Vaccine against RSV

Field of the invention

The invention relates to the field of medicine. More in particular, the invention relates to vaccines against RSV.

Background of the invention

After discovery of the respiratory syncytial virus (RSV) in the 1950s, the virus soon became a recognized pathogen associated with lower and upper respiratory tract infections in humans. Worldwide, it is estimated that 64 million RSV infections occur each year resulting in 160.000 deaths (WHO Acute Respiratory Infections Update September 2009). The most severe disease occurs particularly in premature infants, the elderly and immunocompromised individuals. In children younger than 2 years, RSV is the most common respiratory tract pathogen, accounting for approximately 50% of the hospitalizations due to respiratory infections, and the peak of hospitalization occurs at 2-4 months of age. It has been reported that almost all children have been infected by RSV by the age of two. Repeated infection during lifetime is attributed to ineffective natural immunity. In the elderly, the RSV disease burden is similar to those caused by non-pandemic influenza A infections.

RSV is a paramyxovirus, belonging to the subfamily of pneumovirinae. Its genome encodes for various proteins, including the membrane proteins known as RSV Glycoprotein (G) and RSV fusion (F) protein which are the major antigenic targets for neutralizing antibodies. Antibodies against the fusion-mediating part of the F1 protein can prevent virus uptake in the cell and thus have a neutralizing effect.

A vaccine against RSV infection is currently not available, but is desired due to the high disease burden. The RSV fusion glycoprotein (RSV F) is an attractive vaccine antigen

since as stated above it is the principal target of neutralizing antibodies in human sera. Thus, a neutralizing monoclonal antibody against RSV F (Palivizumab) can prevent severe disease and has been approved for prophylaxis in infants.

RSV F fuses the viral and host-cell membranes by irreversible protein refolding from the labile pre-fusion conformation to the stable post-fusion conformation. Structures of both conformations have been determined for RSV F (McLellan JS, *et al. Science* **342**, 592-598 (2013); McLellan JS, *et al. Nat Struct Mol Biol* **17**, 248-250 (2010); McLellan JS, *et al. Science* **340**, 1113-1117 (2013); Swanson KA, *et al. Proceedings of the National Academy of Sciences of the United States of America* **108**, 9619-9624 (2011)), as well as for the fusion proteins from related paramyxoviruses, providing insight into the mechanism of this complex fusion machine. Like other type I fusion proteins, the inactive precursor, RSV F_0, requires cleavage during intracellular maturation by a furin-like protease. RSV F contains two furin sites, which leads to three polypeptides: F2, p27 and F1, with the latter containing a hydrophobic fusion peptide (FP) at its N-terminus. In order to refold from the pre-fusion to the post-fusion conformation, the refolding region 1 (RR1) between residue 137 and 216, that includes the FP and heptad repeat A (HRA) has to transform from an assembly of helices, loops and strands to a long continuous helix. The FP, located at the N-terminal segment of RR1, is then able to extend away from the viral membrane and insert into the proximal membrane of the target cell. Next, the refolding region 2 (RR2), which forms the C-terminal stem in the pre-fusion F spike and includes the heptad repeat B (HRB), relocates to the other side of the RSV F head and binds the HRA coiled-coil trimer with the HRB domain to form the six-helix bundle. The formation of the RR1 coiled-coil and relocation of RR2 to complete the six-helix bundle are the most dramatic structural changes that occur during the refolding process.

Most neutralizing antibodies in human sera are directed against the pre-fusion conformation, but due to its instability the pre-fusion conformation has a propensity to prematurely refold into the post-fusion conformation, both in solution and on the surface of the virions. An RSV F protein that has both high expression levels and maintains a stable pre-fusion conformation would be a promising candidate for use in a subunit or vector-based vaccine against RSV.

Summary of the invention

The present invention provides compositions comprising stable, recombinant, pre-fusion respiratory syncytial virus (RSV) fusion (F) polypeptides, i.e. recombinant RSV F polypeptides that are stabilized in the pre-fusion conformation. The RSV F polypeptides of the invention comprise at least one epitope that is specific to the pre-fusion conformation F protein. In certain embodiments, the pre-fusion RSV F polypeptides are soluble pre-fusion RSV F polypeptides.

The invention also provides compositions comprising nucleic acid molecules encoding the stable pre-fusion RSV F polypeptides.

In certain embodiments, the nucleic acid molecules encode a full-length membrane-bound RSV F protein that is stabilized in the pre-fusion conformation. In certain embodiments, the nucleic acid molecules encode soluble stabilized pre-fusion RSV F polypeptides.

In certain embodiments, the nucleic acid molecules are present in a vector. In certain embodiments, the nucleic acid encoding the RSV F polypeptide is codon optimized for expression in human cells.

The invention further provides compositions as described herein for use in inducing an immune response against RSV F protein, in particular for use as a vaccine.

The invention also relates to methods for inducing an anti-respiratory syncytial virus (RSV) immune response in a subject, comprising administering to the subject an effective amount of a composition as described herein. Preferably, the induced immune response is characterized by neutralizing antibodies to RSV and/or protective immunity against RSV. In particular aspects, the invention relates to a method for inducing neutralizing anti-respiratory syncytial virus (RSV) F protein antibodies in a subject, comprising administering to the subject an effective amount of a composition comprising a pre-fusion RSV F polypeptide, a nucleic acid molecule encoding said RSV F polypeptide, and/or a vector comprising said nucleic acid molecule.

The invention further provides a method for vaccinating a subject against RSV, the method comprising administering to the subject a composition according to the invention.

In certain embodiments, the compositions are administered intramuscularly.

In certain embodiments, a composition according to the invention is administered to the subject more than once.

The invention also provides a method for reducing infection and/or replication of RSV in, e.g. the nasal tract and lungs of, a subject, comprising administering to the subject a composition according to the invention. This will reduce adverse effects resulting from RSV infection in a subject, and thus contribute to protection of the subject against such adverse effects upon administration of the vaccine. In certain embodiments, adverse effects of RSV infection may be essentially prevented, i.e. reduced to such low levels that they are not clinically relevant.

Brief description of the Figures

FIG 1: RSV F mutations that stabilize the pre-fusion conformation. The percentage of surface-expressed RSV F mutants remaining in the pre-fusion conformation after a heat

shock at increasing temperatures. Experiments were performed 2–5 times at various concentrations. Where error bars are shown, they represent the standard deviations of at least two data points from independent experiments.

Detailed description of the invention

The fusion protein (F) of the respiratory syncyctial virus (RSV) is involved in fusion of the viral membrane with a host cell membrane, which is required for infection. The RSV F mRNA is translated into a 574 amino acid precursor protein designated F0, which contains a signal peptide sequence at the N-terminus (e.g. amino acid residues 1-26 of SEQ ID NO: 1) that is removed by a signal peptidase in the endoplasmic reticulum. F0 is cleaved at two sites (between amino acid residues 109/110 and 136/137) by cellular proteases (in particular furin) in the trans-Golgi, removing a short glycosylated intervening sequence (also referred to a p27 region, comprising the amino acid residues 110 to 136, and generating two domains or subunits designated F1 and F2. The F1 domain (amino acid residues 137-574) contains a hydrophobic fusion peptide at its N-terminus and the C-terminus contains the transmembrane (TM) (amino acid residues 530-550) and cytoplasmic region (amino acid residues 551-574). The F2 domain (amino acid residues 27-109) is covalently linked to F1 by two disulfide bridges. The F1-F2 heterodimers are assembled as homotrimers in the virion.

A vaccine against RSV infection is not currently available, but is desired. Most neutralizing antibodies in human sera are directed against the pre-fusion conformation, but due to its instability the pre-fusion conformation has a propensity to prematurely refold into the post-fusion conformation, both in solution and on the surface of the virions.

The present invention provides compositions comprising a stable recombinant pre-fusion RSV F polypeptide, i.e. a RSV F polypeptide that is stabilized in the pre-fusion conformation, wherein said RSV F polypeptide comprises at least one mutation as compared

to a wild type RSV F polypeptide, wherein the at least one mutation is selected from the group consisting of: a) a mutation of the amino acid aspartic acid (D) on position 486, b) a mutation of the amino acid aspartic acid (D) on position 489, or c) a mutation of the amino acid serine (S) on position 398 and/or the amino acid lysine (K) on position 394.

In certain embodiments, the RSV F polypeptide is a soluble RSV polypeptide.

The present invention further provides compositions comprising an isolated nucleic acid molecule encoding an RSV F polypeptide as described herein, i.e. encoding a RSV F polypeptide comprising at least one mutation as compared to a wild type RSV F polypeptide, wherein the at least one mutation is selected from the group consisting of: a) a mutation of the amino acid aspartic acid (D) on position 486, b) a mutation of the amino acid aspartic acid (D) on position 489, or c) a mutation of the amino acid serine (S) on position 398 and/or the amino acid lysine (K) on position 394.

In certain embodiments, the nucleic acid molecule encodes a full-length membrane-bound RSV F protein that is stabilized in the pre-fusion conformation. After administration of the composition, the stable, full-length RSV protein expressed from said nucleic acid molcule will be presented on the cell membrane of cells of the subject to which the nucleic acid molecule has been administered.

In certain embodiments, the nucleic acid molecule encodes a soluble RSV F polypeptide.

In certain embodiments, the nucleic acid molecules encoding the polypeptides according to the invention are codon-optimized for expression in mammalian cells, preferably human cells. Methods of codon-optimization are known and have been described previously (e.g. WO 96/09378). A sequence is considered codon-optimized if at least one non-preferred codon as compared to a wild type sequence is replaced by a codon that is more preferred. Herein, a non-preferred codon is a codon that is used less frequently in an organism than

another codon coding for the same amino acid, and a codon that is more preferred is a codon that is used more frequently in an organism than a non-preferred codon. The frequency of codon usage for a specific organism can be found in codon frequency tables, such as in http://www.kazusa.or.jp/codon. Preferably more than one non-preferred codon, preferably most or all non-preferred codons, are replaced by codons that are more preferred. Preferably the most frequently used codons in an organism are used in a codon-optimized sequence. Replacement by preferred codons generally leads to higher expression.

It will be understood by a skilled person that numerous different polynucleotides and nucleic acid molecules can encode the same polypeptide as a result of the degeneracy of the genetic code. It is also understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the nucleic acid molecules to reflect the codon usage of any particular host organism in which the polypeptides are to be expressed. Therefore, unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. Nucleotide sequences that encode proteins and RNA may or may not include introns.

Nucleic acid sequences can be cloned using routine molecular biology techniques, or generated de novo by DNA synthesis, which can be performed using routine procedures by service companies having business in the field of DNA synthesis and/or molecular cloning (e.g. GeneArt, GenScripts, Invitrogen, Eurofins).

In certain embodiments, the nucleic acid molecule is part of a vector. Thus, the invention also provides compositions comprising a vector comprising a nucleic acid molecule as described above. Such vectors can easily be manipulated by methods well known to the person skilled in the art, and can for instance be designed for being capable of replication in prokaryotic and/or eukaryotic cells. Alternatively, the vectors are designed for not being

capable of replication. Suitable vectors according to the invention are e.g. adenovectors, including Ad26 or AD35, alphavirus, paramyxovirus, vaccinia virus, herpes virus, retroviral vectors etc. The person skilled in the art is capable of choosing suitable expression vectors, and inserting the nucleic acid sequences of the invention in a functional manner.

According to the present invention, it has surprisingly been found that the mutations as described herein, either individually or in combination, are capable of stabilizing the RSV F protein in the pre-fusion conformation. The RSV F polypeptides that are present in the compositions of the present invention thus comprise at least one mutation as compared to a wild-type RSV F protein, in particular as compared to the RSV F protein of SEQ ID NO: 1.

In certain embodiments, the stable RSV F polypeptides comprise the full-length RSV F protein. According to the invention, the full-length RSV F protein is not present within an RSV virion. Thus, the invention relates to recombinantly expressed RSV F polypeptides.

The stable pre-fusion RSV F polypeptides of the present invention are in the pre-fusion conformation, i.e. they comprise (display) at least one epitope that is specific to the pre-fusion conformation F protein. An epitope that is specific to the pre-fusion conformation F protein is an epitope that is not presented in the post-fusion conformation. Without wishing to be bound by any particular theory, it is believed that the pre-fusion conformation of RSV F protein may contain epitopes that are the same as those on the RSV F protein expressed on natural RSV virions, and therefore may provide advantages for eliciting protective neutralizing antibodies.

In certain embodiments, the polypeptides of the invention comprise at least one epitope that is recognized by a pre-fusion specific monoclonal antibody, comprising a heavy chain CDR1 region of SEQ ID NO: 4, a heavy chain CDR2 region of SEQ ID NO: 5, a heavy chain CDR3 region of SEQ ID NO: 6 and a light chain CDR1 region of SEQ ID NO: 7, a light chain CDR2 region of SEQ ID NO: 8, and a light chain CDR3 region of SEQ ID NO: 9

(hereafter referred to as CR9501) and/or a pre-fusion specific monoclonal antibody, comprising a heavy chain CDR1 region of SEQ ID NO: 10, a heavy chain CDR2 region of SEQ ID NO: 11, a heavy chain CDR3 region of SEQ ID NO: 12 and a light chain CDR1 region of SEQ ID NO: 13, a light chain CDR2 region of SEQ ID NO: 14, and a light chain CDR3 region of SEQ ID NO: 15 (referred to as CR9502). CR9501 and CR9502 comprise the heavy and light chain variable regions, and thus the binding specificities, of the antibodies 58C5 and 30D8, respectively, which have previously been shown to bind specifically to RSV F protein in its pre-fusion conformation and not to the post-fusion conformation (see WO2012/006596).

In certain embodiments, the pre-fusion RSV F polypeptide comprises a mutation of the amino acid residue aspartic acid (D) at position 486 into asparagine (N) (D489Y).

In certain embodiments, the pre-fusion RSV F polypeptide comprises a mutation of the amino acid residue aspartic acid (D) at position 489 into tyrosine (Y) (D489Y).

In certain embodiments, the stable pre-fusion RSV F polypeptide according to the invention comprises a mutation of the amino acid residue serine (S) at position 398 into leucine (L) S398L) and/or a mutation of amino acid residue lysine (K) at position 394 into arginine (R) (K394R). In certain embodiments, the stable pre-fusion RSV F polypeptide comprises a mutation of the amino acid residue serine (S) at position 398 into leucine (L) S398L) and a mutation of amino acid residue lysine (K) at position 394 into arginine (R) (K394R).

According to the present invention it was surprisingly shown that these mutations are capable of stabilizing the RSV F protein in the pre-fusion conformation, in particular when the RSV F protein is the full-length, membrane-bound RSV F protein.

In certain embodiments, the stabilized RSV F polypeptides are soluble RSV F polypeptides.

In certain embodiments, the present invention thus provides compositions comprising stable soluble pre-fusion RSV F polypeptides. In certain embodiments, the RSV F protein has been truncated by deletion of the transmembrane (TM) and the cytoplasmic region to create a soluble secreted F protein (sF). Because the TM region is responsible for membrane anchoring and trimerization, the anchorless soluble F protein is considerably more labile than the full-length protein and will readily refold into the post-fusion end-state. In order to obtain soluble F protein in the stable pre-fusion conformation that shows high expression levels and high stability, the pre-fusion conformation thus needs to be stabilized. Soluble RSV F polypeptides that are stabilized with a C-terminal heterologous trimerization domain and two stabilizing mutations in the apex of the protein have been described in WO 2014/174018 and WO2014/202570. It was shown that, in particular, the mutations N67I and S215P were capable of stabilizing the soluble recombinant RSV F polypeptides in the pre-fusion conformation. The modifications according to the present invention further stabilize the soluble RSV F proteins as described in WO 2014/174018 and WO2014/202570.

In certain embodiments, the present invention thus provides compositions comprising a soluble pre-fusion RSV F polypeptide, wherein the RSV F polypeptide comprise at least one of the modifications as described above, in combination with a mutation of the amino acid residue asparagine (N) or threonine (T) on position 67 and/or a mutation of amino acid residue serine (S) on position 215.

In certain embodiments, the soluble pre-fusion RSV F polypeptides in the compositions of the invention comprise at least one of the mutations as described herein in combination with a mutation of the amino acid residue asparagine (N) or threonine (T) on position 67 into isoleucine (I) (N/T67I) into I, and/or a mutation of amino acid residue serine (S) on position 215 into proline (P) (S215P).

In certain embodiments, the soluble pre-fusion RSV F polypeptides further comprise a heterologous trimerization domain linked to a truncated F1 domain, as described in WO2014/174018 and WO2014/202570. As used herein a "truncated" F1 domain refers to a F1 domain that is not a full length F1 domain, i.e. wherein either N-terminally or C-terminally one or more amino acid residues have been deleted. According to the invention, at least the transmembrane domain and cytoplasmic tail have been deleted to permit expression as a soluble ectodomain.

In certain embodiments, the trimerization domain comprises SEQ ID NO: 3 and is linked to amino acid residue 513 of the RSV F1 domain, either directly or through a linker. In certain embodiments, the linker comprises the amino acid sequence SAIG.

It is known that RSV exists as a single serotype having two antigenic subgroups: A and B. The amino acid sequences of the mature processed F proteins of the two groups are about 93% identical. As used throughout the present application, the amino acid positions are given in reference to the sequence of RSV F protein from the A2 strain (SEQ ID NO: 1). As used in the present invention, the wording "the amino acid at position "x" of the RSV F protein thus means the amino acid corresponding to the amino acid at position "x" in the RSV F protein of the RSV A2 strain of SEQ ID NO: 1. Note that, in the numbering system used throughout this application 1 refers to the N-terminal amino acid of an immature F0 protein (SEQ ID NO: 1) When a RSV strain other than the A2 strain is used, the amino acid positions of the F protein are to be numbered with reference to the numbering of the F protein of the A2 strain of SEQ ID NO: 1 by aligning the sequences of the other RSV strain with the F protein of SEQ ID NO: 1 with the insertion of gaps as needed. Sequence alignments can be done using methods well known in the art, e.g. by CLUSTALW, Bioedit or CLC Workbench.

An amino acid according to the invention can be any of the twenty naturally occurring (or 'standard' amino acids) or variants thereof, such as e.g. D-amino acids (the D-enantiomers

of amino acids with a chiral center), or any variants that are not naturally found in proteins, such as e.g. norleucine. The standard amino acids can be divided into several groups based on their properties. Important factors are charge, hydrophilicity or hydrophobicity, size and functional groups. These properties are important for protein structure and protein–protein interactions. Some amino acids have special properties such as cysteine, that can form covalent disulfide bonds (or disulfide bridges) to other cysteine residues, proline that induces turns of the polypeptide backbone, and glycine that is more flexible than other amino acids. Table 1 shows the abbreviations and properties of the standard amino acids.

It will be appreciated by a skilled person that the mutations can be made to the protein by routine molecular biology procedures. The pre-fusion RSV F polypeptides in the compositions according to the invention are stable, i.e. do not readily change into the post-fusion conformation upon processing of the polypeptides, such as e.g. purification, freeze-thaw cycles, and/or storage etc.

In certain embodiments, the pre-fusion RSV F polypeptides according to the invention have an increased stability when subjected to heat, as compared to RSV F polypeptides without said mutation(s). In certain embodiments, the pre-fusion RSV F polypeptides are heat stable for at least 10 minutes at a temperature of 55° C, preferably at 58° C, more preferably at 60° C With "heat stable" it is meant that the polypeptides still display the at least one pre-fusion specific epitope after having been subjected for at least 10 minutes to an increased temperature (i.e. a temperature of 55°C or above), e.g. as determined using a method as described in Example 1.

In certain embodiments, the RSV F polypeptides are derived from an RSV A strain. In certain embodiments the RSV F polypeptides are derived from the RSV A2 strain of SEQ ID NO: 1.

In certain embodiments, the RSV F polypeptides are derived from an RSV B strain. In certain embodiments the F1 and/or F2 domain are from the RSV B strain of SEQ ID NO: 2.

In certain preferred embodiments, the pre-fusion RSV F polypeptide of the invention comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 21-26

As used throughout the present application nucleotide sequences are provided from 5' to 3' direction, and amino acid sequences from N-terminus to C-terminus, as custom in the art.

In certain embodiments, the polypeptides according to the invention further comprise a leader sequence, also referred to as signal sequence or signal peptide, corresponding to amino acids 1-26 of SEQ ID NO: 1 or the amino acids 1-26 of SEQ ID NO: 2. This is a short (typically 5-30 amino acids long) peptide present at the N-terminus of the majority of newly synthesized proteins that are destined towards the secretory pathway. In certain embodiments, the polypeptides according to the invention do not comprise a leader sequence.

In certain embodiments, the polypeptides comprise a HIS-Tag. A His-Tag or polyhistidine-tag is an amino acid motif in proteins that consists of at least five histidine (H) residues, often at the N- or C-terminus of the protein, which is generally used for purification purposes.

As described herein, the present invention provides compositions comprising a stable pre-fusion RSV F polypeptide, i.e.an RSV F polypeptide that displays an epitope that is present in a pre-fusion conformation of the RSV F protein but is absent in the post-fusion conformation and/or a nucleic acid molecule encoding such stable pre-fusion RSV F polypeptide.

The invention further provides pharmaceutical compositions comprising a pre-fusion RSV F polypeptide, a nucleic acid molecule and/or a vector as described herein, and a pharmaceutically acceptable carrier or excipient. In the present context, the term "pharmaceutically acceptable" means that the carrier or excipient, at the dosages and

concentrations employed, will not cause any unwanted or harmful effects in the subjects to which they are administered. Such pharmaceutically acceptable carriers and excipients are well known in the art (see Remington's Pharmaceutical Sciences, 18th edition, A. R. Gennaro, Ed., Mack Publishing Company [1990]; Pharmaceutical Formulation Development of Peptides and Proteins, S. Frokjaer and L. Hovgaard, Eds., Taylor & Francis [2000]; and Handbook of Pharmaceutical Excipients, 3rd edition, A. Kibbe, Ed., Pharmaceutical Press [2000]). The RSV F polypeptides, or nucleic acid molecules, preferably are formulated and administered as a sterile solution although in some cases it may also be possible to utilize lyophilized preparations. Sterile solutions are prepared by sterile filtration or by other methods known per se in the art. The solutions are then lyophilized or filled into pharmaceutical dosage containers. The pH of the solution generally is in the range of pH 3.0 to 9.5, e.g. pH 5.0 to 7.5. The RSV F polypeptides typically are in a solution having a suitable pharmaceutically acceptable buffer, and the composition may also contain a salt. In certain embodiments, the RSV F polypeptides may be formulated into an injectable preparation.

Further provided are methods for inducing an immune response against RSV F protein in a subject, comprising administering to the subject an effective amount of a composition according to the invention. Also provided are compositions according to the invention for use in inducing an immune response against RSV F protein in a subject, in particular for use as a vaccine. Further provided is the use of the compositions according to the invention for the manufacture of a medicament for use in inducing an immune response against RSV F protein in a subject. Preferably, the induced immune response is characterized by neutralizing antibodies to RSV and/or protective immunity against RSV.

In particular aspects, the invention relates to a method for inducing neutralizing anti-respiratory syncytial virus (RSV) F protein antibodies in a subject, comprising administering to the subject an effective amount of a composition as described herein.

The invention also provides a method for reducing infection and/or replication of RSV in, e.g. the nasal tract and lungs of, a subject, comprising administering to the subject a composition according to the invention. This will reduce adverse effects resulting from RSV infection in a subject, and thus contribute to protection of the subject against such adverse effects upon administration of the vaccine. In certain embodiments, adverse effects of RSV infection may be essentially prevented, i.e. reduced to such low levels that they are not clinically relevant.

The compositions of the invention may be used for prevention (prophylaxis) and/or treatment of RSV infections. In certain embodiments, the prevention and/or treatment may be targeted at patient groups that are susceptible RSV infection. Such patient groups include, but are not limited to e.g., the elderly (e.g. $\geq$ 50 years old, $\geq$ 60 years old, and preferably $\geq$ 65 years old), the young (e.g. $\leq$ 5 years old, $\leq$ 1 year old), hospitalized patients and patients who have been treated with an antiviral compound but have shown an inadequate antiviral response.

The compositions according to the invention may be used e.g. in stand-alone treatment and/or prophylaxis of a disease or condition caused by RSV, or in combination with other prophylactic and/or therapeutic treatments, such as (existing or future) vaccines, antiviral agents and/or monoclonal antibodies.

The invention further provides methods for preventing and/or treating RSV infection in a subject utilizing the compositions according to the invention. In a specific embodiment, a method for preventing and/or treating RSV infection in a subject comprises administering to a subject in need thereof a compositions comprising an effective amount of a pre-fusion RSV F polypeptide, nucleic acid molecule and/or a vector, as described herein. A therapeutically effective amount refers to an amount of a polypeptide, nucleic acid molecule or vector that is effective for preventing, ameliorating and/or treating a disease or condition resulting from

infection by RSV. Prevention encompasses inhibiting or reducing the spread of RSV or inhibiting or reducing the onset, development or progression of one or more of the symptoms associated with infection by RSV. Amelioration as used in herein may refer to the reduction of visible or perceptible disease symptoms, viremia, or any other measurable manifestation of influenza infection.

In certain embodiments, the compositions according to the invention further comprise one or more adjuvants. Adjuvants are known in the art to further increase the immune response to an applied antigenic determinant. 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 RSV F polypeptides of the invention. Examples of suitable adjuvants include aluminium salts such as aluminium hydroxide and/or aluminium phosphate; oil-emulsion compositions (or oil-in-water compositions), including squalene-water emulsions, such as MF59 (see e.g. WO 90/14837); saponin formulations, such as for example QS21 and Immunostimulating Complexes (ISCOMS) (see e.g. US 5,057,540; WO 90/03184, WO 96/11711, WO 2004/004762, WO 2005/002620); bacterial or microbial derivatives, examples of which are monophosphoryl lipid A (MPL), 3-O-deacylated MPL (3dMPL), CpG-motif containing oligonucleotides, ADP-ribosylating bacterial toxins or mutants thereof, such as *E. coli* heat labile enterotoxin LT, cholera toxin CT, and the like; eukaryotic proteins (e.g. antibodies or fragments thereof (e.g. directed against the antigen itself or CD1a, CD3, CD7, CD80) and ligands to receptors (e.g. CD40L, GMCSF, GCSF, etc), which stimulate immune response upon interaction with recipient cells. In certain embodiments the compositions of the invention comprise aluminium as an adjuvant, e.g. in the form of aluminium hydroxide, aluminium phosphate, aluminium potassium phosphate, or combinations thereof, in concentrations of 0.05 – 5 mg, e.g. from 0.075-1.0 mg, of aluminium content per dose.

In certain embodiments, the compositions according to the invention are for use as a vaccine against respiratory syncytial virus (RSV). The term "vaccine" refers to a composition containing an active component effective to induce a certain degree of immunity in a subject against a certain pathogen or disease, which will result in at least a decrease (up to complete absence) of the severity, duration or other manifestation of symptoms associated with infection by the pathogen or the disease. In the present invention, the vaccine comprises an effective amount of a pre-fusion RSV F polypeptide and/or a nucleic acid molecule encoding a pre-fusion RSV F polypeptide, and/or a vector comprising said nucleic acid molecule, which results in an immune response against the F protein of RSV. The vaccine may be used to prevent serious lower respiratory tract disease leading to hospitalization and to decrease the frequency of complications such as pneumonia and bronchiolitis due to RSV infection and replication in a subject. In certain embodiments, the vaccine may be a combination vaccine that further comprises other components that induce an immune response, e.g. against other proteins of RSV and/or against other infectious agents. The administration of further active components may for instance be done by separate administration or by administering combination products of the vaccines of the invention and the further active components.

The invention further provides a method for vaccinating a subject against RSV, the method comprising administering to the subject a composition according to the invention.

Compositions according to the invention may be administered to a subject, e.g. a human subject. Determining the recommended dose will be carried out by experimentation and is routine for those skilled in the art.

Administration of the compositions according to the invention can be performed using standard routes of administration. Non-limiting embodiments include parenteral administration, such as intradermal, intramuscular, subcutaneous, transcutaneous, or mucosal

administration, e.g. intranasal, oral, and the like. In one embodiment a composition is administered by intramuscular injection. The skilled person knows the various possibilities to administer a composition, e.g. a vaccine in order to induce an immune response to the antigen(s) in the vaccine. In certain embodiments, a composition of the invention is administered intramuscularly.

A subject as used herein preferably is a mammal, for instance a rodent, e.g. a mouse, a cotton rat, or a non-human-primate, or a human. Preferably, the subject is a human subject.

The compositions according to the invention may be administered, either as prime, or as boost, in a homologous or heterologous prime-boost regimen. If a boosting vaccination is performed, typically, such a boosting vaccination will be administered to the same subject at a time between one week and one year, preferably between two weeks and four months, after administering the composition to the subject for the first time (which is in such cases referred to as 'priming vaccination'). In certain embodiments, the administration comprises a prime and at least one booster administration.

The invention further provides a method for stabilizing the pre-fusion conformation of an RSV F polypeptide, comprising introducing a mutation in the RSV F protein, as compared to the wild-type RSV F protein, wherein the one or more mutations are selected from the group consisting of:

Stabilized pre-fusion RSV F polypeptides obtainable and/or obtained by such method also form part of the invention, as well as the uses thereof as described above.

The invention is further explained in the following examples. The examples do not limit the invention in any way. They merely serve to clarify the invention.

Examples

EXAMPLE 1

Preparation of stable pre-fusion RSV F polypeptides

Therapeutic small molecules that bind the respiratory syncytial virus (RSV) F protein inhibit membrane fusion and bind to a 3-fold symmetric pocket within the central cavity of the metastable RSV F pre-fusion conformation. Inhibitor binding stabilizes this conformation by tethering two regions that need to undergo a large structural rearrangement to facilitate membrane fusion. According to the invention surprisingly escape mutations have been identified that paradoxically stabilize the pre-fusion conformation. According to the invention it has thus been shown that amino acid substitutions corresponding to this class of escape mutations can be used to stabilize RSV F in the pre-fusion conformation.

In the research that led to the present invention a temperature-based triggering assay was developed to assess the effect of mutations on pre-fusion F stability. HEK293 cells expressing wild-type RSV F or mutant RSV F were heat shocked at increasing temperatures for 10 minutes so that a melting curve could be determined. Mutations such as the D489Y variant substantially increased the temperature required for triggering (Fig. 1), thus indicating that the mutations stabilized the RSV F polypeptide. Full-length RSV F proteins (wild-type and comprising one or more of the mutations according to the present inventions) were transiently expressed in HEK293T cells. 48 h post-transfection, cells were detached using an EDTA-containing buffer and heat-shocked for 10 minutes. The cells were stained with AlexaFluor647-conjugated antibodies that were either specific for pre-fusion RSV F (antibody CR9501) or recognized both the pre- and post-fusion conformations (antibody CR9503, which comprises the heavy and light chain variable regions of the RSV F antibody Motavizumab). Propidium iodide (Invitrogen) was used as a live-dead stain, and cells were analyzed by flow cytometry on a FACS Canto II instrument (BD Biosciences). The data were

analyzed using FlowJo 9.6 software, and mean fluorescence intensities (MFI) were calculated, with heat-shocked samples normalized to untreated (37 °C) samples.

The constructs were synthesized and codon-optimized at Gene Art (Life Technologies, Carlsbad, CA). The constructs were cloned into pCDNA2004 or generated by standard methods widely known within the field involving site-directed mutagenesis and PCR and sequenced.

Table 1. Standard amino acids, abbreviations and properties

Amino Acid	3-Letter	1-Letter	Side chain polarity	Side chain charge (pH 7.4)
alanine	Ala	A	non-polar	Neutral
arginine	Arg	R	polar	Positive
asparagine	Asn	N	polar	Neutral
aspartic acid	Asp	D	polar	Negative
cysteine	Cys	C	non-polar	Neutral
glutamic acid	Glu	E	polar	Negative
glutamine	Gln	Q	polar	Neutral
glycine	Gly	G	non-polar	Neutral
histidine	His	H	polar	positive(10%) neutral(90%)
isoleucine	Ile	I	non-polar	Neutral
leucine	Leu	L	non-polar	Neutral
lysine	Lys	K	polar	Positive
methionine	Met	M	non-polar	Neutral
phenylalanine	Phe	F	non-polar	Neutral
proline	Pro	P	non-polar	Neutral
serine	Ser	S	polar	Neutral
threonine	Thr	T	polar	Neutral
tryptophan	Trp	W	non-polar	Neutral
tyrosine	Tyr	Y	polar	Neutral
valine	Val	V	non-polar	Neutral

Table 2

Ab	VH domain	VH CDR1	VH CDR2	VH CDR3
CR9501	Amino acids 1-125 of SEQ ID NO: 16	GASINSDNYYWT (SEQ ID NO:4)	HISYTGNTYYTPSLKS (SEQ ID NO:5)	CGAYVLISNCGWFDS (SEQ ID NO:6)
CR9502	Amino acids 1-121 of SEQ ID NO:18	GFTFSGHTIA (SEQ ID NO:10)	WVSTNNGNTEYAQKIQG (SEQ ID NO:11)	EWLVMGGFAFDH (SEQ ID NO:12)

Ab	VL domain	VL CDR1	VL CDR2	VL CDR3
CR9501	Amino acids 1-107 of SEQ ID NO: 17	QASQDISTYLN (SEQ ID NO: 7)	GASNLET (SEQ ID NO:8)	QQYQYLPYT (SEQ ID NO:9)
CR9502	Amino acids 1-110 of SEQ ID NO: 19	GANNIGSQNVH (SEQ ID NO:13)	DDRDRPS (SEQ ID NO:14)	QVWDSSRDQAVI (SEQ ID NO:15)

Sequences

RSV F protein A2 full length sequence (SEQ ID NO: 1)

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKKNKCNGTDAKIKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSV
ITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE
GKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELLHNVNAVKST
TNIMITTIIIVIIVILLSLIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN

RSV F protein B1 full length sequence (SEQ ID NO: 2)

MELLIHRLSAIFLTLAINALYLTSSQNITEEFYQSTCSAVSRGYFSALRTGWYTSVITIE
LSNIKETKCNGTDTKVKLIKQELDKYKNAVTELQLLMQNTPAANNRARREAPQYMN
YTINTTKNLNVSISKKRKRRFLGFLLGVGSAIASGIAVSKVLHLEGEVNKIKNALLSTN
KAVVSLSNGVSVLTSKVLDLKNYINNQLLPIVNQQSCRISNIETVIEFQQKNSRLLEIN
REFSVNAGVTTPLSTYMLTNSELLSLINDMPITNDQKKLMSSNVQIVRQQSYSIMSIIK
EEVLAYVVQLPIYGVIDTPCWKLHTSPLCTTNIKEGSNICLTRTDRGWYCDNAGSVSF
FPQADTCKVQSNRVFCDTMNSLTLPSEVSLCNTDIFNSKYDCKIMTSKTDISSSVITSL
GAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKLEGKN
LYVKGEPIINYYDPLVFPSDEFDASISQVNEKINQSLAFIRRSDELLHNVNTGKSTTNI
MITTIIIVIIVVLLSLIAIGLLLYCKAKNTPVTLSKDQLSGINNIAFSK

SEQ ID NO: 3

GYIPEAPRDGQAYVRKDGEWVLLSTFL

CR9501 heavy chain (SEQ ID NO: 16):

QVQLVQSGPGLVKPSQTLALTCNVSGASINSDNYYWTWIRQRPGGGLEWIGHISYTG
NTYYTPSLKSRLSMSLETSQSQFSLRLTSVTAADSAVYFCAACGAYVLISNCGWFDS

WGQGTQVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

CR9501 light chain (SEQ ID NO: 17):

EIVMTQSPSSLSASIGDRVTITCQASQDISTYLNWYQQKPGQAPRLLIYGASNLETGVP
SRFTGSGYGTDFSVTISSLQPEDIATYYCQQYQYLPYTFAPGTKVEIKRTVAAPSVFIF
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

CR9502 heavy chain (SEQ ID NO: 18):

EVQLLQSGAELKKPGASVKISCKTSGFTFSGHTIAWVRQAPGQGLEWMGWVSTNNG
NTEYAQKIQGRVTMTMDTSTSTVYMELRSLTSDDTAVYFCAREWLVMGGFAFDHW
GQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC

CR9502 light chain (SEQ ID NO: 19):

QSVLTQASSVSVAPGQTARITCGANNIGSQNVHWYQQKPGQAPVLVVYDDRDRPSG
IPDRFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSRDQAVIFGGGTKLTVLGQPK
AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQS
NNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTIAPTECS

PreF, RSV A2, fibritin (SEQ ID NO: 20) (soluble, wt with fibritin)

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSV
ITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE
GKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELLSAIGGYIPEAPR
DGQAYVRKDGEWVLLSTFL

PreF, RSV A2, (SEQ ID NO: 21) D486N

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSV
ITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE
GKSLYVKGEPIINFYDPLVFPS**N**EFDASISQVNEKINQSLAFIRKSDELLHNVNAVKST
TNIMITTIIIVIIVILLSLIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN

PreF, RSV A2, (SEQ ID NO: 22) D489Y

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSV
ITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE
GKSLYVKGEPIINFYDPLVFPSDEF**Y**ASISQVNEKINQSLAFIRKSDELLHNVNAVKST
TNIMITTIIIVIIVILLSLIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN

PreF, RSV A2, (SEQ ID NO:23) S398L, K394R

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDC**R**IMT**L**KTDVSSS
VITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQ

EGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELLHNVNAVKS
TTNIMITTIIIVIIVILLSLIAVGLLLYCKARSTPVTLSKDQLSGINNIAFSN

Soluble PreF, RSV A2, (SEQ ID NO: 24) D486N

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSV
ITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE
GKSLYVKGEPIINFYDPLVFPS**N**EFDASISQVNEKINQSLAFIRKSDELL
SAIGGYIPEAPRDGQAYVRKDGEWVLLSTFL

Soluble PreF, RSV A2, (SEQ ID NO: 25) D489Y

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS
VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSV
ITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE
GKSLYVKGEPIINFYDPLVFPSDEF**Y**ASISQVNEKINQSLAFIRKSDELL
SAIGGYIPEAPRDGQAYVRKDGEWVLLSTFL

Soluble PreF, RSV A2, (SEQ ID NO: 26) S398L, K394R

MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIE
LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFMN
YTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVSKVLHLEGEVNKIKSALLS
TNKAVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETVIEFQQKNNRLLE
ITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMSI
IKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGS

VSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDC**R**IMT**L**KTDVSSS
VITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQ
EGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL
SAIGGYIPEAPRDGQAYVRKDGEWVLLSTFL

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Claims

1. A composition comprising a recombinant respiratory syncytial virus (RSV) Fusion (F) polypeptide, wherein the polypeptide comprises SEQ ID NO: 21.

2. A composition comprising a recombinant respiratory syncytial virus (RSV) Fusion (F) polypeptide, wherein, as compared to a wild type RSV F polypeptide, the recombinant RSV F polypeptide comprises: (i) a mutation of the amino acid at position 486 from aspartic acid (D) to asparagine (N), and (ii) at least one of a. a mutation of the amino acid residue at position 67 from asparagine (N) or threonine (T) to isoleucine (I), and b. a mutation of the amino acid residue at position 215 from serine (S) to proline (P).

3. The composition of claim 2, wherein the recombinant RSV F polypeptide comprises: (i) the mutation of the amino acid at position 486 from aspartic acid (D) to asparagine (N), (ii) the mutation of the amino acid residue at position 67 from asparagine (N) or threonine (T) to isoleucine (I), and (iii) the mutation of the amino acid residue at position 215 from serine (S) to proline (P).