassette comprising a marker and/or selection gene operably linked to a poxviral promoter.

Suitable marker or selection genes are, e.g., the genes encoding the green fluorescent protein, β- galactosidase, neomycin-phosphoribosyltransferase or other markers. The use of selection or marker cassettes simplifies the identification and isolation of the generated recombinant poxvirus. However, a recombinant poxvirus can also be identified by PCR technology. Subsequently, a further cell can be infected with the recombinant poxvirus obtained as described above and transfected with a second vector comprising a second foreign or heterologous gene or genes. In case, this gene shall be introduced into a different insertion site of the poxviral genome, the second vector also differs in the poxvirus-homologous sequences directing the integration of the second foreign gene or genes into the genome of the poxvirus. After homologous recombination has occurred, the recombinant virus comprising

two or more foreign or heterologous genes can be isolated. For introducing additional foreign genes into the recombinant virus, the steps of infection and transfection can be repeated by using the recombinant virus isolated in previous steps for infection and by using a further vector comprising a further foreign gene or genes for transfection.

Alternatively, the steps of infection and transfection as described above are interchangeable, i.e., a suitable cell can at first be transfected by the plasmid vector comprising the foreign gene and, then, infected with the poxvirus. As a further alternative, it is also possible to introduce each foreign gene into different viruses, co-infect a cell with all the obtained recombinant viruses and screen for a recombinant including all foreign genes. A third alternative is ligation of DNA genome and foreign sequences in vitro and reconstitution of the recombined vaccinia virus DNA genome using a helper virus. A fourth alternative is homologous recombination in E.coli or another bacterial species between a vaccinia virus genome, such as MVA, cloned as a bacterial artificial chromosome (BAC) and a linear foreign sequence flanked with DNA sequences homologous to sequences flanking the desired site of integration in the vaccinia virus genome.

The heterologous filovirus gene may be under the control of (i.e., operably linked to) one or more poxvirus promoters. In certain embodiments, the poxvirus promoter is a Pr7.5 promoter, a hybrid early/late promoter, or a PrS promoter, a PrS5E promoter, a synthetic or natural early or late promoter, or a cowpox virus ATI promoter.

Immunogenic Compositions

Immunogenic compositions are compositions comprising an immunologically effective amount of purified or partially purified adenovirus or MVA vectors for use in the invention. Said compositions may be formulated as a vaccine (also referred to as an "immunogenic composition") according to methods well known in the art. Such compositions may include adjuvants to enhance immune responses. The optimal ratios of each component in the formulation may be determined by techniques well known to those skilled in the art in view of the present disclosure.

The preparation and use of immunogenic compositions are well known to those of skill in the art. 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.

The compositions of the invention may comprise other filovirus antigens or the priming or boosting inoculations may comprise other antigens. The other antigens used in combination with the adenovirus vectors of the invention are not critical to the invention and may be, for example, filovirus antigens and nucleic acids expressing them.

The immunogenic compositions useful in the invention can comprise adjuvants.

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-I, GcMAF, B-alethine, MPC-026, Adjuvax, CpG ODN, Betafectin, Alum, and MF59.

Other 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-I, IL-2, IL-4, IL-6, IL-8, IL-IO, and IL-12 or encoding nucleic acids therefore.

The compositions of the invention can 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., intramuscular, subcutaneous, oral, intravenous, cutaneous, intramucosal (e.g., gut), intranasal or intraperitoneal routes.

Method for Inducing Protective Immunity Against Filovirus Infection

The present invention provides a method of priming and boosting an immune response to one or more Filoviruses in an individual using an adenoviral vector in combination with another adenoviral vector and/or an MVA vector.

According to one general aspect of the present invention, a method of inducing an immune response against a filovirus in a subject comprises:

a. administering to the subject a first composition comprising an immunologically effective amount of an adenovirus vector comprising a nucleic acid encoding an antigenic protein of a first filovirus subtype; and

b. administering to the subject a second composition comprising an immunologically effective amount of an MVA vector comprising a nucleic acid encoding antigenic proteins of at least two strains of filovirus

wherein steps (a) and (b) are conducted in either order. In a preferred embodiment the later step is conducted 1-12 weeks after the first step.

In certain additional aspects of the invention, the first composition further comprises one or more additional adenovirus vectors comprising a nucleic acid encoding an antigenic protein of a second filovirus subtype. In other embodiments the first composition further comprises one or more additional adenovirus vectors comprising a nucleic acid encoding an antigenic protein of a third filovirus subtype.

In one embodiment of the disclosed methods, an adenovirus vector is used to prime the immune response, and another adenovirus and/or MVA vector is used to boost the immune response about 1-12 weeks after the priming vaccination. Boosting compositions are generally administered weeks or months after administration of the priming composition, for example, about 1 or 2 weeks or 3 weeks, or 4 weeks, or 6 weeks, or 8 weeks, or 12 weeks, or 16 weeks, or 20 weeks, or 24 weeks, or 28 weeks, or 32 weeks or one to two years after administration of the priming composition.

In a preferred embodiment of the present invention, the adenovirus vectors disclosed herein include a rAd26 or rAd35 vector. In one exemplary embodiment, an rAd26 or rAd35 vector is used to prime the immune response, and an MVA vector is used to boost the immune response, or vice versa.

In a more preferred embodiment according to this method, an rAd26 vector is used for the priming followed by a boosting with an MVA vector. Preferably, the boosting composition is administered 1-12 weeks after priming, more preferably 1, 2, 4 or 8 weeks after priming. In a preferred embodiment, the boosting composition is administered 8 weeks after priming. In

another preferred embodiment, the boosting composition is administered 1 week after priming. In another preferred embodiment, the boosting composition is administered 2 weeks after priming. In another preferred embodiment, the boosting composition is administered 4 weeks after priming.

In a more preferred embodiment according to this method, an MVA vector is used for the priming followed by a boosting with an rAd26 vector. Preferably, the boosting composition is administered 1-12 weeks after priming, more preferably 1, 2, 4 or 8 weeks after priming. In a preferred embodiment, the boosting composition is administered 8 weeks after priming. In another preferred embodiment, the boosting composition is administered 1 week after priming. In another preferred embodiment, the boosting composition is administered 2 weeks after priming. In another preferred embodiment, the boosting composition is administered 4 weeks after priming.

The present invention is also related to methods of inducing immune responses against more than one subtype of filoviruses by priming and boosting the immune responses, preferably with a combination of heterologous vectors.

According to another aspect of the present invention, a method of inducing an immune response against a plurality of subtypes of filoviruses in a subject comprises:

a. administering to the subject an immunologically effective amount of a plurality of rAd26 or rAd35 vectors comprising a plurality of nucleic acids encoding glycoproteins or substantially similar glycoproteins of the plurality subtypes of filoviruses; and
b. administering to the subject an immunologically effective amount of a plurality of MVA vectors comprising a plurality of nucleic acids encoding the glycoproteins or the substantially similar glycoproteins,

wherein steps (a) and (b) are conducted in either order.

In one or more embodiments of the described method, a plurality of rAd26 or rAd35 vectors are used to prime the immune response, and a plurality of MVA vectors are used to boost the immune response, or vice versa.

In a preferred embodiment according to the method herein, a plurality of rAd26 vectors are used for the priming followed by a boosting with a plurality of MVA vectors. Preferably,

the boosting inoculation is administered 1-12 weeks after priming, more preferably 1, 2, 4 or 8 weeks after priming.

The antigens in the respective priming and boosting compositions (however many boosting compositions are employed) need not be identical, but should share antigenic determinants or be substantially similar to each other.

Administration of the immunogenic compositions comprising the vectors is typically intramuscular or subcutaneous. However other modes of administration such as intravenous, cutaneous, intradermal or nasal can be envisaged as well. Intramuscular administration of the immunogenic compositions may be achieved by using a needle to inject a suspension of the adenovirus vector. An alternative is the use of a needleless injection device to administer the composition (using, e.g., Biojector(TM)) or a freeze-dried powder containing the vaccine.

For intravenous, cutaneous or subcutaneous injection, or injection at the site of affliction, the vector will be in the form of a parenterally acceptable aqueous solution which is pyrogen-free and has suitable pH, isotonicity and stability. Those of 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 also be employed

Typically, administration will have a prophylactic aim to generate an immune response against a filovirus antigen 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. In other embodiments, the adenovirus and MVA vectors can be administered for post-exposure prophylactics.

The immunogenic compositions containing the adenovirus vectors are administered to a subject, giving rise to an anti-filovirus immune response in the subject. An amount of a composition sufficient to in induce a detectable immune response is defined to be an "immunologically effective dose." As shown below, the immunogenic compositions of the invention induce a humoral as well as a cell-mediated immune response. In a typical embodiment the immune response is a protective immune response.

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.

Following production of adenovirus and MVA vectors and optional formulation of such particles into compositions, the vectors may be administered to an individual, particularly human or other primate. Administration may be to humans, or another mammal, e.g., mouse, rat, hamster, guinea pig, rabbit, sheep, goat, pig, horse, cow, donkey, monkey, dog or cat. 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 the adenovirus or MVA vectors.

In one exemplary regimen, the adenovirus vector is administered (e.g., intramuscularly) in a volume ranging between about 100 µl to about 10 ml containing concentrations of about 10^4 to 10^{12} virus particles/ml. Preferably, the adenovirus vector is administered in a volume ranging between 0.25 and 1.0 ml. More preferably the adenovirus vector is administered in a volume of 0.5 ml.

Typically, the adenovirus is administered in an amount of about 10^9 to about 10^{12} viral particles (vp) to a human subject during one administration, more typically in an amount of about 10^{10} to about 10^{12} vp. In a preferred embodiment, the adenovirus vector is administered in an amount of about $5x10^{10}$ vp. In another preferred embodiment, the adenovirus vector is administered in an amount of about $0.8x10^{10}$ vp. In another preferred embodiment, the adenovirus vector is administered in an amount of about $2x10^{10}$ vp. In another preferred embodiment, the adenovirus vector is administered in an amount of about $4x10^{10}$ vp. In certain embodiments, adenoviruses are formulated as a trivalent composition, wherein three adenoviruses with each a different insert, are mixed together. In a trivalent composition, each distinct adenovirus is preferably present in an amount of about $4x10^{10}$ vp. In said trivalent

composition, the total number of adenovirus particles per dose amounts to about $1.2x10^{11}$ vp. In another preferred embodiment, each distinct adenovirus in the trivalent composition is present in an amount of about $1x10^{11}$ vp. In said trivalent composition the total number of adenovirus particles per dose then amounts to about $3x10^{11}$ vp. The initial vaccination is followed by a boost as described above.

In another exemplary regimen, the MVA vector is administered (*e.g.*intramuscularly) in a volume ranging between about 100 µl to about 10 ml of saline solution containing a dose of about $1x10^7$ $TCID_{50}$ to $1x10^9$ $TCID_{50}$ (50% Tissue Culture Infective Dose) or Inf.U. (Infectious Unit). Preferably, the MVA vector is administered in a volume ranging between 0.25 and 1.0 ml. More preferably the MVA vector is administered in a volume of 0.5 ml.

Typically, the MVA vector is administered in a dose of about $1x10^7$ $TCID_{50}$ to $1x10^9$ $TCID_{50}$ (or Inf.U.) to a human subject during one administration. In a preferred embodiment, the MVA vector is administered in an amount of about $5x10^7$ $TCID_{50}$ to $5x10^8$ $TCID_{50}$ (or Inf.U.). In a more preferred embodiment, the MVA vector is administered in an amount of about $5x10^7$ $TCID_{50}$ (or Inf.U.). In a more preferred embodiment, the MVA vector is administered in an amount of about $1x10^8$ $TCID_{50}$ (or Inf.U.). In another preferred embodiment, the MVA vector is administered in an amount of about $1.9x10^8$ $TCID_{50}$ (or Inf.U). In yet another preferred embodiment, the MVA vector is administered in an amount of about $4.4x10^8$ $TCID_{50}$ (or Inf.U.). In a more preferred embodiment, the MVA vector is administered in an amount of about $5x10^8$ $TCID_{50}$ (or Inf.U.)

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.

The compositions of the invention may be administered alone or in combination with other treatments, either simultaneously or sequentially dependent upon the condition to be treated.

EXAMPLES

The following examples are offered to illustrate, but not to limit the claimed invention.

Example 1

An animal study was conducted with a goal of identifying a multivalent filovirus vaccine with real efficacy ≥ 80% against multiple [e.g., Marburg, Ebola (aka Zaire) & Sudan] Filoviruses for continued advance development. The study tested an extended vaccination schedule using two or three vaccinations and impact of using heterologous (as opposed to homologous) vaccine combinations on subsequent NHP immune responses to the target Filoviruses. The vaccinated NHP was challenged with Ebola virus Kikwit to test the efficacy of the applied vaccinations.

Animal Manipulations

These studies complied with all applicable sections of the Final Rules of the Animal Welfare Act regulations (9 CFR Parts 1, 2, and 3) and *Guide for the Care and Use of Laboratory Animals – National Academy Press, Washington D.C. Eight Edition (the Guide).*

A total of 16 Cynomolgus macaques (Macaca fascicularis) (NHPs) (12 males and 4 females), Mauritian-origin, cynomolgus macaques, 4-5 years old, approx.. 4−8 kg each, were purchased from PrimGen (Hines, IL). Animals were experimentally naive to Reston virus (RESTV) by ELISA prior to vaccination. Animals with prior exposure to Mycobacterium tuberculosis, Simian Immunodeficiency Virus (SIV), Simian T-Lymphotropic Virus-1(STLV-1), Macacine herpesvirus 1 (Herpes B virus), and Simian Retrovirus (SRV1 and SRV2) were excluded, and active infections with Salmonella and Shigella were tested, and confirmed negative for *Mycobacterium tuberculosis*.

Filoviruses are Risk Group 4 (High Containment) Pathogens; therefore all manipulations involving Zaire ebolavirus, Sudan ebolavirus, or Marburgviruses were carried out in the CDC- accredited Biosafety Level (BSL)-4/Animal Biosafety Level (ABSL-4) containment facility.

Vaccine materials

The rAd vectors were manufactured by Crucell Holland B.V. They are purified E1/E3- deleted replication deficient recombinant Adenovirus type 26 or type 35 vaccine vectors (Ad26 and Ad35, respectively) containing the Filovirus Glycoprotein (GP) genes inserted at the E1 position. These vectors were rescued in PER.C6® cells, plaque purified,

upscaled and then purified by a two-step CsCl banding procedure and subsequently formulated in a TRIS-based formulation buffer and stored below -65°C. Release for in vivo use of these vectors includes bioburden test, low endotoxin level (<5EU/ml) and confirmation of expression and integrity of the transgene.

In particular, the rAd vectors expressed EBOV Mayinga GP (SEQ ID NO:1), SUDV Gulu GP (SEQ ID NO:2) and MARV Angola GP (SEQ ID NO:3). Each rAd vector expressed one single antigenic protein (GP).

The MVA vectors were manufactured by Bavarian Nordic. In particular, the MVA-multi vector (MVA-BN-Filo) expressed 4 different antigenic proteins: EBOV Mayinga GP (SEQ ID NO:1); SUDV Gulu GP (SEQ ID NO:2); MARV Musoke GP (SEQ ID NO:4); and Taï forest virus (TAFV) NP (SEQ ID NO:5).

The vaccine materials were stored at -80°C in a controlled temperature freezer.

Vaccination and Experimental Design

See Figures 1 and 2 for the study grouping and experimental design.

Cynomolgus macaques (Macaca fascicularis) (NHPs) were vaccinated using two different vaccine platforms, 2 animals per group, in addition to a control group consisting of two naïve (empty vector) challenge controls. Animals were first vaccinated with the recombinant vector(s) in groups shown in Figure 1. Each macaque was anesthetized and received an intramuscular (IM) injection of the vaccine into the left hind thigh. Priming and boosting doses were given 4 or 8 weeks apart (Fig.1). Each dose of adenoviruses consisted of a single IM injection into the left posterior thigh. The MVA vectors were administered subcutaneously.

EDTA or heparin whole blood were shipped overnight at room temperature to Texas Biomed on D28, D56 and D63. Additionally, Heparin or EDTA whole blood was collected on D77 while animals were housed at Texas Biomed. At all these time-points, EDTA whole blood will be processed for PBMC and plasma at Texas Biomed.

PBMC were used in an IFN-g ELISPOT assay using Ebola Zaire peptide pools 1 and 2, Sudan Gulu peptide pools 1 and 2, an Ebolavirus consensus peptide pool, Marburg Angola peptide pool 1 and 2 and a Marburgvirus consensus peptide pool, together with a DMSO only

negative control and an anti-CD3 stimulation positive control. All stimulations were performed in duplicate, for a total of 20 wells per NHP.

Additionally, whole blood without anticoagulant was processed for serum at Bioqual on D0, D28, D56 and D68, and on D77 at Texas Biomed. Aliquots of the serum collected at Bioqual will be sent frozen to Texas Biomed on D68. Each serum was assayed in a ZEBOV GP specific ELISA. Additionally, serum from D0, D56 and D77 were assayed in a SEBOV GP and a MARVA GP specific ELISA (two different assays).

Table 1: Parameters measured before challenge with Ebola virus

Parameter	Study weeks					
	0	4	8	9	10	11
PBMC and plasma processing		X	X	X		X
ZEBOV GP ELISA – all animals	X	X	X		X	X
SEBOV GP ELISA – all animals	X		X			X
MARVA GP ELISA – all animals	X		X			X
Filovirus ELISPOT – all animals		X	X	X		X

Filovirus Inoculum for Animal Challenges

As shown in Fig. 2, about 4 weeks after the boosting vaccination, the animals were challenged with EBOV. In particular, EBOV kikwit-9510621 was used for animal challenges and was supplied by Texas Biomed. A second cell-culture passage (P2) of EBOV kikwit-9510621 was obtained from Dr. Tom Ksiazek (at NIAID's WRCEVA at UTMB's Health Galveston National Laboratory) in 2012 and propagated at Texas Biomed for a third time in Vero E6 cells and had a titer of 2.1×10^5 PFU/ml. EBOV kikwit-9510621. LOT No. 2012099171.

Titer at harvest: 2.1×10^5 PFU/ml was used for the study.

The challenge stock has been confirmed to be wild-type EBOV kikwit 9510621 by deep sequencing with only 1 SNP difference from the Genbank P2 consensus sequence. The challenge stock was stored in liquid nitrogen vapor phase as 500 ± 50 µl aliquots containing media (MEM) containing 10% FBS. For a 100 PFU challenge, the filovirus challenge agent was diluted to a target dose of 200 PFU/ml in phosphate buffered saline. Briefly, stock virus was diluted via three consecutive 1:10 dilutions in PBS to achieve a 200 PFU/ml challenge material concentration. A total of 0.5 ml of challenge material was given to each animal.

Prior to virus injection, monkeys were sedated via intramuscular injection with Telazol (2 to 6 mg/kg; 5 to 8 mg/kg ketamine IM prn for supplemental anesthesia). On Study Day 0, blood was collected and each monkey was subsequently challenged with a targeted dose of 100 PFU of EBOV in a 0.5 ml volume via intramuscular injection in the right deltoid muscle of the arm. The challenge site was recorded.

Following virus administration, each monkey was returned to its home cage and observed until it has recovered from anesthesia (sternal recumbancy/ability to maintain an upright posture). Endpoints in this study were survival/nonsurvival. Nonsurvival is defined by an animal having terminal illness or being moribund. Animals' health was evaluated on a daily clinical observation score sheet.

Anti-EBOV GP IgG ELISA

Filovirus-specific humoral response was determined at time points described in table 1 by a modified enzyme-linked immunosorbent assay (ELISA), as previously described in Sulivan et al. (2006) (Immune protection of nonhuman primates against Ebola virus with single low-dose adenovirus vectors encoding modified GPs. PLoS Medicine 3, e177), which is incorporated by reference herein in its entirety. Briefly, ELISA plates were coated over night with Galanthus Nivalis Lectin at 10μg/ml. Then, after blocking, the plates were coated with either an Ebola or a Marburg strain specific GP supernatant. These supernatants were produced by transient transfection of Hek293T with expression plasmids coding for filovirus glycoprotein deleted of the transmembrane domain and cytoplasmic tail. Monkey serum samples were tested in a 4-fold dilution series starting at 1:50. Bound IgG was detected by colorimetry at 492nm. Relative serum titers were calculated against a filovirus glycoprotein strain specific reference serum. The results of the Elisa assay are shown in Figures 4-6.

IFN-g ELISPOT Assay

Filovirus-specific cellular immune response was determined at time points described in table 1 by interferon gamma Enzyme-linked immunospot assay (ELISPOT) as previously described in Ophorst et al. 2007 (Increased immunogenicity of recombinant Ad35-based malaria vaccine through formulation with aluminium phosphate adjuvant. Vaccine 25, 6501-6510), which is incorporated by reference herein in its entirety. The peptide pools used for

stimulation for each Ebola and Marburg strain glycoprotein consist of 15-mers overlapping by 11 amino acids. To minimize undesired effects of a too high number of peptides in a pool, each glycoprotein peptide pool was divided into two, one N-terminal and one C-terminal half.

Peptides that overlap with more than nine consecutive amino acids within three Ebolavirus (Zaire, Sudan and Taï Forest) or two Marburg virus (Marburg and Ravn viruses) were combined in a consensus pool. The peptide pools and single peptides were used at a final concentration of 1μg/ml for each single peptide. The results of the ELISPOT assay are shown in Figure 7.

As shown by results summarized in Figs 3-7, the animal study herein demonstrated the utility of rAd and MVA vectors in prime-boost combinations for preventing filovirus infections in primates. In particular, the administration of one or more rAd26 vectors expressing GP(s) of one or more types of filoviruses or MVA vectors expressing multiple filovirus antigens resulted in efficient priming of the humoral response to the one or more types of filoviruses. After boost immunization at week 8 with the heterologous vector, all vaccine regimes induced a similar humoral and cellular immune response to the one or more types of filoviruses and provided 100% protection against a highly pathogenic Ebola Zaire challenge.

Example 2

A second NHP study was performed to confirm the immunogenicity and protective efficacy of 2 prime-boost regimens at 0-4 week and at 0-8 week intervals. One comprising a monovalent Ad26.ZEBOV vaccine as a prime and a MVA-BN-Filo as a boost; the other one comprising a MVA-BN-Filo as a prime and an Ad26.ZEBOV as a boost. All immunizations were Intra muscular. Ad26.ZEBOV ($5x10^{10}$ vp) was used as a prime for the 0-8 week regimen, and was combined with a boost of $1x10^{8}$ $TCID_{50}$ of MVA-BN-Filo (4 NHPs) and $5x10^{8}$ $TCID_{50}$ MVA-BN-Filo (4 NHPs) to assess the impact of a standard and a high dose of MVA in this regimen. Two additional groups of 4 NHPs were primed with $1x10^{8}$ $TCID_{50}$ of MVA-BN-Filo and $5x10^{8}$ $TCID_{50}$ MVA-BN-Filo, respectively; in both cases followed by a boost with Ad26.ZEBOV ($5x10^{10}$ vp) after 4 weeks, to test the impact of the MVA-BN-Filo dose as a prime in a 4-week regimen. In addition, 2 NHPs were primed with Ad26.ZEBOV

($5x10^{10}$ vp) followed by $1x10^{8}$ $TCID_{50}$ of MVA-BN-Filo. Finally, 2 NHPs were immunized with empty Ad26 vector (not expressing any Filovirus antigens, $5x10^{10}$ vp IM) and TBS as negative immunization control for the study. All animals were challenged 4 weeks after the last immunization with 100 pfu of EBOV Kikwit 1995 wild-type P3 challenge virus. The grouping of this study is summarized in 2.

Table 2: Experimental Grouping of Protection Study in Non-human Primates Challenged With EBOV

Group	Immunization 1 (Dose 1)	Immunization 2 (Dose 2)	Immunization Schedule (Weeks)	Challenge After 4 Weeks	Survival Ratio (%)
1/A	Ad26.empty (5×10^{10} vp)	MVA negative control (TBS)	0 - 8	EBOV (Kikwit)	0/2 (0%)
2/B	Ad26.ZEBOV (5×10^{10} vp)	MVA-BN-Filo (5×10^{8} $TCID_{50}$)	0 - 8	EBOV (Kikwit)	**4/4 (100%)**
3/C	MVA-BN-Filo (5×10^{8} $TCID_{50}$)	Ad26.ZEBOV (5×10^{10} vp)	4 – 8	EBOV (Kikwit)	2/4 (50%)
4/D	Ad26.ZEBOV (5×10^{10} vp)	MVA-BN-Filo (1×10^{8} $TCID_{50}$)	0 – 8	EBOV (Kikwit)	**4/4 (100%)**
5/E	MVA-BN-Filo (1×10^{8} $TCID_{50}$)	Ad26.ZEBOV (5×10^{10} vp)	4 – 8	EBOV (Kikwit)	2/4 (50%)
6/F	Ad26.ZEBOV (5×10^{10} vp)	MVA-BN-Filo (1×10^{8} $TCID_{50}$)	4 – 8	EBOV (Kikwit)	**2/2 (100%)**

Abbreviations: TBS: Tris-buffered saline; $TCID_{50}$: 50% tissue culture infective dose; vp: viral particles.
100% survival are in bold.

Immunogenicity

The immune response in NHP is characterized with respect to Filovirus GP-binding and neutralizing antibodies (ELISA) as well as cytokine producing T cells (ELISpot).

ELISA:

EBOV Mayinga GP reactive antibodies were analyzed by GP-specific ELISA for all timepoints (see Figure 20).

The Anti-EBOV GP IgG ELISA was performed as described in experiment 1. ELISA titers were not observed in control-vaccinated animals. The vaccine regimens were immunogenic in all animals. The highest titers were observed in Group B, receiving Ad26.ZEBOV and a high dose of MVA-BN-Filo with an 8-week interval.

Protective Efficacy

Both 8-week Ad26.ZEBOV/MVA-BN-Filo prime/boost regimens resulted in complete survival after EBOV challenge, irrespective of the dose of MVA-BN-Filo (1×10^8 $TCID_{50}$ or 5×10^8 $TCID_{50}$). Additionally, a 4-week regimen of Ad26.ZEBOV/MVA-BN-Filo gave protection in 2 out of 2 NHPs. Both 4-week MVA-BN-Filo/Ad26.ZEBOV regimens gave protection in 2 out of 4 NHPs.

Example 3

A clinical study is performed in humans for evaluating the safety, tolerability and immunogenicity of regimens using MVA-BN-Filo at a dose of $1x10^8$ $TCID_{50}$ and Ad26.ZEBOV at a dose of $5x10^{10}$ vp. The study consisted of two parts.

The main study is a randomized, placebo-controlled, observer-blind study being conducted in 72 healthy adult subjects who never received an experimental Ebola candidate vaccine before and have no known exposure to an Ebola virus or diagnosis of Ebola disease. In this study 4 regimens are tested: 2 regimens have MVA-BN-Filo as prime and Ad26.ZEBOV as boost at a 28- or 56-day interval, and 2 regimens have Ad26.ZEBOV as prime and MVA-BN-Filo as boost at a 28- or 56-day interval.

The substudy consists of an open-label, uncontrolled non-randomized treatment arm evaluating the safety, tolerability and immunogenicity of a regimen with Ad26.ZEBOV at a dose of $5x10^{10}$ vp as prime, and MVA-BN-Filo at a dose of $1x10^8$ $TCID_{50}$ as boost 14 days later, and is conducted in 15 healthy adult subjects.

The study consists of a vaccination period in which subjects are vaccinated at baseline (Day 1) followed by a boost on Day 15, 29 or 57, and a post-boost follow-up until all subjects have had their 21-day post-boost visit (Day 36, 50 or 78) or discontinued earlier.

Subjects in the main study are enrolled into 4 different groups of 18 healthy subjects each. Overall, subjects are randomized within a group in a 5:1 ratio to receive active vaccine or placebo (0.9% saline) through IM injections (0.5 ml) as follows:

- MVA-BN-Filo ($1x10^8$ $TCID_{50}$) on Day 1, followed by a booster of Ad26.ZEBOV ($5x10^{10}$ vp) on Day 29 (Group 1) or Day 57 (Group 2), or

- Ad26.ZEBOV ($5x10^{10}$ vp) on Day 1, followed by a booster of MVA-BN-Filo ($1x10^{8}$ $TCID_{50}$) on Day 29 (Group 3) or Day 57 (Group 4).

The 15 subjects in the substudy receive active vaccine through IM injections (0.5 ml) as follows:

- Ad26.ZEBOV ($5x10^{10}$ vp) on Day 1, followed by a booster of MVA-BN-Filo ($1x10^{8}$ $TCID_{50}$) on Day 15 (Group 5).

The exemplary study vaccination schedules are summarized in Table 3.

Table 3 : Study Vaccination Schedules

Group	N		Day 1	Day 15	Day 29	Day 57
1	18	15	MVA-BN-Filo $1x10^{8}$ $TCID_{50}$	-	Ad26.ZEBOV $5x10^{10}$ vp	-
		3	placebo (0.9% saline)	-	placebo (0.9% saline)	-
2	18	15	MVA-BN-Filo $1x10^{8}$ $TCID_{50}$	-	-	Ad26.ZEBOV $5x10^{10}$ vp
		3	placebo (0.9% saline)	-	-	placebo (0.9% saline)
3	18	15	Ad26.ZEBOV $5x10^{10}$ vp	-	MVA-BN-Filo $1x10^{8}$ $TCID_{50}$	-
		3	placebo (0.9% saline)	-	placebo (0.9% saline)	-
4	18	15	Ad26.ZEBOV $5x10^{10}$ vp	-	-	MVA-BN-Filo $1x10^{8}$ $TCID_{50}$
		3	placebo (0.9% saline)	-	-	placebo (0.9% saline)
5	15		Ad26.ZEBOV $5x10^{10}$ vp	MVA-BN-Filo $1x10^{8}$ $TCID_{50}$	-	-

N: number of subjects to receive study vaccine; $TCID_{50}$: 50% Tissue Culture Infective Dose; vp: viral particles

Safety is assessed by collection of solicited local and systemic adverse events, unsolicited adverse events and serious adverse events, and by physical examination. In addition, standard chemistry, hematologic (including coagulation parameters) and urinalysis parameters are assessed at multiple time points.

Immunogenicity is assessed using the immunologic assays summarized in Tables 4 and 5. The exploratory assay package may include, but is not limited to, the listed assays.

Table 4: Summary of Immunologic Assays (Serology)

Assay	Purpose
Secondary endpoints	
Virus neutralization assay	Analysis of neutralizing antibodies to EBOV GP
ELISA	Analysis of antibodies binding to EBOV GP
Exploratory endpoints	
Adenovirus/MVA neutralization assay	Neutralizing antibodies to adenovirus/MVA
Molecular antibody characterization	Analysis of anti-EBOV GP, SUDV GP, MARV GP and/or TAFV NP antibody characteristics, including IgG subtyping
Exploratory ELISA	Analysis of binding antibodies to a different source of EBOV GP

EBOV: Ebola virus; ELISA: enzyme-linked immunosorbent assay; GP: glycoprotein; IgG: immunoglobulin G; MARV: Marburg virus; MVA: Modified Vaccinia Ankara; NP: nucleoprotein; SUDV: Sudan virus; TAFV: Taï Forest virus

Table 5: Summary of Immunologic Assays (Cellular)

Assay	Purpose
Secondary endpoints	
ELISpot	T-cell IFN-γ responses to EBOV GP
Exploratory endpoints	
ICS of frozen PBMC	Analysis of T-cell responses to EBOV GP, SUDV GP, MARV GP and/or TAFV NP (including CD4/8, IL-2, IFN-γ, TNF-α and/or activation markers)
ICS and/or ELISpot of fresh PBMC	Analysis of T cell responses to EBOV GP including CD4-positive and low-magnitude T cell responses

EBOV: Ebola virus; ELISpot: enzyme-linked immunospot; GP: glycoprotein; ICS: intracellular cytokine staining; IFN: interferon; IL: interleukin; MARV: Marburg virus; NP: nucleoprotein; PBMC: peripheral blood mononuclear cells; SUDV: Sudan virus; TAFV: Taï Forest virus; TNF: tumor necrosis factor

The clinical study is on-going. Some of the initial results are described below.

Safety assessment

Safety was assessed by collection of solicited local and systemic adverse events, unsolicited adverse events and serious adverse events, and by physical examination. In addition, standard chemistry, hematologic (including coagulation parameters) and urinalysis parameters were assessed at multiple time points.

The safety data from this first in human showed that both vaccines appear to be well-tolerated at this stage with transient reactions normally expected from vaccination. No significant adverse events were associated with the vaccine regimen. The majority of events were mild, occurring one to two days post-vaccination, and lasting one to two days on average. Very few cases of fever were observed.

Assessment of immune response

Immunogenicity was assessed up to 21 days post-boost immunization using an ELISA assay to analyze antibodies binding to EBOV GP, an ELISpot assay to analyze an EBOV GP-specific T cell response, and ICS assays to detect CD4+ and CD8+ T-cell responses to EBOV GP. Samples for the analysis of the humoral and cellular immune response induced by the study vaccines were collected on Days 1, 8, 29, 36 and 50 in Groups 1 and 3 and on Days 1, 8, 29, 57, 64 and 78 for Groups 2 and 4.

Assessment of humoral immune response

The binding antibody responses induced by study vaccines was assessed by an anti-EBOV GP ELISA assay (Fig. 8). Importantly, all subjects who have received a vaccine regimen showed seroconversion at 21 days post-boost immunization. A robust immunogenic response has been observed in all immunized subjects.

While the EBOV GP-specific immune response post-prime with MVA-BN-Filo was only observed at low levels in 7 to 40% of the subjects , a strong antigen-specific response was observed post-boost with Ad26.ZEBOV administered at 28 days or 56 days post-prime. Surprisingly, this response is of higher magnitude than the one induced by the reverse vaccine regimen at the same prime-boost time interval (Group 3 and Group 4, Ad26.ZEBOV prime followed by MVA-BN-Filo boost 28 or 56 days later, respectively) at 21 days post-boost immunization [Geometric mean titers with 95% confidence interval of EU/mL 10573 (6452; 17327) and 4274 (2350; 7775) for groups 1 and 3 ,respectively, and 18729 (12200; 28751) and 7553 (511; 1115) for groups 2 and 4, respectively].

It must be noted that in nonhuman primate (NHP), boosting an MVA prime with Ad26 had resulted in an EBOV GP-specific immune response that was comparable in magnitude to that induced by the reverse vaccine regimen (Ad/MVA), at the same prime-boost time interval (see Fig. 4) or that was inferior in magnitude (Fig. 20). Thus, the immune responses observed for one specific prime-boost regimen in NHP were not predictive for the immune responses observed following that same prime-boost regimen in humans.

Assessment of cellular immune response

The EBOV GP-specific cellular immune response was measured by interferon gamma (IFN-γ) ELISpot and ICS. To assess the cellular immune response, stored PBMC (peripheral blood mononuclear cells) were thawed and stimulated with peptides organized in 2 pools (Pools 1 and 2). The sum of the T-cell responses stimulated per pool are shown in Figure 9.

By ELISpot analysis (Fig. 9), an IFN-γ response could readily be detected in 50 to 60% of the subjects at day 29 after prime immunization with Ad26.ZEBOV (median IFN-γ response 103 and 58 spots forming units per million PBMC for Group 3 and 4, respectively) and in 86% of the subjects at day 57 post Ad26.ZEBOV prime immunization (Group 4, median IFN-γ response 283 spots forming units per million (SFU/10^6) PBMC). These responses were further boosted by immunization on Day 29 or Day 57 with MVA-BN-Filo (87% responders, median IFN-γ response 463 SFU/10^6 PBMC for Group 3, 86% responders, 648 SFU/10^6 PBMC for Group 4) and maintained at that level up to day 21 post-boost (79% responders, median IFN-γ response 390 SFU/10^6 PBMC for Group 3 and 100% responders, 464 SFU/10^6 PBMC for Group 4).

Results for the cellular assays measuring specific CD4+ and CD8+ T cell responses by ICS are shown in Figures 10-15.

As expected, no EBOV GP-specific CD8+ or CD4+ T cell response was observed in placebo immunized individuals (Figs. 10 and 13). No CD8+ cytokine responses were observed on Day 29 or Day 57 after prime immunization with MVA-BN-Filo (Group 1 and 2). However, a vaccine-induced CD8+ T cell response was observed in 53% of subjects 7 days post-boost with Ad26.ZEBOV (median total cytokine response: 0.08% and 0.07%, when Ad26 boost immunization administered at day 29 or day 57, respectively; Fig. 10). This response was maintained at day 21 post boost immunization (median total cytokine response: 0.1% and 0.06%, when Ad26 boost immunization administered at day 29 or day 57, respectively; Fig. 10). In comparison, 57% of subjects receiving a prime immunization with Ad26.ZEBOV (Group 3 and Group 4) showed at Day 29 a CD8+ T cell response (median total cytokine response: 0.12 and 0.05%, respectively), 86% of the subjects at day 57 post Ad26.ZEBOV prime immunization (Group 4) showed a CD8+ T cell response (median total cytokine response: 0.19%). This response was further enhanced after boost immunization with

MVA-BN-Filo on day 29, with 67% and 73% of subjects responding 7 and 21 days post-boost, respectively (median response: 0.27% on both days).

Surprisingly, while a smaller percentage of responders was observed in Group 1 (MVA-Ad26 prime-boost 0-28 day schedule) compared to Group 3 (Ad26-MVA prime-boost 0-28 day schedule), the proportion of polyfunctional CD8+ T cells (CD8+ T cells expressing more than one cytokine) induced by the MVA-Ad26 prime-boost regimen in these responders was higher post-boost than that induced by the Ad26-MVA prime-boost regimen (Fig. 11). This difference was not observed when the prime and boost were administered at day 57. Using this schedule, both the MVA prime Ad26 boost (Group 2) and the Ad26 prime MVA boost (Group 4) regimens induced similarly high proportion of polyfunctional CD8+ T cells (Fig.12).

Surprisingly, prime immunization with MVA-BN-Filo followed by a boost with Ad26.ZEBOV given at 28 days interval (Group 1) induced a very robust CD4+ T cell response which peaked 7 days post-boost immunization (93% responders, median total cytokine response 0.37%; Fig. 13). At the peak, this CD4+ T cell response was of a higher magnitude than that seen in Group 3 after prime immunization with Ad26.ZEBOV followed by a MVA-BN-Filo boost at 28 days interval (67% responders, median total cytokine response 0.11%). 21 days post-boost, the CD4+ T cell responses induced by both regimens were comparable. Extending the interval of the MVA-BN-Filo/Ad26.ZEBOV regimen to 56 days resulted in lower CD4+ T cell responses. The Ad26.ZEBOV/MVA-BN-Filo regimen induced slightly lower CD4+ T cell responses at a 28-day interval and comparable responses at a 56-day interval. The CD4+ T cells induced by both vaccine combinations were predominantly polyfunctional (Fig. 14 and 15).

Results of the substudy assessing the immunogenicity of a prime with Ad26.ZEBOV at $5x10^{10}$ vp followed by a boost 14 days later using $1x10^{8}$ $TCID_{50}$ of MVA-BN-Filo are summarized below.

Overall, this relatively short regimen using a 14-days interval between prime and boost has been shown to be immunogenic. The humoral immune response to vaccinations was assessed by ELISA. As observed for longer intervals, all subjects seroconverted by 21 days

post boost immunization (Figure 16A). Furthermore, a cellular immune response was observed by ELISpot in 92% of the subjects 21 days post boost immunization (Figure 16B). This cellular immune response consisted of both CD4+ (67% responders, median response 0.08% at day 21 post boost) and CD8+ (64% responders, median response 0.15% at day 7 post boost) specific T cells. The immune response induced using a 2 weeks interval appeared somewhat lower than the response induced when using longer intervals between prime and boost (refer to previous section).

Example 4

A randomized, placebo-controlled, observer-blind study (preceded by an initial open-label vaccination of a total of 6 sentinel study subjects) is performed to evaluate the safety, tolerability and immunogenicity of a heterologous regimen of (a) a single dose of MVA-BN-Filo ($1x10^8$ $TCID_{50}$) or placebo (0.9% saline) as prime followed by a single dose of Ad26.ZEBOV ($5x10^{10}$ vp) or placebo as boost at different time points (14, 28, or 56 days after prime; Groups 1 to 3) and (b) a single dose of Ad26.ZEBOV ($5x10^{10}$ vp) or placebo as prime followed by a single dose of MVA-BN-Filo ($1x10^8$ $TCID_{50}$) or placebo as boost at 28 days after prime (Group 4).

In order to assess the safety of the 2 vaccines independently, Groups 5 and 6 are included where homologous regimens of 2 single doses of MVA-BN-Filo ($1x10^8$ $TCID_{50}$) or placebo, or 2 single doses of Ad26.ZEBOV ($5x10^{10}$ vp) or placebo are administered with the shorter prime-boost schedule of 1 and 15 days. This study is conducted in a target of approximately 92 healthy subjects, aged between 18 and 50 years (inclusive) who have never received an experimental Ebola candidate vaccine before and have no known exposure to or diagnosis of Ebola disease.

The study consists of a vaccination period in which subjects are vaccinated at their baseline visit (Day 1) followed by a boost on Day 15, 29, or 57, and a post-boost follow-up period until all subjects have had their 21-day post-boost visit, or discontinued earlier. At that time, the study will be unblinded.

Subjects are enrolled in 6 different groups, comprising 18 (Groups 1 to 4) or 10 (Groups 5 and 6) healthy subjects each. Within Groups 1 to 4, subjects are randomized in a

5:1 ratio to receive active vaccine or placebo throughout the study. Groups 5 and 6 each start with a Sentinel Cohort of 3 subjects who receive active vaccine in an open-label fashion, followed by a blinded cohort of 7 subjects, who are randomized in a 6:1 ratio to receive active vaccine or placebo. The study vaccination schedules in the different groups are summarized in Table 6.

Safety is assessed by collection of solicited local and systemic adverse events, unsolicited adverse events and serious adverse events, and by physical examination. In addition, standard chemistry, hematologic (including coagulation parameters) and urinalysis parameters are assessed at multiple time points.

Immunogenicity is assessed using the immunologic assays summarized in Table 7 and 8. The exploratory assay package may include, but is not limited to, the listed assays.

Table 6: Study Vaccination Schedules

Group	N	n	Day 1	Day 15	Day 29	Day 57
1	18	15	MVA-BN-Filo	Ad26.ZEBOV		
		3	Placebo	Placebo		
2	18	15	MVA-BN-Filo		Ad26.ZEBOV	
		3	Placebo		Placebo	
3	18	15	MVA-BN-Filo			Ad26.ZEBOV
		3	Placebo			Placebo
4	18	15	Ad26.ZEBOV		MVA-BN-Filo	
		3	Placebo		Placebo	
5	10	3	MVA-BN-Filo *(sentinel)*	MVA-BN-Filo *(sentinel)*		
		6	MVA-BN-Filo	MVA-BN-Filo		
		1	Placebo	Placebo		
6	10	3	Ad26.ZEBOV *(sentinel)*	Ad26.ZEBOV *(sentinel)*		
		6	Ad26.ZEBOV	Ad26.ZEBOV		
		1	Placebo	Placebo		

N: number of subjects to receive study vaccine
MVA-BN-Filo dose level is $1x10^8$ $TCID_{50}$ (50% Tissue Culture Infective Dose) in all groups; Ad26.ZEBOV dose level is $5x10^{10}$ vp (viral particles) in all groups; Placebo is 0.9% saline

Table 7: Summary of Immunologic Assays (Serology)

Assay	Purpose
Secondary endpoints	
Virus neutralization assay	Analysis of neutralizing antibodies to EBOV GP
ELISA	Analysis of antibodies binding to EBOV GP
Exploratory endpoints	
Adenovirus/MVA neutralization assay	Neutralizing antibodies to adenovirus/MVA
Molecular antibody characterization	Analysis of anti-EBOV GP, SUDV GP, MARV GP and/or TAFV NP antibody characteristics, including IgG subtyping
Exploratory ELISA	Analysis of binding antibodies to a different source of EBOV GP

EBOV: Ebola virus; ELISA: enzyme-linked immunosorbent assay; GP: glycoprotein; IgG: immunoglobulin G; MARV: Marburg virus; MVA: Modified Vaccinia Ankara; NP: nucleoprotein; SUDV: Sudan virus; TAFV: Taï Forest virus

Table 8: Summary of Immunologic Assays (Cellular)

Assay	Purpose
Secondary endpoints	
ELISpot	T-cell IFN-γ responses to EBOV GP
Exploratory endpoints	
ICS of frozen PBMC	Analysis of T-cell responses to EBOV GP, SUDV GP, MARV GP and/or TAFV NP (including CD4/8, IL-2, IFN-γ, TNF-α and/or activation markers)
ICS and/or ELISpot of fresh PBMC	Analysis of T cell responses to EBOV GP including CD4-positive and low-magnitude T cell responses

EBOV: Ebola virus; ELISpot: enzyme-linked immunospot; GP: glycoprotein; ICS: intracellular cytokine staining; IFN: interferon; IL: interleukin; MARV: Marburg virus; NP: nucleoprotein; PBMC: peripheral blood mononuclear cells; SUDV: Sudan virus; TAFV: Taï Forest virus; TNF: tumor necrosis factor

The clinical study is ongoing. Some of the initial results are described below.

Assessment of humoral immune response

Initial results confirm the immunogenicity of the combination of Ad26.ZEBOV at $5x10^{10}$ vp and MVA-BN-Filo at $1x10^{8}$ $TCID_{50}$ when either vaccine is used as a prime and the other as a boost.

As shown in Figure 17, all subjects seroconverted 21 days post boost immunization when assessed by ELISA. Similar to previous experiments, a higher immune response was observed at 21 days post boost immunization when MVA was used as a prime and Ad26 administered as a boost 28 days later (Group 2, Geometric Mean Concentration of EU/mL 6987) compared to the reverse order of vaccine immunization (Group 4, Geometric Mean Concentration of EU/mL 2976).

The strength of the humoral immune response correlated with the interval between the prime and the boost, with higher antibody concentrations observed when using a 56 days interval between MVA prime and Ad26 boost (group 3, Geometric Mean Concentration of EU/mL 14048) compared to a shorter schedule (group 1, 14 days interval, Geometric Mean Concentration of EU/mL 4418 and group 2, 28 days interval, Geometric Mean Concentration of EU/mL 6987).

Surprisingly, a robust humoral immune response as assessed by ELISA was observed when MVA-BN-Filo was used as a prime and followed by a boost immunization with Ad26.ZEBOV 14 days later. All subjects receiving the vaccine regimen seroconverted by 21 days post boost immunization, and the antibody concentration at this time point reached similar or higher levels than when using the Ad26 prime MVA boost combination at a 28 day intervals (Geometric Mean Titer of EU/mL 4418 and 2976, respectively). Surprisingly, the antibody concentrations induced by this MVA/Ad26 prime boost combination at 14 days interval were strikingly higher than the response induced by the reverse vaccine regimen at the same prime-boost time interval (refer to example 2, figure 16A, Geometric Mean Concentration of EU/mL 915). This confirms the induction of a robust immune response by an MVA prime Ad26 boost combination and the advantage of such combination when using a short prime boost interval (14 days).

Assessment of cellular immune response

The EBOV GP-specific cellular immune response was measured by interferon gamma (IFN-γ) ELISpot and ICS. To assess the cellular immune response, stored PBMC (peripheral blood mononuclear cells) were thawed and stimulated with peptides organized in 2 pools (Pools 1 and 2). The sum of the T cell responses stimulated per pool are shown in Figures 18-19.

ELISpot analysis (Fig. 18) confirmed the induction of an IFN-γ response using both Ad26.ZEBOV prime followed by MVA-BN-Filo boost or the reverse vaccine regimen. For all prime boost interval studies, the cellular response was enhanced after the boost immunization. The IFN-γ response was highest when using Ad26 as a prime followed by MVA as a boost 28

days later (87% responders, median IFN-γ response 687 and 600 SFU/10^6 PBMC for Group 4 at day 7 and day 21 post boost, respectively). Surprisingly, when using MVA-BN-Filo as a prime followed by Ad26.ZEBOV as a boost, a stronger IFN-γ response was observed when using a shorter 14 days interval between prime and boost (87 and 93% responders, 395 and 577 SFU/10^6 PBMC for Group 1 at day 7 and 21 post boost, respectively) compared to the response induced by a 28 days (Group 2, 73 and 67% responders, median IFN-γ response 427 and 375 SFU/10^6 PBMC for day 7 and day 21 post boost) or 56 days interval (Group 3, 47% responders, median IFN-γ response 118 and 153 SFU/10^6 PBMC for day 7 and day 21 post boost).

Remarkably, the cellular immune response induced by the MVA-BN-Filo prime Ad26.ZEBOV boost at a 14 days interval was well balanced with both EBOV GP-specific CD8+ and CD4+ T cell response (73% responders for both CD4+ and CD8+ T cells, CD4+ median total cytokine response 0.15 and 0.19% at day 7 and 21 post boost, respectively; CD8+ median total cytokine response 0.19 and 0.34% at day 7 and 21 post boost, respectively; Fig. 19 A and B). Both the CD8+ and CD4+ T cells induced by this vaccine combination were predominantly polyfunctional (Fig. 19 C and D).

The following tables 9-12 are presented as summaries of the clinical studies presented herein. The studies presented in example 3 and 4 are numbered study 1001 and 1002 respectively.

Table 9 is a summary of the humoral immune responses as determined in ELISA assays during the studies as described in example 3 and 4.

Table 9: Overview of ELISA titers in clinical studies

Study Day	Ad26/ MVA 0, 14	Ad26/ MVA 0, 28	Ad26/ MVA 0, 28	Ad26/ MVA 0, 56	MVA/ Ad26 0, 14	MVA/ Ad26 0, 28	MVA/ Ad26 0, 28	MVA/ Ad26 0, 56
Study	**1001**	**1001**	**1002**	**1001**	**1002**	**1001**	**1002**	**1001**
d8	22 (13)	18 (0)	20 (7)	22 (0)	19 (7)	18 (0)	22 (0)	21 (0)
d15	164 (79)*	-	-	-	22 (13)*	-	-	-
d22	298 (83)	-	-	-	293 (87)	-	-	-
d29	-	533 (93)*	477 (100)*	582 (100)	-	36 (40)*	55 (47)*	22 (7)
d36	**915 (100)**	946 (100)	965 (100)	-	**4418 (100)**	269 (80)	1025 (93)	-
d50	-	**4274 (100)**	**2976 (100)**	-	-	**10573 (100)**	**6987 (100)**	-
d57	-	-	-	854 (100)*	-	-	-	21 (7)*
d64	-	-	-	1554 (100)	-	-	-	568 (100)
d78	-	-	-	**7553 (100)**	-	-	-	**18729 (100)**

The data are presented as geometric mean concentration (GMC) in ELISA per mL. Percentage of responders at each time points is indicated in brackets;. Ad26: Immunization with Ad26.ZEBOV; MVA: Immunization with MVA-BN-Filo; Prime boost schedule is indicated in headers. 0, 14: 14 days interval between prime and boost immunizations; 0, 28: 28 days interval between prime and boost immunizations; 0, 56: 56 days interval between prime and boost immunizations; *: day of boost; GMC: Geometric Mean Concentration. Study 1001 was described in example 3 and study 1002 was described in example 4.

Table 10 is a summary of the cellular immune responses as determined in ELISpot assays during the studies as described in example 3 and 4.

Table 10: Overview of cellular immune responses in clinical studies as determined by ELISpot

Study Day	Ad26/ MVA 0, 14	Ad26/ MVA 0, 28	Ad26/ MVA 0, 56	MVA/ Ad26 0, 14	MVA/ Ad26 0, 28	MVA/ Ad26 0, 56
Study	**1001**	**1001**	**1001**	**1002**	**1001**	**1001**
d8	25 (13)	25 (7)	25 (7)	25 (13)	25 (0)	25 (0)
d15	113 (79)*	-	-	52 (20)*	-	-
d22	354 (75)	-	-	**293 (87)**	-	-
d29	-	103 (60)*	58 (50)	-	25 (7)*	25 (0)
d36	203 (92)	**463 (87)**	-	**552 (100)**	**882 (93)**	-
d50	-	**390 (79)**	-	-	**455 (73)**	-
d57	-	-	243 (86)*	-	-	25 (0)*
d64	-	-	**648 (86)**	-	-	**440 (100)**
d78	-	-	**464 (100)**	-	-	**238 (87)**

Data are represented as median SFU/10^6 PBMC. Percentage of responders at each time points is indicated in brackets; Ad26: Immunization with Ad26.ZEBOV; MVA: Immunization with MVA-BN-Filo; Prime boost schedule is indicated in headers. 0, 14: 14 days interval between prime and boost immunizations; 0, 28: 28 days interval between prime and boost immunizations; 0, 56: 56 days interval between prime and boost immunizations; *: day of boost; SFU: Spot Forming Units; PBMC: Peripheral blood mononuclear cells. Study 1001 was described in example 3 and study 1002 was described in example 4. Study 1001 was described in example 3 and study 1002 was described in example 4.

Table 11 is a summary of CD4+ T cell responses as determined by intracellular cytokine staining (ICS) during the studies as described in example 3 and 4.

Table 11: Overview of the CD4+ T cell immune response as measured by ICS in clinical studies

Study Day	Ad26/ MVA 0, 14	Ad26/ MVA 0, 28	Ad26/ MVA 0, 56	MVA/ Ad26 0, 14	MVA/ Ad26 0, 28	MVA/ Ad26 0, 56
Study	**1001**	**1001**	**1001**	**1002**	**1001**	**1001**
d8	0.02 (0)	0.02 (0)	0.02 (0)	0.02 (0)	0.02 (0)	0.02 (0)
d15	0.06 (36)*	-	-	0.02 (7)*	-	-
d22	0.06 (45)	-	-	**0.15 (73)**	-	-
d29	-	0.07 (43)*	0.06 (31)	-	0.02 (13)*	0.02 (7)
d36	0.08 (67)	**0.11 (64)**	-	**0.19 (73)**	**0.37 (93)**	-
d50	-	**0.15 (60)**	-	-	**0.16 (67)**	-
d57	-	-	0.05 (36)*	-	-	0.02 (0)*
d64	-	-	**0.16 (71)**	-	-	**0.17 (67)**
d78	-	-	**0.12 (57)**	-	-	**0.08 (53)**

Data are represented as median total CD4+ cytokine response in %. Percentage of responders at each time points is indicated in brackets; Ad26: Immunization with Ad26.ZEBOV; MVA: Immunization with MVA-BN-Filo; Prime boost schedule is indicated in headers. 0, 14: 14 days interval between prime and boost immunizations; 0, 28: 28 days interval between prime and boost immunizations; 0, 56: 56 days interval between prime and boost immunizations; *: day of boost. Study 1001 was described in example 3 and study 1002 was described in example 4.

Table 12 is a summary of CD8+ T cell responses as determined by intracellular cytokine staining (ICS) during the studies as described in example 3 and 4.

Table 12: Overview of the CD8+ T cell immune response as measured by ICS in clinical studies

Study Day	Ad26/ MVA 0, 14	Ad26/ MVA 0, 28	Ad26/ MVA 0, 56	MVA/ Ad26 0, 14	MVA/ Ad26 0, 28	MVA/ Ad26 0, 56
Study	**1001**	**1001**	**1001**	**1002**	**1001**	**1001**
d8	0.02 (0)	0.02 (0)	0.02 (0)	0.02 (0)	0.02 (0)	0.02 (0)
d15	0.02 (29)*	-	-	0.02 (0)*	-	-
d22	0.15 (64)	-	-	**0.19 (73)**	-	-
d29	-	0.12 (57)*	0.05 (57)	-	0.02 (0)*	0.02 (0)
d36	0.07 (50)	**0.27 (67)**	-	**0.34 (73)**	0.08 (53)	-
d50	-	**0.27 (73)**	-	-	0.1 (53)	-
d57	-	-	0.19 (86)*	-	-	0.02 (0)*
d64	-	-	**0.24 (86)**	-	-	0.07 (53)
d78	-	-	**0.24 (79)**	-	-	0.06 (47)

Data are presented as median total CD8+ cytokine response in %. Percentage of responders at each time points is indicated in brackets;. Ad26: Immunization with Ad26.ZEBOV; MVA: Immunization with MVA-BN-Filo; Prime boost schedule is indicated in headers. 0, 14: 14 days interval between prime and boost immunizations; 0, 28: 28 days interval between prime and boost immunizations; 0, 56: 56 days interval between prime and boost immunizations; *: day of boost. Study 1001 was described in example 3 and study 1002 was described in example 4.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims.

SEQUENCE LISTING

SEQ ID NO:1
Glycoprotein Ebola virus Zaire, strain Mayinga (Amino Acid sequence):

MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQVSDVDKLVCRDKLSSTNQLR
SVGLNLEGNGVATDVPSATKRWGFRSGVPPKVVNYEAGEWAENCYNLEIKKPDGSECLPAAPDG
IRGFPRCRYVHKVSGTGPCAGDFAFHKEGAFFLYDRLASTVIYRGTTFAEGVVAFLILPQAKKD
FFSSHPLREPVNATEDPSSGYYSTTIRYQATGFGTNETEYLFEVDNLTYVQLESRFTPQFLLQL
NETIYTSGKRSNTTGKLIWKVNPEIDTTIGEWAFWETKKNLTRKIRSEELSFTVVSNGAKNISG
QSPARTSSDPGTNTTTEDHKIMASENSSAMVQVHSQGREAAVSHLTTLATISTSPQSLTTKPGP
DNSTHNTPVYKLDISEATQVEQHHRRTDNDSTASDTPSATTAAGPPKAENTNTSKSTDFLDPAT
TTSPQNHSETAGNNNTHHQDTGEESASSGKLGLITNTIAGVAGLITGGRRTRREAIVNAQPKCN
PNLHYWTTQDEGAAIGLAWIPYFGPAAEGIYIEGLMHNQDGLICGLRQLANETTQALQLFLRAT
TELRTFSILNRKAIDFLLQRWGGTCHILGPDCCIEPHDWTKNITDKIDQIIHDFVDKTLPDQGD
NDNWWTGWRQWIPAGIGVTGVIIAVIALFCICKFVF

SEQ ID NO:2
Glycoprotein Ebola virus Sudan, strain Gulu (Amino Acid sequence):

MGGLSLLQLPRDKFRKSSFFVWVIILFQKAFSMPLGVVTNSTLEVTEIDQLVCKDHLASTDQLK
SVGLNLEGSGVSTDIPSATKRWGFRSGVPPKVVSYEAGEWAENCYNLEIKKPDGSECLPPPPDG
VRGFPRCRYVHKAQGTGPCPGDYAFHKDGAFFLYDRLASTVIYRGVNFAEGVIAFLILAKPKET
FLQSPPIREAVNYTENTSSYYATSYLEYEIENFGAQHSTTLFKIDNNTFVRLDRPHTPQFLFQL
NDTIHLHQQLSNTTGRLIWTLDANINADIGEWAFWENKKNLSEQLRGEELSFEALSLNETEDDD
AASSRITKGRISDRATRKYSDLVPKNSPGMVPLHIPEGETTLPSQNSTEGRRVGVNTQETITET
AATIIGTNGNHMQISTIGIRPSSSQIPSSSPTTAPSPEAQTPTTHTSGPSVMATEEPTTPPGSS
PGPTTEAPTLTTPENITTAVKTVLPQESTSNGLITSTVTGILGSLGLRKRSRRQTNTKATGKCN
PNLHYWTAQEQHNAAGIAWIPYFGPGAEGIYTEGLMHNQNALVCGLRQLANETTQALQLFLRAT
TELRTYTILNRKAIDFLLRRWGGTCRILGPDCCIEPHDWTKNITDKINQIIHDFIDNPLPNQDN
DDNWWTGWRQWIPAGIGITGIIIAIIALLCVCKLLC

SEQ ID NO:3
Glycoprotein Marburg virus Angola (Amino Acid sequence):

MKTTCLLISLILIQGVKTLPILEIASNIQPQNVDSVCSGTLQKTEDVHLMGFTLSGQKVADSPL
EASKRWAFRAGVPPKNVEYTEGEEAKTCYNISVTDPSGKSLLLDPPTNIRDYPKCKTIHHIQGQ
NPHAQGIALHLWGAFFLYDRIASTTMYRGKVFTEGNIAAMIVNKTVHKMIFSRQGQGYRHMNLT
STNKYWTSSNGTQTNDTGCFGTLQEYNSTKNQTCAPSKKPLPLPTAHPEVKLTSTSTDATKLNT
TDPNSDDEDLTTSGSGSGEQEPYTTSDAATKQGLSSTMPPTPSPQPSTPQQGGNNTNHSQGVVT
EPGKTNTTAQPSMPPHNTTTISTNNTSKHNLSTPSVPIQNATNYNTQSTAPENEQTSAPSKTTL
LPTENPTTAKSTNSTKSPTTTVPNTTNKYSTSPSPTPNSTAQHLVYFRRKRNILWREGDMFPFL
DGLINAPIDFDPVPNTKTIFDESSSSGASAEEDQHASPNISLTLSYFPKVNENTAHSGENENDC
DAELRIWSVQEDDLAAGLSWIPFFGPGIEGLYTAGLIKNQNNLVCRLRRLANQTAKSLELLLRV
TTEERTFSLINRHAIDFLLARWGGTCKVLGPDCCIGIEDLSRNISEQIDQIKKDEQKEGTGWGL
GGKWWTSDWGVLTNLGILLLLSIAVLIALSCICRIFTKYIG

SEQ ID NO:4
Glycoprotein Marburg virus Musoke (Amino Acid sequence):

MKTTCFLISLILIQGTKNLPILEIASNNQPQNVDSVCSGTLQKTEDVHLMGFTLSGQKVADSPL
EASKRWAFRTGVPPKNVEYTEGEEAKTCYNISVTDPSGKSLLLDPPTNIRDYPKCKTIHHIQGQ
NPHAQGIALHLWGAFFLYDRIASTTMYRGKVFTEGNIAAMIVNKTVHKMIFSRQGQGYRHMNLT
STNKYWTSSNGTQTNDTGCFGALQEYNSTKNQTCAPSKIPPPLPTARPEIKLTSTPTDATKLNT
TDPSSDDEDLATSGSGSGEREPHTTSDAVTKQGLSSTMPPTPSPQPSTPQQGGNNTNHSQDAVT
ELDKNNTTAQPSMPPHNTTTISTNNTSKHNFSTLSAPLQNTTNDNTQSTITENEQTSAPSITTL
PPTGNPTTAKSTSSKKGPATTAPNTTNEHFTSPPPTPSSTAQHLVYFRRKRSILWREGDMFPFL
DGLINAPIDFDPVPNTKTIFDESSSSGASAEEDQHASPNISLTLSYFPNINENTAYSGENENDC
DAELRIWSVQEDDLAAGLSWIPFFGPGIEGLYTAVLIKNQNNLVCRLRRLANQTAKSLELLLRV
TTEERTFSLINRHAIDFLLTRWGGTCKVLGPDCCIGIEDLSKNISEQIDQIKKDEQKEGTGWGL
GGKWWTSDWGVLTNLGILLLLSIAVLIALSCICRIFTKYIG

SEQ ID NO:5
Nucleoprotein Ebola virus Taï Forest / Ivory coast (Amino Acid sequence):

MESRAHKAWMTHTASGFETDYHKILTAGLSVQQGIVRQRVIQVHQVTNLEEICQLIIQAFEAGV
DFQESADSFLLMLCLHHAYQGDYKQFLESNAVKYLEGHGFRFEVRKKEGVKRLEELLPAASSGK
SIRRTLAAMPEEETTEANAGQFLSFASLFLPKLVVGEKACLEKVQRQIQVHSEQGLIQYPTAWQ
SVGHMMVIFRLMRTNFLIKFLLIHQGMHMVAGHDANDAVIANSVAQARFSGLLIVKTVLDHILQ
KTEHGVRLHPLARTAKVKNEVNSFKAALSSLAQHGEYAPFARLLNLSGVNNLEHGLFPQLSAIA
LGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQKYAESRELDHLGLDDQEKKILKDFHQKKN
EISFQQTTAMVTLRKERLAKLTEAITSTSLLKTGKQYDDDNDIPFPGPINDNENSEQQDDDPTD
SQDTTIPDIIVDPDDGRYNNYGDYPSETANAPEDLVLFDLEDGDEDDHRPSSSSENNNKHSLTG
TDSNKTSNWNRNPTNMPKKDSTQNNDNPAQRAQEYARDNIQDTPTPHRALTPISEETGSNGHNE
DDIDSIPPLESDEENNTETTITTTKNTTAPPAPVYRSNSEKEPLPQEKSQKQPNQVSGSENTDN
KPHSEQSVEEMYRHILQTQGPFDAILYYYMMTEEPIVFSTSDGKEYVYPDSLEGEHPPWLSEKE
ALNEDNRFITMDDQQFYWPVMNHRNKFMAILQHHK

Claim

1. A vaccine combination comprising

(i) a first composition comprising an immunologically effective amount of a recombinant adenovirus 26 (rAd26) adenovirus vector comprising a nucleic acid encoding an antigenic glycoprotein of a first filovirus subtype, wherein said first filovirus subtype is an Ebolavirus subtype, together with a pharmaceutically acceptable carrier; and

(ii) a second composition comprising an immunologically effective amount of a Modified Vaccinia Ankara (MVA) vector comprising a nucleic acid encoding an antigenic glycoprotein of an Ebolavirus subtype and additionally encoding at least one antigenic glycoprotein of another filovirus subtype, together with a pharmaceutically acceptable carrier;
wherein the first composition is to be used for priming said immune response and the second composition is to be used for boosting said immune response.

2. A vaccine combination according to claim 1, wherein the first composition (i) further comprises an adenovirus vector comprising a nucleic acid encoding an antigenic glycoprotein of a second filovirus subtype.

3. A vaccine combination according to claim 2, wherein the first composition (i) further comprises an adenovirus vector comprising a nucleic acid encoding an antigenic glycoprotein of a third filovirus subtype.

4. A vaccine combination according to claim 1, wherein the adenovirus vector in the first composition (i) comprises a nucleic acid encoding an antigenic glycoprotein with SEQ ID NO:1.

5. A vaccine combination according to claim 4, wherein composition (i) further comprises an adenovirus comprising a nucleic acid encoding an antigenic glycoprotein with SEQ ID NO:2.

6. A vaccine combination according to claim 5, wherein composition (i) further comprises an adenovirus comprising a nucleic acid encoding an antigenic glycoprotein with SEQ

ID NO:3.

7. A vaccine combination according to any one of claims 1-6, wherein the MVA vector in composition (ii) comprises a nucleic acid encoding antigenic glycoproteins of at least four filovirus subtypes.

8. A vaccine combination according to any one of claims 1-7, wherein the MVA vector in composition (ii) comprises a nucleic acid encoding antigenic glycoproteins from four different filovirus subtypes having SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, and SEQ ID NO: 5.

9. A vaccine combination according to any one of claims 1-8 for use in generating a protective immune response against at least one filovirus subtype, wherein the first composition is to be used for priming said immune response and the second composition is to be used for boosting said immune response.

10. A vaccine combination according to any one of claims 1-8 for use in the preparation of a pharmaceutical composition or medicament.

11. A kit comprising the vaccine combination according to any one of claims 1-8, wherein the first composition is to be used for priming said immune response and the second composition is to be used for boosting said immune response.

12. Use of a first composition comprising an immunologically effective amount of an adenovirus vector comprising a nucleic acid encoding an antigenic glycoprotein of a first filovirus subtype, wherein the first filovirus subtype is an Ebolavirus subtype, together with a pharmaceutically acceptable carrier; and a second composition comprising an immunologically effective amount of an MVA vector comprising a nucleic acid encoding antigenic glycoproteins of at least two filovirus subtypes, wherein the at least two filovirus subtypes are Ebolavirus subtypes, together with a pharmaceutically acceptable carrier; each in the manufacture of a

medicament for the combined treatment of a filovirus infection, wherein the first composition is a priming composition and the second composition is a boosting composition.