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(54) Title: SWINE INFLUENZA HEMAGGLUTININ VARIANTS

(57) Abstract: Polypeptides, polynucleotides, methods, compositions, and vaccines comprising influenza hemagglutinin and neuraminidase variants are provided.

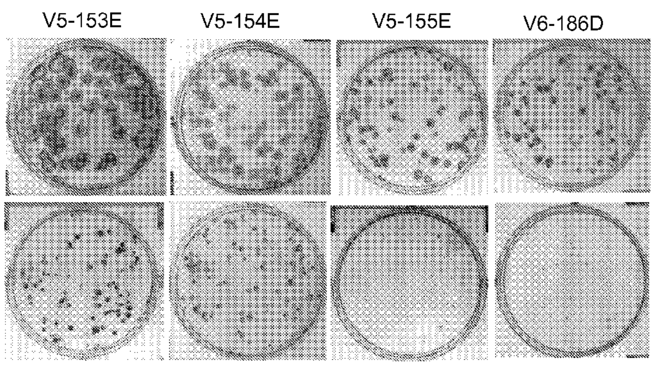

Fig. 1A

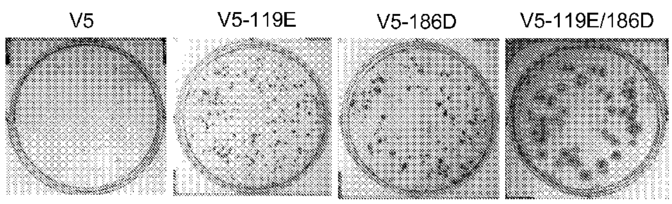

Fig. 1B

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SWINE INFLUENZA HEMAGGLUTININ VARIANTS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application Serial Nos.: 61/220,426, filed June 25, 2009; 61/227,986, filed July 23, 2009; 61/234,021, filed August 14, 2009; and 61/258,890, filed November 6, 2009. Each of these applications is expressly incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

The global spread of swine-origin influenza A (H1N1) viruses in humans in April 2009 marked the first influenza pandemic in 41 years. Over 35,000 people were infected with this novel H1N1 virus as of June 15, 2009. Last century, an H1N1 influenza virus also caused the devastating 1918-19 pandemic. In addition, an H1N1 virus derived from swine caused an abortive pandemic in 1976. The 1918 influenza virus caused a mild outbreak in the spring of 1918 and a lethal wave globally in the fall of that year, killing as many as 50 million people worldwide. Although the 2009 swine-origin H1N1 influenza virus was viewed as mild in early 2009, the possibility exists that this virus may mutate and become more virulent by the fall of 2009. Therefore there is an urgent need to develop an effective vaccine to prevent a severe pandemic caused by the 2009 H1N1 viruses.

6:2 reassortant influenza viruses (having the HA and NA segments of swine-origin influenza A (H1N1) viruses and the "backbone" segments of attenuated influenza viruses) useful for vaccine development, both live and killed vaccine have been isolated yet most strains isolated thus far display low titers in eggs. The same isolates infect MDCK cells poorly and form tiny plaques with poor CPE. Additionally, a severe loss of virus potency is observed after virus filtration. Accordingly, the initially isolated H1N1 reassortant influenza virus strains are poor candidates for the development of a vaccine strain.

The present invention provides new and/or newly isolated swine influenza H1 hemagglutinin variants that are capable of use for the production of numerous types of vaccines as well as in research, diagnostics, etc. The present invention further provides methods of improving the replication efficiency of H1 influenza viruses. Numerous other benefits will become apparent upon review of the following.

SUMMARY OF THE INVENTION

As described herein, 6:2 reassortant influenza strains suitable for use in the development of H1N1 vaccines were generated by reverse genetics. The initially isolated reassortant viruses comprising the wild type HA and NA genome segments, which grew poorly in eggs, were modified such that their growth in eggs is significantly improved. Sequence analysis of the modified reassortant viruses indicated that amino acid changes at positions 119, 153, 154 and 186 of the H1 swine hemagglutinin were responsible for the growth advantage in eggs and MDCK cells. Amino acid substitutions at HA residue 155, previously shown to increase swine 1976 virus replication, were also found to increase reassortant A/CA/7/09 virus replication in eggs. Viruses having amino acid changes at HA residues 119 and 186 increased egg growth without significantly altering virus antigenicity. The H1 HA variants described herein conferred increased growth phenotype on 6:2 reassortant viruses comprising the 6 internal genome segment of the PR8 or A/Ann Arbor/6/60 virus strains. Moreover, the variant viruses comprising the *ca* A/Ann Arbor/6/60 backbone and an H1 HA variant having an amino acid substitution at HA residue 119 or 186 were attenuated and very immunogenic in ferrets. These data indicates that the reassortant influenza virus variants comprising an amino acid substitution at HA residue 119 and/or 186 are suitable for development of an H1N1 swine influenza vaccine for human use.

DETAILED DESCRIPTION

The present invention includes polypeptide and polynucleotide sequences of influenza hemagglutinin as well as vectors, viruses, vaccines, compositions and the like comprising such sequences and methods of their use. Additional features of the invention are described in more detail herein.

In some aspects, the invention provides isolated or recombinant hemagglutinin polypeptides. In one embodiment, an isolated or recombinant HA polypeptide of the invention is an H1 HA polypeptide. In another embodiment, the isolated or recombinant HA polypeptide of the invention may be a swine influenza HA polypeptide.

In one embodiment, an isolated or recombinant HA polypeptide of the invention may comprise a non naturally occurring amino acid at the position corresponding to amino acid residue position 119 of SEQ ID NO: 1 or the position corresponding to amino acid residue position 186 of SEQ ID NO: 1. In another embodiment, an isolated or recombinant HA polypeptide of the invention may comprise a non naturally occurring amino acid at the position corresponding to amino acid residue position 119 of SEQ ID NO: 1 and the position corresponding to amino acid residue position 186 of SEQ ID NO: 1. In a further embodiment, an isolated or recombinant HA polypeptide of the invention comprises at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D.

In a specific embodiment, an isolated or recombinant HA polypeptide of the invention comprises the amino acid sequence of SEQ ID NO:1 comprising at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D. In another specific embodiment, an isolated or recombinant HA polypeptide of the invention may comprise a glutamic acid (E) at the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1, and an aspartic acid (D) at the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1. In a further specific embodiment, an isolated or recombinant HA polypeptide of the invention may comprise an asparagine (N) at the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1, and an aspartic acid (D) at the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1.

In a further embodiment, an isolated or recombinant HA polypeptide of the invention may further comprise the H273Y substitution.

In a further embodiment, an isolated or recombinant HA polypeptide of the invention may further comprise the D222G and/or Q223R substitution.

In a specific embodiment, an HA polypeptide of the invention comprises the amino acid sequence of SEQ ID NO:6 or 8. In another embodiment, an HA polypeptide of the invention comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a further embodiment, an HA polypeptide of the invention comprises the amino acid sequence of

SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

In a specific embodiment, an HA polypeptide of the invention comprises the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In another embodiment, an HA polypeptide of the invention comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In a further embodiment, an HA polypeptide of the invention comprises the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

The invention also encompasses nucleic acids encoding polypeptides of the invention and reassortant or recombinant influenza viruses comprising such polypeptides and/or nucleic acids of the invention.

In a specific embodiment, a nucleic acid of the invention comprises the nucleotide sequence of SEQ ID NO:7. In another embodiment, a nucleic acid of the invention comprises a nucleotide sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the nucleotide sequence of SEQ ID NO:7. In a further embodiment, a nucleic acid of the invention comprises the nucleotide sequence of SEQ ID NO:7 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 nucleotide substitutions, deletions or insertions.

In a specific embodiment, a nucleic acid of the invention comprises the nucleotide sequence of residues 84 to 1064 of SEQ ID NO:7. In another embodiment, a nucleic acid of the invention comprises a nucleotide sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the nucleotide sequence of 84 to 1064 of SEQ ID NO:7. In a further embodiment, a nucleic acid of the invention comprises the nucleotide sequence of 84 to 1064 of SEQ ID NO:7 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 nucleotide substitutions, deletions or insertions.

In one embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Ann Arbor/6/60, a first genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8, and a second genome segment encoding a neuramidinase polypeptide. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the second genome segment comprises the nucleotide sequence of SEQ ID NO:5. In a specific embodiment, the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO:4. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml , at least about 8 $\log_{10}$ PFU/ml, at least about 8.5 $\log_{10}$ PFU/ml, at least about 9 $\log_{10}$ PFU/ml, at least about 9.5 $\log_{10}$ PFU/ml, at least about 10 $\log_{10}$ PFU/ml, at least about 10.5 $\log_{10}$ PFU/ml or at least about 11 $\log_{10}$ PFU/ml in embryonated eggs. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml , at least about 8 $\log_{10}$ PFU/ml, at least about 8.5 $\log_{10}$ PFU/ml, at least about 9 $\log_{10}$ PFU/ml, at least about 9.5 $\log_{10}$ PFU/ml, at least about 10 $\log_{10}$ PFU/ml, at least about 10.5 $\log_{10}$ PFU/ml or at least about 11 $\log_{10}$ PFU/ml in tissue cultures.

In another embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Ann Arbor/6/60, a first genome segment encoding an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8, and a second genome segment encoding a neuramidinase polypeptide. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 SEQ ID NO:6. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the second genome segment comprises the nucleotide sequence of SEQ ID NO:5. In a specific embodiment, the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO:4. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in embryonated eggs. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in tissue cultures.

In one embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Puerto Rico/8/34, a first genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8, and a second genome segment encoding a neuramidinase polypeptide. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the second genome segment comprises the nucleotide sequence of SEQ ID NO:5. In a specific embodiment, the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO:4. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in embryonated eggs. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in tissue cultures.

In another embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Puerto Rico/8/34, a first genome segment encoding an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8, and a second genome segment encoding a neuramidinase polypeptide. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8. In a specific embodiment, the first genome segment may encode an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the second genome segment comprises the nucleotide sequence of SEQ ID NO:5. In a specific embodiment, the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO:4. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in embryonated eggs. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in tissue cultures.

In one embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Ann Arbor/6/60, a first genome segment comprising the nucleotide sequence of SEQ ID NO:7, and a second genome segment encoding a neuramidinase polypeptide. In another embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Ann Arbor/6/60, a first genome segment comprising the nucleotide sequence of residues 84-1064 of SEQ ID NO:7, and a second genome segment encoding a neuramidinase polypeptide. In a further embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Puerto Rico/8/34, a first genome segment comprising the nucleotide sequence of SEQ ID NO:7, and a second genome segment encoding a neuramidinase polypeptide. In another embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments from A/Puerto Rico/8/34, a first genome segment comprising the nucleotide sequence of residues 84-1064 of SEQ ID NO:7, and a second genome segment encoding a neuramidinase polypeptide. In a specific embodiment, the second genome segment comprises the nucleotide sequence of SEQ ID NO:5. In a specific embodiment, the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO:4. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml , at least about 8 $\log_{10}$ PFU/ml, at least about 8.5 $\log_{10}$ PFU/ml, at least about 9 $\log_{10}$ PFU/ml, at least about 9.5 $\log_{10}$ PFU/ml, at least about 10 $\log_{10}$ PFU/ml, at least about 10.5 $\log_{10}$ PFU/ml or at least about 11 $\log_{10}$ PFU/ml in embryonated eggs. In a specific embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml , at least about 8 $\log_{10}$ PFU/ml, at least about 8.5 $\log_{10}$ PFU/ml, at least about 9 $\log_{10}$ PFU/ml, at least about 9.5 $\log_{10}$ PFU/ml, at least about 10 $\log_{10}$ PFU/ml, at least about 10.5 $\log_{10}$ PFU/ml or at least about 11 $\log_{10}$ PFU/ml in tissue cultures.

In other aspects, the invention comprises a sterile composition with one or more polypeptide listed above, or fragments thereof. The invention also encompasses immunogenic compositions comprising an immunologically effective amount of one or more of the polypeptides described above, as well as methods for stimulating the immune system of an individual to produce a protective immune response against an influenza virus comprising administering to the individual an immunologically effective amount of one or more of the polypeptides described above. In a specific embodiment, an immunogenic composition of the invention comprises a polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8. In another embodiment, an immunogenic composition of the invention comprises a polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a further embodiment, an immunogenic composition of the invention comprises a polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, an immunogenic composition of the invention comprises a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In another embodiment, an immunogenic composition of the invention comprises a polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In a further embodiment, an immunogenic composition of the invention comprises a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

In one embodiment, an immunogenic composition of the invention is a monovalent immunogenic composition comprising a single reassortant influenza virus. In one embodiment, an immunogenic composition of the invention is a trivalent immunogenic composition comprising three reassortant influenza viruses. In one embodiment, an immunogenic composition of the invention is a trivalent immunogenic composition comprising two reassortant influenza A viruses and a reassortant influenza B virus. In one embodiment, an immunogenic composition of the invention is a trivalent immunogenic composition comprising a reassortant influenza A virus of the H1 type, a reassortant influenza A virus of the H3 type and a reassortant influenza B virus. In another embodiment, an immunogenic composition of the invention is a tetravalent immunogenic composition comprising four reassortant influenza viruses. In one embodiment, an immunogenic composition of the invention is a tetravalent immunogenic composition comprising two reassortant influenza A viruses and two reassortant influenza B viruses. In one embodiment, an immunogenic composition of the invention is a tetravalent immunogenic composition comprising a reassortant influenza A virus of the H1 type, a reassortant influenza A virus of the H3 type, a reassortant influenza B virus of the Victoria lineage and a reassortant influenza B virus of the Yamagata lineage. In a specific embodiment, an immunogenic composition of the invention comprises a reassortant or recombinant influenza virus comprising a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8. In another embodiment, an immunogenic composition of the invention comprises a reassortant or recombinant influenza virus comprising a genome segment encoding an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least

99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a further embodiment, an immunogenic composition of the invention comprises a reassortant or recombinant influenza virus comprising a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, an immunogenic composition of the invention comprises a reassortant or recombinant influenza virus comprising a genome segment encoding an HA polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In another embodiment, an immunogenic composition of the invention comprises a reassortant or recombinant influenza virus comprising a genome segment encoding an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In a further embodiment, an immunogenic composition of the invention comprises a reassortant or recombinant influenza virus comprising a genome segment encoding an HA polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

Additionally, the invention encompasses a reassortant influenza virus that comprises a genome segment encoding one or more of the polypeptides described above. Further, the invention encompasses immunogenic compositions comprising an immunologically effective amount of such reassortant influenza virus. Methods for stimulating the immune system of an individual to produce a protective immune response against influenza virus comprising administering an immunologically effective amount of such reassortant influenza virus in a physiologically acceptable carrier are also part of the invention. In one embodiment, a reassortant influenza virus of the invention is a 6:2 reassortant virus comprising 6 internal genome segments from one or more donor virus (e.g. A/AA/6/60 or A/Puerto Rico/8/34, which is more commonly known as PR8) and further comprising 2 genome segments (typically and preferably encoding HA and NA or fragments thereof). Immunogenic compositions comprising such reassortant (recombinant) virus are also features of the invention.

In one embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Ann Arbor/6/60 and a genome segment encoding an HA polypeptide. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having at least one substitution, deletion or insertion. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having the H273Y substitution. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having the D222G and/or Q223R substitution. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Ann Arbor/6/60 and a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:1 having the D222G, K119E and A186D substitutions. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Ann Arbor/6/60 and a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:1 having Q223R and A186D substitutions. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Ann Arbor/6/60 and a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:1 having Q223R, H273Y and A186D substitutions. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Ann Arbor/6/60 and an HA genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

In one embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Puerto Rico/8/34 (PR8) and a genome segment encoding an HA polypeptide. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having at least one substitution, deletion or insertion. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having the D222G and/or Q223R substitution. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D. The HA polypeptide may comprise the amino acid sequence of SEQ ID NO:1 having the H273Y substitution. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Puerto Rico/8/34 (PR8) and a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:1 having the D222G, K119E and A186D substitutions. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Puerto Rico/8/34 (PR8) and a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:1 having the Q223R and A186D substitutions. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Puerto Rico/8/34 (PR8) and a genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:1 having the Q223R, H273Y and A186D substitutions. In a specific embodiment, a reassortant or recombinant influenza virus of the invention comprises 6 internal genome segments of A/Puerto Rico/8/34 (PR8) and an HA genome segment encoding an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8. In a specific embodiment, the HA genome segment may encode an HA polypeptide comprising the amino acid sequence of residues 1-327 SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

Also within the invention are reassortant influenza viruses comprising a polynucleotide encoding a polypeptide of the invention. In one embodiment such reassortant viruses are 6:2 reassortant viruses comprising 6 internal genome segments from one or more donor virus (e.g., A/AA/6/60 or A/Puerto Rico/8/34), a first genome segment encoding a hemagglutinin polypeptide of the invention, and a second genome segment encoding a neuramidinase polypeptide. Immunogenic compositions comprising immunologically effective amounts of such a reassortant/recombinant influenza virus are also within purview of the current invention.

Reassortant or recombinant viruses of the invention display high rate of replication in tissue cultures or embryonated eggs. In one embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in embryonated eggs. In another embodiment, a reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml , at least about 8 log_{10} PFU/ml, at least about 8.5 log_{10} PFU/ml, at least about 9 log_{10} PFU/ml, at least about 9.5 log_{10} PFU/ml, at least about 10 log_{10} PFU/ml, at least about 10.5 log_{10} PFU/ml or at least about 11 log_{10} PFU/ml in tissue cultures.

Methods of producing a reassortant/recombinant influenza virus through culturing a host cell harboring a polynucleotide of the invention are also contemplated.

In other embodiments herein, the invention comprises immunogenic compositions having an immunologically effective amount of one or more of the above described reassortant influenza viruses of the invention. In one embodiment, an immunogenic composition of the invention comprises a live virus of the invention. Other embodiments include methods for stimulating the immune system of an individual to produce a protective immune response against influenza virus comprising administering to the individual an immunologically effective amount of one or more of the reassortant influenza viruses described above (optionally in a physiologically effective carrier).

The invention also encompasses vaccines comprising a recombinant or reassortant influenza virus of the invention. In one embodiment, a vaccine of the invention is a split vaccine or killed vaccine. In another embodiment, a vaccine of the invention is a live attenuated influenza virus vaccine. In a further embodiment, a vaccine of the invention may be a monovalent, bivalent, trivalent or tetravalent vaccine.

Methods of producing an influenza virus vaccine are also included in the invention. In one embodiment, a vaccine of the invention may be a monovalent, bivalent, trivalent or tetravalent vaccine.

The present invention also relates to methods and compositions for increasing the replication capacity of influenza viruses in, for example, embryonated hens' eggs and/or cell culture. The invention is based, in part, on the identification of particular H1 protein amino acids associated with increased replication capacity. By using an H1 HA gene encoding an H1 HA protein that comprises one or more of these particular amino acids, improved influenza viral yields can be achieved. In one embodiment, a method is provided for increasing the replication capacity of a reassortant or recombinant influenza virus comprising altering an amino acid residue of the hemagglutinin polypeptide at a position corresponding to the amino acid residue of position 119 or 186 of SEQ ID NO: 1, thereby increasing the replication capacity of the reassortant or recombinant influenza virus. A recombinant influenza virus produced by the method is also provided.

The present invention also relates to methods and compositions for increasing the replication capacity of H1N1 reassortant influenza viruses in, for example, embryonated hens' eggs and/or cell culture. In one embodiment, a method is provided for increasing the replication capacity of a H1N1 reassortant or recombinant influenza virus comprising altering an amino acid residue of the hemagglutinin polypeptide at a position corresponding to the amino acid residue of position 119 or 186 of SEQ ID NO: 1, thereby increasing the replication capacity of the reassortant or recombinant influenza virus. A recombinant influenza virus produced by the method is also provided.

In one embodiment, the replication capacity of a reassortant or recombinant influenza virus of the invention, which comprises a hemagglutinin polypeptide of the invention having a non naturally occurring amino acid is increased at least 2-fold, at least 4-fold, at least 6-fold, at least 8-fold, at least 10-fold, at least 20-fold, at least 40-fold, at least 50-fold, or at least 100-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid at the same position. In another embodiment, the replication capacity of a reassortant or recombinant influenza virus of the invention, which comprises a hemagglutinin polypeptide of the invention having a non naturally occurring amino acid is increased at between 2-fold and 10-fold, between 2-fold and 20-fold, between 2-fold and 40-fold, between 2-fold and 100-fold, between 5-fold and 10-fold, between 5-fold and 20-fold, between 5-fold and 40-fold, or between 5-fold and 100-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid at the same position.

In one embodiment, the peak titer in embryonated eggs for a reassortant or recombinant influenza virus of the invention, which comprises a hemagglutinin polypeptide of the invention having a non naturally occurring amino acid is increased at least 2-fold, at least 4-fold, at least 6-fold, at least 8-fold, at least 10-fold, at least 20-fold, at least 40-fold, at least 50-fold, or at least 100-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid at the same position. In another embodiment, the peak titer in embryonated eggs for a reassortant or recombinant influenza virus of the invention, which comprises a hemagglutinin polypeptide of the invention having a non naturally occurring amino acid is increased at between 2-fold and 10-fold, between 2-fold and 20-fold, between 2-fold and 40-fold, between 2-fold and 100-fold, between 5-fold and 10-fold, between 5-fold and 20-fold, between 5-fold and 40-fold, or between 5-fold and 100-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid at the same position.

In a specific embodiment, a recombinant influenza virus is provided which comprises an HA polypeptide of an H1N1 virus which polypeptide comprises an amino acid selected from the group consisting of K119E, K119N and A186D. In a specific embodiment, a recombinant influenza virus is provided which comprises an HA polypeptide of an H1N1 virus which polypeptide comprises an amino acid selected from the group consisting of K119X and A186X, wherein X is any amino acid not naturally occurring in said H1N1 virus. In a specific embodiment, the recombinant influenza viruses of the invention are 6:2 reassortant viruses comprising at least 5 or 6 segments of (or derived from) an attenuated virus. In a specific embodiment, the recombinant influenza viruses of the invention are 6:2 reassortant viruses comprising at least 5 or 6 segments of (or derived from) an attenuated virus selected from the group consisting of: Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17. In a specific embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8. In another embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a further embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In another embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In a further embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

In a specific embodiment, the recombinant influenza viruses of the invention are 6:2, or 7:1 reassortant viruses comprising an HA polypeptide of the invention. In a specific embodiment, the recombinant influenza viruses of the invention are 6:2, or 7:1 reassortant viruses comprising an HA polypeptide of the invention and at least 5 or 6 segments of (or derived from) an attenuated virus selected from the group consisting of:

A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17. In one embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide of (or derived from) A/CA/04/09 or A/CA/07/09 having 1, 2, or 3 substitutions (e.g., at positions 119, 186). In one embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide of (or derived from) A/CA/04/09 or A/CA/07/09 having a glutamic acid or an asparagine at amino acid position 119 and an aspartic acid at position 186. In one embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide of (or derived from) A/CA/04/09 or A/CA/07/09 having an amino acid substitution at amino acid position 119 and position 186. In one embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide of (or derived from) an H1N1 swine flu virus having an amino acid substitution at amino acid position 119 and position 186. In a specific embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8.In another embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6 or 8. In a further embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions. In a specific embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In another embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8. In a further embodiment, the recombinant influenza viruses of the invention comprise an HA polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6 or 8 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

One skilled in the art will recognize that the exact position of an amino acid can vary depending on the particular influenza strain used in the vectors, methods, and viruses of the invention. For example, the HA protein of a particular influenza strain may comprise an insertion or deletion in the HA gene encoding the HA protein such that the position corresponding to position 119 of SEQ ID NO:1 is found at, for example, residue 93 or 97 of the HA protein of that particular influenza strain. In particular, as shown in Table 3, position 119 and 186 of the A/CA/07/09 HA polypeptide (SEQ ID NO:1) corresponds to position 118 and 185, respectively of the A/South Dakota/6/07 H1 HA polypeptide. One skilled in the art can readily recognize whether a particular amino acid position corresponds to a position that, when altered, is associated with increased replication capacity using techniques conventional to the art. One such conventional technique is to align the amino acid sequence of SEQ ID NO:1 and the particular influenza strain HA polypeptide using algorithms available in the art.

These and other objects and features of the invention will become more fully apparent when the following detailed description is read in conjunction with the accompanying figures and claims.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Plaque morphology of variants selected from MDCK cells and the indicated variants containing introduced amino acid changes (**A**). Plaque assay was performed in MDCK cells, incubated at 33°C for 4 days and immunostained with polyclonal antiserum against influenza A virus. The plaque morphology of double mutant V5-119E/186D is compared with single 119E and 186D mutant in panel **B**.

Figure 2. HA1 protein sequence comparison of A/California/7/09, A/Swine/Iowa/1/1976 (nucleotide sequence accession code CY022069), A/Swine/1931 (nucleotide sequence accession code CY009628), and A/South Dakota/6/07. The amino acids at positions 119, 153, 154, 155, 186 and 278 are highlighted.

Figure 3. Protein composition of virus preparations purified from embryonated eggs.

Figure 4. Protein composition of virus preparations purified from embryonated eggs.

Figure 5. Protein composition of purified virus preparations harvested from embryonated eggs at (A) 48 hrs and (B) 60 hrs.

Figure 6. Quantitative comparison of the HA1 protein produced by two reassortant H1N1 viruses in embryonated eggs.

DEFINITIONS

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. The following definitions supplement those in the art and are directed to the current application and are not necessarily to be imputed to any related or unrelated case, e.g., to any commonly owned patent or application. Although any methods and materials similar or equivalent to those described herein can be used in the practice for testing of the present invention, the preferred materials and methods are described herein. Accordingly, the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting. Additional terms are defined and described throughout.

The phrase “substantially identical,” in the context of two nucleic acids or polypeptides (e.g., DNAs encoding a HA or NA molecule, or the amino acid sequence of a HA or NA molecule) refers to two or more sequences or subsequences that have at least about 90%, preferably 91%, most preferably 92%, 93%, 94%, 95%, 96%, 97%, 98%, 98.5%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9% or more nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using a sequence comparison algorithm or by visual inspection.

The term “variant” with respect to a polypeptide refers to an amino acid sequence that is altered by one or more amino acids with respect to a reference sequence. The variant can have “conservative” changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. Alternatively, a variant can have “non-conservative” changes, e.g., replacement of a glycine with a tryptophan. Analogous minor variation can also include amino acid deletion or insertion, or both. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without eliminating biological or immunological activity can be found using computer programs well known in the art, for example, DNASTAR software. Examples of conservative substitutions are also described herein.

The “neuraminidase” polypeptides of the invention show immunological cross reactivity with one or more known neuraminidase molecule from an influenza virus. The literature is replete with examples of such known neuraminidases (e.g., in GenBank, in publications from the CDC, etc.). Similarly, the “hemagglutinin” polypeptides of the invention may show immunological cross-reactivity with one or more known hemagglutinin molecule from an influenza virus. Again, the literature is replete with examples of such known hemagglutinin molecules.

Genes also include non-expressed nucleic acid segments that, for example, form recognition sequences for other proteins. Non-expressed regulatory sequences include “promoters” and “enhancers,” to which regulatory proteins such as transcription factors bind, resulting in transcription of adjacent or nearby sequences. A “tissue specific” promoter or enhancer is one that regulates transcription in a specific tissue type or cell type, or types.

Expression of a gene” or “expression of a nucleic acid” typically means transcription of DNA into RNA (optionally including modification of the RNA, e.g., splicing) or transcription of RNA into mRNA, translation of RNA into a polypeptide (possibly including subsequent modification of the polypeptide, e.g., post-translational modification), or both transcription and translation, as indicated by the context.

An “open reading frame” or “ORF” is a possible translational reading frame of DNA or RNA (e.g., of a gene), which is capable of being translated into a polypeptide. That is, the reading frame is not interrupted by stop codons. However, it should be noted that the term ORF does not necessarily indicate that the polynucleotide is, in fact, translated into a polypeptide.

The term “vector” refers to the means by which a nucleic acid can be propagated and/or transferred between organisms, cells, or cellular components. Vectors include plasmids, viruses, bacteriophages, pro-viruses, phagemids, transposons, artificial chromosomes, and the like, that replicate autonomously or can integrate into a chromosome of a host cell. A vector can also be a naked RNA polynucleotide, a naked DNA polynucleotide, a polynucleotide composed of both DNA and RNA within the same strand, a poly-lysine-conjugated DNA or RNA, a peptide-conjugated DNA or RNA, a liposome-conjugated DNA, or the like, that is not autonomously replicating. In many, but not all, common embodiments, the vectors of the present invention are plasmids.

An "expression vector" is a vector, such as a plasmid that is capable of promoting expression, as well as replication of a nucleic acid incorporated therein. Typically, the nucleic acid to be expressed is "operably linked" to a promoter and/or enhancer, and is subject to transcription regulatory control by the promoter and/or enhancer.

A "bi-directional expression vector" is characterized by two alternative promoters oriented in the opposite direction relative to a nucleic acid situated between the two promoters, such that expression can be initiated in both orientations resulting in, e.g., transcription of both plus (+) or sense strand, and negative (-) or antisense strand RNAs.

In the context of the invention, the term "isolated" refers to a biological material, such as a virus, a nucleic acid or a protein, which is substantially free from components that normally accompany or interact with it in its naturally occurring environment. The isolated biological material optionally comprises additional material not found with the biological material in its natural environment, e.g., a cell or wild-type virus. For example, if the material is in its natural environment, such as a cell, the material can have been placed at a location in the cell (e.g., genome or genetic element) not native to such material found in that environment. For example, a naturally occurring nucleic acid (e.g., a coding sequence, a promoter, an enhancer, etc.) becomes isolated if it is introduced by non-naturally occurring means to a locus of the genome (e.g., a vector, such as a plasmid or virus vector, or amplicon) not native to that nucleic acid. Such nucleic acids are also referred to as "heterologous" nucleic acids. An isolated virus, for example, is in an environment (e.g., a cell culture system, or purified from cell culture) other than the native environment of wild-type virus (e.g., the nasopharynx of an infected individual).

The term "chimeric" or "chimera," when referring to a virus, indicates that the virus includes genetic and/or polypeptide components derived from more than one parental viral strain or source. Similarly, the term "chimeric" or "chimera," when referring to a viral protein, indicates that the protein includes polypeptide components (i.e., amino acid subsequences) derived from more than one parental viral strain or source. As will be apparent herein, such chimeric viruses are typically reassortant/recombinant viruses. Thus, in some embodiments, a chimera can optionally include, e.g., a sequence (e.g., of HA and/or NA) from an A influenza virus placed into a backbone comprised of, or constructed/derived from a B influenza virus (e.g., B/AA/1/66, etc.) or a B influenza virus sequence placed into an A influenza virus backbone (i.e., donor virus) such as, e.g., A/AA/6/60, etc.

The term “recombinant” indicates that the material (e.g., a nucleic acid or protein) has been artificially or synthetically (non-naturally) altered by human intervention. The alteration can be performed on the material within, or removed from, its natural environment or state. Specifically, e.g., an influenza virus is recombinant when it is produced by the expression of a recombinant nucleic acid. For example, a “recombinant nucleic acid” is one that is made by recombining nucleic acids, e.g., during cloning, DNA shuffling or other procedures, or by chemical or other mutagenesis; a “recombinant polypeptide” or “recombinant protein” is a polypeptide or protein which is produced by expression of a recombinant nucleic acid; and a “recombinant virus,” e.g., a recombinant influenza virus, is produced by the expression of a recombinant nucleic acid.

The term “reassortant,” when referring to a virus (typically herein, an influenza virus), indicates that the virus includes genetic and/or polypeptide components derived from more than one parental viral strain or source. For example, a 7:1 reassortant includes 7 viral genome segments (or gene segments) derived from a first parental virus, and a single complementary viral genome segment, e.g., encoding a hemagglutinin or neuraminidase described herein. A 6:2 reassortant includes 6 genome segments, most commonly the 6 internal genome segments from a first parental virus, and two complementary segments, e.g., hemagglutinin and neuraminidase genome segments, from one or more different parental virus. Reassortant viruses can also, depending upon context herein, be termed as “chimeric” and/or “recombinant.”

The term “introduced” when referring to a heterologous or isolated nucleic acid refers to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid can be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA). The term includes such methods as “infection,” “transfection,” “transformation,” and “transduction.” In the context of the invention a variety of methods can be employed to introduce nucleic acids into cells, including electroporation, calcium phosphate precipitation, lipid mediated transfection (lipofection), etc.

The term “host cell” means a cell that contains a heterologous nucleic acid, such as a vector or a virus, and supports the replication and/or expression of the nucleic acid. Host cells can be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, avian or mammalian cells, including human cells. Exemplary host cells can include, e.g., Vero (African green monkey kidney) cells, BHK (baby hamster kidney) cells, primary chick kidney (PCK) cells, Madin-Darby Canine Kidney (MDCK) cells, Madin-Darby Bovine Kidney (MDBK) cells, 293 cells (e.g., 293T cells), and COS cells (e.g., COS1, COS7 cells), etc. In other embodiments, host cells can optionally include eggs (e.g., hen eggs, embryonated hen eggs, etc.).

An "immunologically effective amount" of influenza virus is an amount sufficient to enhance an individual's (e.g., a human's) own immune response against a subsequent exposure to influenza virus. Levels of induced immunity can be monitored, e.g., by measuring amounts of neutralizing secretory and/or serum antibodies, e.g., by plaque neutralization, complement fixation, enzyme-linked immunosorbent, or microneutralization assay.

A "protective immune response" against influenza virus refers to an immune response exhibited by an individual (e.g., a human) that is protective against disease when the individual is subsequently exposed to and/or infected with wild-type influenza virus. In some instances, the wild-type (e.g., naturally circulating) influenza virus can still cause infection, but it cannot cause a serious or life-threatening infection. Typically, the protective immune response results in detectable levels of host engendered serum and secretory antibodies that are capable of neutralizing virus of the same strain and/or subgroup (and possibly also of a different, non-vaccine strain and/or subgroup) *in vitro* and *in vivo*.

As used herein, an "antibody" is a protein comprising one or more polypeptides substantially or partially encoded by immunoglobulin genes or fragments of immunoglobulin genes. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon and mu constant region genes, as well as myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. A typical immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively. Antibodies exist as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to VH-CH1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region thereby converting the (Fab')2 dimer into a Fab' monomer. The Fab' monomer is essentially a Fab with part of the hinge region (*see* Fundamental Immunology, W. E. Paul, ed., Raven Press, N.Y. (1999) for a more detailed description of other antibody fragments). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such Fab' fragments may be synthesized *de novo* either chemically or by utilizing recombinant DNA methodology. Thus, the term antibody, as used herein, includes antibodies or fragments either produced by the modification of whole antibodies or synthesized *de novo* using recombinant DNA methodologies. Antibodies include, e.g., polyclonal antibodies, monoclonal antibodies, multiple or single chain antibodies, including single chain Fv (sFv or scFv) antibodies in which a variable heavy and a variable light chain are joined together (directly or through a peptide linker) to form a continuous polypeptide, and humanized or chimeric antibodies.

INFLUENZA VIRUS

The polypeptides and polynucleotides of the invention are variants of influenza HA and/or NA sequences. *See*, e.g., the Sequence Listing in Figures 1 and 2 below. In general, influenza viruses are made up of an internal ribonucleoprotein core containing a segmented single-stranded RNA genome and an outer lipoprotein envelope lined by a matrix protein. The genome of influenza viruses is composed of eight segments of linear (-) strand ribonucleic acid (RNA), encoding the immunogenic hemagglutinin (HA) and neuraminidase (NA) proteins, and six internal core polypeptides: the nucleocapsid nucleoprotein (NP); matrix proteins (M); non-structural proteins (NS); and 3 RNA polymerase (PA, PB1, PB2) proteins. During replication, the genomic viral RNA is transcribed into (+) strand messenger RNA and (-) strand genomic cRNA in the nucleus of the host cell. Each of the eight genomic segments is packaged into ribonucleoprotein complexes that contain, in addition to the RNA, NP and a polymerase complex (PB1, PB2, and PA). The hemagglutinin molecule consists of a surface glycoprotein and acts to bind to N-AcetylNeuraminic acid (NeuNAc), also known as sialic acid, on host cell surface receptors. In some embodiments herein, the polypeptides of the invention (and polypeptides encoded by the polynucleotides of the invention) can act to bind NeuNAc whether *in vitro* or *in vivo*. Such action can in some embodiments also be done by fragments of hemagglutinin which retain hemagglutinin activity. Hemagglutinin is made up of two subunits, HA1 and HA2 and the entire structure is about 550 amino acids in length and about 220 kD. Neuraminidase molecules cleave terminal sialic acid residues from cell surface receptors of influenza virus, thereby releasing virions from infected cells. Neuraminidase also removes sialic acid from newly made hemagglutinin and neuraminidase molecules. In some embodiments herein, the polypeptides of the invention (and polypeptides encoded by the polynucleotides of the invention) can act to cleave sialic acid residues whether *in vitro* or *in vivo*. This action can also be done in some embodiments by fragments of neuraminidase which retain neuraminidase activity. The neuraminidase polypeptides of the invention show immunological cross reactivity with one or more known neuraminidase molecule from an influenza virus. The literature is replete with examples of such known neuraminidases (e.g., in GenBank, in publications from the CDC, etc.). Similarly, the hemagglutinin polypeptides of the invention show immunological cross-reactivity with one or more known hemagglutinin molecule from an influenza virus. Again, the literature is replete with examples of such known hemagglutinin molecules.

Influenza is commonly grouped into influenza A and influenza B categories, as well as a typically less important C category. Influenza A and influenza B viruses each contain eight segments of single stranded RNA with negative polarity. The influenza A genome encodes eleven polypeptides. Segments 1-3 encode three polypeptides, making up a RNA-dependent RNA polymerase. Segment 1 encodes the polymerase complex protein PB2. The remaining polymerase proteins PB1 and PA are encoded by segment 2 and segment 3, respectively. In addition, segment 1 of some influenza strains encodes a small protein, PB1-F2, produced from an alternative reading frame within the PB1 coding region. Segment 4 encodes the hemagglutinin (HA) surface glycoprotein involved in cell attachment and entry during infection. Segment 5 encodes the nucleocapsid nucleoprotein (NP) polypeptide, the major structural component associated with viral RNA. Segment 6 encodes a neuraminidase (NA) envelope glycoprotein. Segment 7 encodes two matrix proteins, designated M1 and M2, which are translated from differentially spliced mRNAs. Segment 8 encodes NS1 and NS2, two nonstructural proteins, which are translated from alternatively spliced mRNA variants. The eight genome segments of influenza B encode 11 proteins. The three largest genes code for components of the RNA polymerase, PB1, PB2 and PA. Segment 4 encodes the HA protein. Segment 5 encodes NP. Segment 6 encodes the NA protein and the NB protein. Both proteins, NB and NA, are translated from overlapping reading frames of a bicistronic mRNA. Segment 7 of influenza B also encodes two proteins: M1 and BM2. The smallest segment encodes two products: NS1 is translated from the full length RNA, while NS2 is translated from a spliced mRNA variant.

Influenza types A and B are typically associated with influenza outbreaks in human populations. However, type A influenza also infects other species as well, e.g., birds, pigs, and other animals. The type A viruses are categorized into subtypes based upon differences within their hemagglutinin and neuraminidase surface glycoprotein antigens. Hemagglutinin in type A viruses has 16 known subtypes and neuraminidase has 9 known subtypes. In humans, currently only about 4 different hemagglutinin and 2 different neuraminidase subtypes are known, e.g., H1, H2, H3, H5, N1, and N2. In particular, two major subtypes of influenza A have been active in humans, namely, H1N1 and H3N2. H1N2, however has recently been of concern. Influenza B viruses are not divided into subtypes based upon their hemagglutinin and neuraminidase proteins.

Different strains of influenza can be categorized based upon, e.g., the ability of influenza to agglutinate red blood cells (RBCs or erythrocytes). Antibodies specific for particular influenza strains can bind to the virus and, thus, prevent such agglutination. Assays determining strain types based on such inhibition are typically known as hemagglutinin inhibition assays (HI assays or HAI assays) and are standard and well known methods in the art to characterize influenza strains. Of course, those of skill in the art will be familiar with other assays, e.g., ELISA, indirect fluorescent antibody assays, immunohistochemistry, Western blot assays, etc. with which to characterize influenza strains and the use of and discussion herein of HI assays should not be necessarily construed as limiting.

Briefly, in typical HI assays, sera to be used for typing or categorization, which is often produced in ferrets, is added to erythrocyte samples in various dilutions, e.g., 2-fold, etc. Optical determination is then made whether the erythrocytes are clumped together (i.e., agglutinated) or are suspended (i.e., non-agglutinated). If the cells are not clumped, then agglutination did not occur due to the inhibition from antibodies in the sera that are specific for that influenza. Thus, the types of influenza are defined as being within the same strain. In some cases, one strain is described as being "like" the other, e.g., strain x is a "y-like" strain, etc. For example, if two samples are within four-fold titer of one another as measured by an HI assay, then they can be described as belonging to the same strain (e.g., both belonging to the "New Caledonia" strain or both being "Moscow-like" strains, etc.). In other words, strains are typically categorized based upon their immunologic or antigenic profile. An HAI titer is typically defined as the highest dilution of a serum that completely inhibits hemagglutination. *See*, e.g., Schild, et al., Bull. Wld Hlth Org., 1973, 48:269-278, etc. Again, those of skill in the art will be quite familiar with categorization and classification of influenza into strains and the methods to do so.

From the above it will be appreciated that the current invention not only comprises the specific sequences listed herein, but also such sequences within various vectors (e.g., ones used for plasmid reassortment and rescue, *see* below) as well as hemagglutinin and neuraminidase sequences within the same strains as the sequences listed herein. Also, such same strains that are within various vectors (e.g., typically ones used for plasmid reassortment and rescue such as A/Ann Arbor/6/60 or B/Ann Arbor/1/66, A/Puerto Rico/8/34, B/Leningrad/14/17/55, B/14/5/1, B/USSR/60/69, B/Leningrad/179/86, B/Leningrad/14/55, or B/England/2608/76, etc.) are also included.

As used herein, the term "similar strain" should be taken to indicate that a first influenza virus is of the same or related strain as a second influenza virus. In typical embodiments such relation is commonly determined through use of an HAI assay. Influenza viruses that fall within a four-fold titer of one another in an HAI assay are, thus, of a "similar strain." Those of skill in the art, however, will be familiar with other assays, etc. to determine similar strains, e.g., FRID, neutralization assays, etc. The current invention also comprises such similar strains (i.e., strains similar to the ones present in the sequence listing herein) in the various plasmids, vectors, viruses, methods, etc. herein. Thus, unless the context clearly dictates otherwise, descriptions herein of particular sequences (e.g., those in the sequence listing) or fragments thereof also should be considered to include sequences from similar strains to those (i.e., similar strains to those strains having the sequences in those plasmids, vectors, viruses, etc. herein). Also, it will be appreciated that the NA and HA polypeptides within such similar strains are, thus, "similar polypeptides" when compared between "similar strains."

INFLUENZA VIRUS VACCINES

The sequences, compositions and methods herein are primarily, but not solely, concerned with production of influenza viruses for vaccines. Historically, influenza virus vaccines have primarily been produced in embryonated hen eggs using strains of virus selected or based on empirical predictions of relevant strains. More recently, reassortant viruses have been produced that incorporate selected hemagglutinin and/or neuraminidase antigens in the context of an approved attenuated, temperature sensitive master strain. Following culture of the virus through multiple passages in hen eggs, influenza viruses are recovered and, optionally, inactivated, e.g., using formaldehyde and/or β-propiolactone (or alternatively used in live attenuated vaccines). Thus, it will be appreciated that HA and NA sequences (as in the current invention) are quite useful in constructing influenza vaccines.

Attempts at producing recombinant and reassortant vaccines in cell culture have been hampered by the inability of some of the strains approved for vaccine production to grow efficiently under standard cell culture conditions. However, prior work by the inventors and their coworkers provided a vector system, and methods for producing recombinant and reassortant viruses in culture, thus, making it possible to rapidly produce vaccines corresponding to one or many selected antigenic strains of virus, e.g., either A or B strains, various subtypes or substrains, etc., e.g., comprising the HA and NA sequences herein. *See*, U.S. Application No. 60/420,708, filed October 23, 2002, U.S. Application No. 10/423,828, filed April 25, 2003, and U.S. Application No. 60/574,117, filed May 24, 2004, all entitled "Multi-Plasmid System for the Production of Influenza Virus." Typically, the cultures are maintained in a system, such as a cell culture incubator, under controlled humidity and CO_2, at constant temperature using a temperature regulator, such as a thermostat to insure that the temperature does not exceed 35°C. Reassortant influenza viruses can be readily obtained by introducing a subset of vectors corresponding to genomic segments of a master influenza virus, in combination with complementary segments derived from strains of interest (e.g., HA and NA antigenic variants herein). Typically, the master strains are selected on the basis of desirable properties relevant to vaccine administration. For example, for vaccine production, e.g., for production of a live attenuated vaccine, the master donor virus strain may be selected for an attenuated phenotype, cold adaptation and/or temperature sensitivity. As explained elsewhere herein and, e.g., in U.S. Patent Application No. 10/423,828, etc., various embodiments of the invention utilize A/Ann Arbor (AA)/6/60 or B/Ann Arbor/1/66 or A/Puerto Rico/8/34, or B/Leningrad/14/17/55, B/14/5/1, B/USSR/60/69, B/Leningrad/179/86, B/Leningrad/14/55, or B/England/2608/76 influenza strain as a "backbone" upon which to add HA and/or NA genes (e.g., such as those sequences listed herein, etc.) to create desired reassortant viruses. Thus, for example, in a 6:2 reassortant, 2 genes (i.e., NA and HA) would be from the influenza strain(s) against which an immunogenic reaction is desired, while the other 6 genes would be from the Ann Arbor strain, or other backbone strain, etc. The Ann Arbor virus is useful for its cold adapted, attenuated, temperature sensitive attributes. Of course, it will be appreciated that the HA and NA sequences herein are capable of reassortment with a number of other virus genes or virus types (e.g., a number of different "backbones" such as A/Puerto Rico/8/34, etc., containing the other influenza genes present in a reassortant, namely, the non-HA and non-NA genes). Live, attenuated influenza A virus vaccines against human influenza viruses were recently licensed in the United States. *See* above. Such vaccines are reassortant H1N1 and H1N2 viruses in which the internal protein genes of A/Ann Arbor (AA)/6/60 (H2N2) cold adapted (ca) virus confer the cold adapted, attenuation and temperature sensitive phenotypes of the AA ca virus on the reassortant viruses (i.e., the ones having the hemagglutinin and neuraminidase genes from the non-Ann Arbor strain). In some embodiments herein, the reassortants can also comprise 7:1 reassortants. In other words, only the HA or the NA is not from the backbone or MDV strain. Previous work has been reported with suitable backbone donor virus strains that optionally are within various embodiments of the current invention. *See*, e.g., U.S. Application No. 60/420,708, filed October 23, 2002, U.S. Application No. 10/423,828, filed April 25, 2003, and U.S. Application No. 60/574,117, filed May 25, 2004, all entitled "Multi-Plasmid System for the Production of Influenza Virus"; Maassab et al., J. of Inf. Dis., 1982, 146:780-790; Cox, et al., Virology, 1988, 167:554-567; Wareing et al., Vaccine, 2001, 19:3320-3330; Clements, et al., J Infect Dis., 1990, 161(5):869-77, etc.

In some embodiments, the sequences herein can optionally have specific regions removed (both or either in the nucleic acid sequence or the amino acid sequence). For example, for those molecules having a polybasic cleavage site, such sites can optionally be removed. Such cleavage sites, in some embodiments herein, are, e.g., modified or altered in their sequences in comparison to the wild-type sequences from which such sequences are derived (e.g., to disable the cleavage or reduce the cleavage there, etc.). Such modifications/alterations can be different in different strains or sequences due to the various sequences of the cleavage sites in the starting sequences. For example, 4 polybasic residues (RRKK) are typically removed in some HA sequences. (as compared to wt). In various embodiments, such polybasic cleavage sites can be modified in a number of ways (all of which are contained within the invention). For example, the polybasic cleavage site can be removed one amino acid at a time (e.g., one R removed, two Rs removed, RRK removed, or RRKK removed). Additionally, an amino acid residue directly upstream of the cleavage site can also be removed or altered (e.g., from an R to a T, etc.); also, the nucleotides encoding the amino acid residue directly after the cleavage site can also be modified. Those of skill in the art will be familiar with various methods of removing such specific regions. The resulting shortened sequences are also contained within the current invention. *See*, e.g., Li et al., J. of Infectious Diseases, 179:1132-8, 1999

The terms "temperature sensitive," "cold adapted" and "attenuated" as applied to viruses (typically used as vaccines or for vaccine production) which optionally encompass the current sequences, are well known in the art. For example, the term "temperature sensitive" (*ts*) indicates, e.g., that the virus exhibits a 100 fold or greater reduction in titer at 39°C relative to 33°C for influenza A strains, or that the virus exhibits a 100 fold or greater reduction in titer at 37°C relative to 33°C for influenza B strains. The term "cold adapted" (*ca*) indicates that the virus exhibits growth at 25°C within 100 fold of its growth at 33°C, while the term "attenuated" (*att*) indicates that the virus replicates in the upper airways of ferrets but is not detectable in their lung tissues, and does not cause influenza-like illness in the animal. It will be understood that viruses with intermediate phenotypes, i.e., viruses exhibiting titer reductions less than 100 fold at 39°C (for A strain viruses) or 37°C (for B strain viruses), or exhibiting growth at 25°C that is more than 100 fold than its growth at 33°C (e.g., within 200 fold, 500 fold, 1000 fold, 10,000 fold less), and/or exhibit reduced growth in the lungs relative to growth in the upper airways of ferrets (i.e., partially attenuated) and/or reduced influenza like illness in the animal, are also useful viruses and can be used in conjunction with the HA and NA sequences herein.

Thus, the present invention can utilize growth, e.g., in appropriate culture conditions, of virus strains (both A strain and B strain influenza viruses) with desirable properties relative to vaccine production (e.g., attenuated pathogenicity or phenotype, cold adaptation, temperature sensitivity, etc.) *in vitro* in cultured cells. Influenza viruses can be produced by introducing a plurality of vectors incorporating cloned viral genome segments into host cells, and culturing the cells at a temperature not exceeding 35ºC. When vectors including an influenza virus genome are transfected, recombinant viruses suitable as vaccines can be recovered by standard purification procedures. Using the vector system and methods of the invention, reassortant viruses incorporating the six internal gene segments of a strain selected for its desirable properties with respect to vaccine production, and the immunogenic HA and NA segments from a selected, e.g., pathogenic strain such as those in the sequence listing herein, can be rapidly and efficiently produced in tissue culture. Thus, the system and methods described herein are useful for the rapid production in cell culture of recombinant and reassortant influenza A and B viruses, including viruses suitable for use as vaccines, including live attenuated vaccines, such as vaccines suitable for intranasal administration.

In such embodiments, typically, a single Master Donor Virus (MDV) strain is selected for each of the A and B subtypes. In the case of a live attenuated vaccine, the Master Donor Virus strain is typically chosen for its favorable properties, e.g., temperature sensitivity, cold adaptation and/or attenuation, relative to vaccine production. For example, exemplary Master Donor Strains include such temperature sensitive, attenuated and cold adapted strains of A/Ann Arbor/6/60 and B/Ann Arbor/1/66, respectively, as well as others mentioned throughout.

For example, a selected master donor type A virus (MDV-A), or master donor type B virus (MDV-B), is produced from a plurality of cloned viral cDNAs constituting the viral genome. Embodiments include those wherein recombinant viruses are produced from eight cloned viral cDNAs. Eight viral cDNAs representing either the selected MDV-A or MDV-B sequences of PB2, PB1, PA, NP, HA, NA, M and NS are optionally cloned into a bi-directional expression vector, such as a plasmid (e.g., pAD3000), such that the viral genomic RNA can be transcribed from an RNA polymerase I (pol I) promoter from one strand and the viral mRNAs can be synthesized from an RNA polymerase II (pol II) promoter from the other strand. Optionally, any gene segment can be modified, including the HA segment (e.g., to remove the multi-basic cleavage site (also known as a polybasic cleavage site)).

Infectious recombinant MDV-A or MDV-B virus can be then recovered following transfection of plasmids bearing the eight viral cDNAs into appropriate host cells, e.g., Vero cells, co-cultured MDCK/293T or MDCK/COS7 cells. Using the plasmids and methods described herein and, e.g., in U.S. Application No. 60/420,708, filed October 23, 2002, U.S. Application No. 10/423,828, filed April 25, 2003, and U.S. Application No. 60/574,117, filed May 24, 2004, all entitled "Multi-Plasmid System for the Production of Influenza Virus"; Hoffmann, E., 2000, PNAS, 97(11):6108-6113; U.S. Published Patent Application No. 20020164770 to Hoffmann; and USPN 6,544,785 issued April 8, 2003 to Palese, et al., the invention is useful, e.g., for generating 6:2 reassortant influenza vaccines by co-transfection of the 6 internal genes (PB1, PB2, PA, NP, M and NS) of the selected virus (e.g., MDV-A, MDV-B) together with the HA and NA derived from different corresponding type (A or B) influenza viruses e.g., as shown in the sequence listings herein. For example, the HA segment is favorably selected from a pathogenically relevant H1, H3 or B strain, as is routinely performed for vaccine production. Similarly, the HA segment can be selected from a strain with emerging relevance as a pathogenic strain such as those in the sequence listing herein. Reassortants incorporating seven genome segments of the MDV and either the HA or NA gene of a selected strain (7:1 reassortants) can also be produced. It will be appreciated, and as is detailed throughout, the molecules of the invention can optionally be combined in any desired combination. For example, the HA and/or NA sequences herein can be placed, e.g., into a reassortant backbone such as A/AA/6/60, B/AA/1/66, A/Puerto Rico/8/34 (i.e., PR8), etc., in 6:2 reassortants or 7:1 reassortants, etc. Thus, as explained more fully below, there would be 6 internal genome segments from the donor virus (again, e.g., A/AA/6/60, etc.) and 2 genome segments from a second strain (e.g., a wild-type strain, not the donor virus). Such 2 genome segments are preferably the HA and NA genes. A similar situation arises for 7:1 reassortants, in which however, there are 7 genome segments from the donor virus and 1 genome segment (either HA or NA) from a different virus (typically wild-type or one to which an immune response is desired). Also, it will be appreciated that the sequences herein (e.g., those in the sequence listing of Figure 1, etc.) can be combined in a number of means in different embodiments herein. Thus, any of the sequences herein can be present singularly in a 7:1 reassortant (i.e., the sequence of the invention present with 7 donor virus genome segments) and/or can be present with another sequence of the invention in a 6:2 reassortant. Within such 6:2 reassortants, any of the sequences of the invention can optionally be present with any other sequence of the invention. Typical, and preferred, embodiments comprise HA and NA from the same original wild-type strains however (or modified wild-type strains such as those with modified polybasic cleavage sites). For example, typical embodiments can comprise a 6:2 reassortant having 6 internal genome segments from a donor virus such as A/AA/6/60 and the HA and NA genome segments described herein. Of course, it will again be appreciated that the invention also includes such reassortant viruses wherein the HA and NA genome segments are from similar strains. The above references are specifically incorporated herein in their entirety for all purposes, e.g., especially for their teachings regarding plasmids, plasmid rescue of virus (influenza virus), multi-plasmid systems for virus rescue/production, etc.

Again, the HA and NA sequences of the current invention are optionally utilized in such plasmid reassortment vaccines (and/or in other *ts*, *cs*, *ca*, and/or *att* viruses and vaccines). However, it should be noted that the HA and NA sequences, etc. of the invention are not limited to specific vaccine compositions or production methods, and can, thus, be utilized in substantially any vaccine type or vaccine production method which utilizes strain specific HA and NA antigens (e.g., the sequences of the invention).

FLUMIST®

As mentioned previously, numerous examples and types of influenza vaccine exist. An exemplary influenza vaccine is FluMist (MedImmune Vaccines Inc., Mt. View, CA) which is a live, attenuated vaccine that protects children and adults from influenza illness (Belshe et al. (1998) *The efficacy of live attenuated, cold-adapted, trivalent, intranasal influenza virus vaccine in children* N Engl J Med 338:1405-12; Nichol et al. (1999) *Effectiveness of live, attenuated intranasal influenza virus vaccine in healthy, working adults: a randomized controlled trial* JAMA 282:137-44). In typical, and preferred, embodiments, the methods and compositions of the current invention are preferably adapted to/used with production of FluMist vaccine. However, it will be appreciated by those skilled in the art that the sequences, methods, compositions, etc. herein are also adaptable to production of similar or even different viral vaccines.

FluMist vaccine strains contain, e.g., HA and NA gene segments derived from the wild-type strains to which the vaccine is addressed (or, in some instances, to related strains) along with six gene segments, PB1, PB2, PA, NP, M and NS, from a common master donor virus (MDV). The HA and NA sequences herein, thus, are optionally part of various FluMist formulations. The MDV for influenza A strains of FluMist (MDV-A), was created by serial passage of the wild-type A/Ann Arbor/6/60 (A/AA/6/60) strain in primary chicken kidney tissue culture at successively lower temperatures (Maassab (1967) *Adaptation and growth characteristics of influenza virus at*

25 degrees C Nature 213:612-4). MDV-A replicates efficiently at 25°C (*ca*, cold adapted), but its growth is restricted at 38 and 39°C (*ts*, temperature sensitive). Additionally, this virus does not replicate in the lungs of infected ferrets (*att*, attenuation). The *ts* phenotype is believed to contribute to the attenuation of the vaccine in humans by restricting its replication in all but the coolest regions of the respiratory tract. The stability of this property has been demonstrated in animal models and clinical studies. In contrast to the *ts* phenotype of influenza strains created by chemical mutagenesis, the *ts* property of MDV-A does not revert following passage through infected hamsters or in shed isolates from children (for a recent review, *see* Murphy & Coelingh (2002) *Principles underlying the development and use of live attenuated cold-adapted influenza A and B virus vaccines* Viral Immunol 15:295-323).

Clinical studies in over 20,000 adults and children involving 12 separate 6:2 reassortant strains have shown that these vaccines are attenuated, safe and efficacious (Belshe et al. (1998) *The efficacy of live attenuated, cold-adapted, trivalent, intranasal influenza virus vaccine in children* N Engl J Med 338:1405-12; Boyce et al. (2000) *Safety and immunogenicity of adjuvanted and unadjuvanted subunit influenza vaccines administered intranasally to healthy adults* Vaccine 19:217-26; Edwards et al. (1994) *A randomized controlled trial of cold adapted and inactivated vaccines for the prevention of influenza A disease* J Infect Dis 169:68-76 ; Nichol et al. (1999) *Effectiveness of live, attenuated intranasal influenza virus vaccine in healthy, working adults: a randomized controlled trial* JAMA 282:137-44). Reassortants carrying the six internal genes of MDV-A and the two HA and NA gene segments of a wild-type virus (i.e., a 6:2 reassortant) consistently maintain *ca*, *ts* and *att* phenotypes (Maassab et al. (1982) *Evaluation of a cold-recombinant influenza virus vaccine in ferrets* J. Infect. Dis. 146:780-900).

Production of such reassorted virus using B strains of influenza is more difficult, however, recent work (*see*, e.g., U.S. Application No. 60/420,708, filed October 23, 2002, U.S. Application No. 10/423,828, filed April 25, 2003, and U.S. Application No. 60/574,117, filed May 24, 2004, all entitled “Multi-Plasmid System for the Production of Influenza Virus”) has shown an eight plasmid system for the generation of influenza B virus entirely from cloned cDNA. Methods for the production of attenuated live influenza A and B virus suitable for vaccine formulations, such as live virus vaccine formulations useful for intranasal administration were also shown.

The system and methods described previously are useful for the rapid production in cell culture of recombinant and reassortant influenza A and B viruses, including viruses suitable for use as vaccines, including live attenuated vaccines, such as vaccines suitable for intranasal administration. The sequences, methods, etc. of the current invention, are optionally used in conjunction with, or in combination with, such previous work involving, e.g., reassorted influenza viruses for vaccine production to produce viruses for vaccines.

METHODS AND COMPOSITIONS FOR PROPHYLACTIC ADMINISTRATION OF VACCINES

As stated above, alternatively, or in addition to, use in production of FluMist™ vaccine, the current invention can be used in other vaccine formulations. In general, recombinant and reassortant viruses of the invention can be administered prophylactically in an immunologically effective amount and in an appropriate carrier or excipient to stimulate an immune response specific for one or more strains of influenza virus as determined by the HA and/or NA sequence. Typically, the carrier or excipient is a pharmaceutically acceptable carrier or excipient, such as sterile water, aqueous saline solution, aqueous buffered saline solutions, aqueous dextrose solutions, aqueous glycerol solutions, ethanol, allantoic fluid from uninfected hen eggs (i.e., normal allantoic fluid or NAF), or combinations thereof. The preparation of such solutions insuring sterility, pH, isotonicity, and stability is effected according to protocols established in the art. Generally, a carrier or excipient is selected to minimize allergic and other undesirable effects, and to suit the particular route of administration, e.g., subcutaneous, intramuscular, intranasal, etc.

A related aspect of the invention provides methods for stimulating the immune system of an individual to produce a protective immune response against influenza virus. In the methods, an immunologically effective amount of a recombinant influenza virus (e.g., an HA and/or an NA molecule of the invention), an immunologically effective amount of a polypeptide of the invention, and/or an immunologically effective amount of a nucleic acid of the invention is administered to the individual in a physiologically acceptable carrier.

Generally, the influenza viruses of the invention are administered in a quantity sufficient to stimulate an immune response specific for one or more strains of influenza virus (i.e., against the HA and/or NA strains of the invention). Preferably, administration of the influenza viruses elicits a protective immune response to such strains. Dosages and methods for eliciting a protective immune response against one or more influenza strains are known to those of skill in the art. *See*, e.g., USPN 5,922,326; Wright et al., Infect. Immun. 37:397-400 (1982); Kim et al., Pediatrics 52:56-63 (1973); and Wright et al., J. Pediatr. 88:931-936 (1976). For example, influenza viruses are provided in the range of about 1-1000 HID_{50} (human infectious dose), i.e., about 10^5 - 10^8 pfu (plaque forming units) per dose administered. Typically, the dose will be adjusted within this range based on, e.g., age, physical condition, body weight, sex, diet, time of administration, and other clinical factors. The prophylactic vaccine formulation is systemically administered, e.g., by subcutaneous or intramuscular injection using a needle and syringe, or a needle-less injection device. Alternatively, the vaccine formulation is administered intranasally, either by drops, large particle aerosol (greater than about 10 microns), or spray into the upper respiratory tract. While any of the above routes of delivery results in a protective systemic immune response, intranasal administration confers the added benefit of eliciting mucosal immunity at the site of entry of the influenza virus. For intranasal administration, attenuated live virus vaccines are often preferred, e.g., an attenuated, cold adapted and/or temperature sensitive recombinant or reassortant influenza virus. *See* above. While stimulation of a protective immune response with a single dose is preferred, additional dosages can be administered, by the same or different route, to achieve the desired prophylactic effect.

Typically, the attenuated recombinant influenza of this invention as used in a vaccine is sufficiently attenuated such that symptoms of infection, or at least symptoms of serious infection, will not occur in most individuals immunized (or otherwise infected) with the attenuated influenza virus. In some instances, the attenuated influenza virus can still be capable of producing symptoms of mild illness (e.g., mild upper respiratory illness) and/or of dissemination to unvaccinated individuals. However, its virulence is sufficiently abrogated such that severe lower respiratory tract infections do not occur in the vaccinated or incidental host.

Alternatively, an immune response can be stimulated by *ex vivo* or *in vivo* targeting of dendritic cells with influenza viruses comprising the sequences herein. For example, proliferating dendritic cells are exposed to viruses in a sufficient amount and for a sufficient period of time to permit capture of the influenza antigens by the dendritic cells.

The cells are then transferred into a subject to be vaccinated by standard intravenous transplantation methods.

While stimulation of a protective immune response with a single dose is preferred, additional dosages can be administered, by the same or different route, to achieve the desired prophylactic effect. In neonates and infants, for example, multiple administrations may be required to elicit sufficient levels of immunity. Administration can continue at intervals throughout childhood, as necessary to maintain sufficient levels of protection against wild-type influenza infection. Similarly, adults who are particularly susceptible to repeated or serious influenza infection, such as, for example, health care workers, day care workers, family members of young children, the elderly, and individuals with compromised cardiopulmonary function may require multiple immunizations to establish and/or maintain protective immune responses. Levels of induced immunity can be monitored, for example, by measuring amounts of neutralizing secretory and serum antibodies, and dosages adjusted or vaccinations repeated as necessary to elicit and maintain desired levels of protection.

Optionally, the formulation for prophylactic administration of the influenza viruses also contains one or more adjuvants for enhancing the immune response to the influenza antigens. Suitable adjuvants include: complete Freund's adjuvant, incomplete Freund's adjuvant, saponin, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil or hydrocarbon emulsions, bacille Calmette-Guerin (BCG), *Corynebacterium parvum*, and the synthetic adjuvants QS-21 and MF59.

If desired, prophylactic vaccine administration of influenza viruses can be performed in conjunction with administration of one or more immunostimulatory molecules. Immunostimulatory molecules include various cytokines, lymphokines and chemokines with immunostimulatory, immunopotentiating, and pro-inflammatory activities, such as interleukins (e.g., IL-1, IL-2, IL-3, IL-4, IL-12, IL-13); growth factors (e.g., granulocyte-macrophage (GM)-colony stimulating factor (CSF)); and other immunostimulatory molecules, such as macrophage inflammatory factor, Flt3 ligand, B7.1; B7.2, etc. The immunostimulatory molecules can be administered in the same formulation as the influenza viruses, or can be administered separately. Either the protein (e.g., an HA and/or NA polypeptide of the invention) or an expression vector encoding the protein can be administered to produce an immunostimulatory effect.

The above described methods are useful for therapeutically and/or prophylactically treating a disease or disorder, typically influenza, by introducing a vector of the invention comprising a heterologous polynucleotide encoding a therapeutically or prophylactically effective HA and/or NA polypeptide (or peptide) or HA and/or NA RNA (e.g., an antisense RNA or ribozyme) into a population of target cells *in vitro*, *ex vivo* or *in vivo*. Typically, the polynucleotide encoding the polypeptide (or peptide), or RNA, of interest is operably linked to appropriate regulatory sequences, e.g., as described herein. Optionally, more than one heterologous coding sequence is incorporated into a single vector or virus. For example, in addition to a polynucleotide encoding a therapeutically or prophylactically active HA and/or NA polypeptide or RNA, the vector can also include additional therapeutic or prophylactic polypeptides, e.g., antigens, co-stimulatory molecules, cytokines, antibodies, etc., and/or markers, and the like.

Although vaccination of an individual with an attenuated influenza virus of a particular strain of a particular subgroup can induce cross-protection against influenza virus of different strains and/or subgroups, cross-protection can be enhanced, if desired, by vaccinating the individual with attenuated influenza virus from at least two, at least three, or at least four influenza virus strains or substrains, e.g., at least two of which may represent a different subgroup. For example, vaccinating an individual with at least four strains or substrains of attenuated influenza virus may include vaccinating the individual with at least two strains or substrains of influenza A virus and at least two strains or substrains of influenza B virus. Vaccinating the individual with the at least four strains or substrains of attenuated influenza virus may include vaccinating the individual with at least three strains or substrains of influenza A virus and at least one strain or substrain of influenza B virus. The vaccination of the individual with at least four influenza virus strains or substrains may require administration of a single tetravalent vaccine which comprises all of the at least four attenuated influenza virus strains or substrains. The vaccination may alternatively require administration of multiple vaccines, each of which comprises one, two, or three of the attenuated influenza virus strains or substrains. Additionally, vaccine combinations can optionally include mixes of pandemic vaccines and non-pandemic strains. Vaccine mixtures (or multiple vaccinations) can comprise components from human strains and/or non-human influenza strains (e.g., avian and human, etc.). Similarly, the attenuated influenza virus vaccines of this invention can optionally be combined with vaccines that induce protective immune responses against other infectious agents. In one embodiment, a vaccine of the invention is a trivalent vaccine comprising three reassortant influenza viruses. In one embodiment, a vaccine of the invention is a trivalent vaccine comprising two reassortant influenza A viruses and a reassortant influenza B virus. In one embodiment, a vaccine of the invention is a trivalent vaccine comprising a reassortant influenza A virus of the H1 type, a reassortant influenza A virus of the H3 type and a reassortant influenza B virus. In another embodiment, a vaccine of the invention is a tetravalent vaccine comprising four reassortant influenza viruses. In one embodiment, a vaccine of the invention is a tetravalent vaccine comprising two reassortant influenza A viruses and two reassortant influenza B viruses. In one embodiment, a vaccine of the invention is a tetravalent vaccine comprising a reassortant influenza A virus of the H1 type, a reassortant influenza A virus of the H3 type, a reassortant influenza B virus of the Victoria lineage and a reasortant influenza B virus of the Yamagata lineage.

Production of recombinant virus

Negative strand RNA viruses can be genetically engineered and recovered using a recombinant reverse genetics approach (USPN 5,166,057 to Palese et al.). Such method was originally applied to engineer influenza viral genomes (Luytjes et al. (1989) Cell 59:1107-1113; Enami et al. (1990) Proc. Natl. Acad. Sci. USA 92:11563-11567), and has been successfully applied to a wide variety of segmented and nonsegmented negative strand RNA viruses, e.g., rabies (Schnell et al. (1994) EMBO J. 13: 4195-4203); VSV (Lawson et al. (1995) Proc. Natl. Acad. Sci. USA 92: 4477-4481); measles virus (Radecke et al.(1995) EMBO J. 14:5773-5784); rinderpest virus (Baron & Barrett (1997) J. Virol. 71: 1265-1271); human parainfluenza virus (Hoffman & Banerjee (1997) J. Virol. 71: 3272-3277; Dubin et al. (1997) Virology 235:323-332); SV5 (He et al. (1997) Virology 237:249-260); canine distemper virus (Gassen et al. (2000) J. Virol. 74:10737-44); and Sendai virus (Park et al. (1991) Proc. Natl. Acad. Sci. USA 88: 5537-5541; Kato et al. (1996) Genes to Cells 1:569-579). Those of skill in the art will be familiar with these and similar techniques to produce influenza virus comprising the HA and NA sequences of the invention. Recombinant influenza viruses produced according to such methods are also a feature of the invention, as are recombinant influenza virus comprising one or more nucleic acids and/or polypeptides of the invention. Of course, as will be appreciated by those of skill in the art, influenza viruses in general (and those of the invention as well) are negative stranded RNA viruses. Thus, when the present invention describes influenza viruses as comprising, e.g., the sequences of Figure 1, etc., it is to be understood to typically mean the corresponding negative stranded RNA version of the sequences. The nucleotide sequences in Figure 1 comprise DNA versions (e.g., coding plus sense, etc.) of the genes (along with some untranslated regions in the nucleotide sequences). Those of skill in the art can easily convert between RNA and DNA sequences (e.g., changing U to T, etc.), and between complementary nucleotide sequences (whether RNA or DNA),etc. Thus, for example, those of skill in the art can easily convert from a nucleotide sequence to the corresponding amino acid sequence or to a corresponding complementary sequence (whether DNA or RNA), etc. Also, as will be evident, when such HA and/or NA sequences are described within DNA vectors, e.g., plasmids, etc., then the corresponding DNA version of the sequences are typically to be understood. Again, nucleic acids of the invention include the explicit sequences in the sequence listings herein, as well as the complements of such sequences (both RNA and DNA), the double stranded form of the sequences in the sequence listings, the corresponding RNA forms of the sequences in the sequence listings (either as the RNA complement to the explicit sequence in the sequence listing or as the RNA version of the sequence in the sequence listing, e.g., of the same sense, but comprised of RNA, with U in place of T, etc.).

Cell Culture and Expression Hosts

The present invention also relates to host cells that are introduced (transduced, transformed or transfected) with vectors of the invention, and the production of polypeptides of the invention by recombinant techniques. Host cells are genetically engineered (i.e., transduced, transformed or transfected) with a vector, such as an expression vector, of this invention. As described above, the vector can be in the form of a plasmid, a viral particle, a phage, etc. Examples of appropriate expression hosts include: bacterial cells, such as *E. coli*, *Streptomyces*, and *Salmonella typhimurium*; fungal cells, such as *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Neurospora crassa*; or insect cells such as *Drosophila* and *Spodoptera frugiperda*.

Most commonly, mammalian cells are used to culture the HA and NA molecules of the invention. Suitable host cells for the replication of influenza virus (e.g., with the HA and/or NA sequences herein) include, e.g., Vero cells, BHK cells, MDCK cells, 293 cells and COS cells, including 293T cells, COS7 cells or the like. Commonly, co-cultures including two of the above cell lines, e.g., MDCK cells and either 293T or COS cells are employed at a ratio, e.g., of 1:1, to improve replication efficiency. Typically, cells are cultured in a standard commercial culture medium, such as Dulbecco's modified Eagle's medium supplemented with serum (e.g., 10% fetal bovine serum), or in serum free medium, under controlled humidity and CO_2 concentration suitable for maintaining neutral buffered pH (e.g., at pH between 7.0 and 7.2). Optionally, the medium contains antibiotics to prevent bacterial growth, e.g., penicillin, streptomycin, etc., and/or additional nutrients, such as L-glutamine, sodium pyruvate, non-essential amino acids, additional supplements to promote favorable growth characteristics, e.g., trypsin, β-mercaptoethanol, and the like.

The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the inserted polynucleotide sequences, e.g., through production of viruses. The culture conditions, such as temperature, pH and the like, are typically those previously used with the particular host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, e.g., Freshney (1994) Culture of Animal Cells, a Manual of Basic Technique, 3rd edition, Wiley- Liss, New York and the references cited therein. Other helpful references include, e.g., Paul (1975) Cell and Tissue Culture, 5th ed., Livingston, Edinburgh; Adams (1980) Laboratory Techniques in Biochemistry and Molecular Biology-Cell Culture for Biochemists, Work and Burdon (eds.) Elsevier, Amsterdam. Additional details regarding tissue culture procedures of particular interest in the production of influenza virus *in vitro* include, e.g., Merten et al. (1996) *Production of influenza virus in cell cultures for vaccine preparation*. in Cohen and Shafferman (eds.) Novel Strategies in Design and Production of Vaccines, which is incorporated herein in its entirety for all purposes. Additionally, variations in such procedures adapted to the present invention are readily determined through routine experimentation and will be familiar to those skilled in the art.

Cells for production of influenza virus (e.g., having the HA and/or NA sequences of the invention) can be cultured in serum-containing or serum free medium. In some cases, e.g., for the preparation of purified viruses, it is typically desirable to grow the host cells in serum free conditions. Cells can be cultured in small scale, e.g., less than 25 ml medium, culture tubes or flasks or in large flasks with agitation, in rotator bottles, or on microcarrier beads (e.g., DEAE-Dextran microcarrier beads, such as Dormacell, Pfeifer & Langen; Superbead, Flow Laboratories; styrene copolymer-tri-methylamine beads, such as Hillex, SoloHill, Ann Arbor) in flasks, bottles or reactor cultures. Microcarrier beads are small spheres (in the range of 100-200 microns in diameter) that provide a large surface area for adherent cell growth per volume of cell culture. For example a single liter of medium can include more than 20 million microcarrier beads providing greater than 8000 square centimeters of growth surface. For commercial production of viruses, e.g., for vaccine production, it is often desirable to culture the cells in a bioreactor or fermenter. Bioreactors are available in volumes from under 1 liter to in excess of 100 liters, e.g., Cyto3 Bioreactor (Osmonics, Minnetonka, MN); NBS bioreactors (New Brunswick Scientific, Edison, NJ); laboratory and commercial scale bioreactors from B. Braun Biotech International (B. Braun Biotech, Melsungen, Germany).

Regardless of the culture volume, in many desired aspects of the current invention, it is important that the cultures be maintained at an appropriate temperature, to insure efficient recovery of recombinant and/or reassortant influenza virus using temperature dependent multi plasmid systems (*see*, e.g., U.S. Application No. 60/420,708, filed October 23, 2002, U.S. Application No. 10/423,828, filed April 25, 2003, and U.S. Application No. 60/574,117, filed May 24, 2004, all entitled “Multi-Plasmid System for the Production of Influenza Virus”), heating of virus solutions for filtration, etc. Typically, a regulator, e.g., a thermostat, or other device for sensing and maintaining the temperature of the cell culture system and/or other solution, is employed to insure that the temperature is at the correct level during the appropriate period (e.g., virus replication, etc.).

In some embodiments herein (e.g., wherein reassorted viruses are to be produced from segments on vectors) vectors comprising influenza genome segments are introduced (e.g., transfected) into host cells according to methods well known in the art for introducing heterologous nucleic acids into eukaryotic cells, including, e.g., calcium phosphate co-precipitation, electroporation, microinjection, lipofection, and transfection employing polyamine transfection reagents. For example, vectors, e.g., plasmids, can be transfected into host cells, such as COS cells, 293T cells or combinations of COS or 293T cells and MDCK cells, using the polyamine transfection reagent TransIT-LT1 (Mirus) according to the manufacturer’s instructions in order to produce reassorted viruses, etc. Thus, in one example, approximately 1 μg of each vector is introduced into a population of host cells with approximately 2 μl of TransIT-LT1 diluted in 160 μl medium, preferably serum-free medium, in a total volume of 200 μl. The DNA:transfection reagent mixtures are incubated at room temperature for 45 minuets followed by addition of 800 μl of medium. The transfection mixture is added to the host cells, and the cells are cultured as described via other methods well known to those skilled in the art. Accordingly, for the production of recombinant or reassortant viruses in cell culture, vectors incorporating each of the 8 genome segments, (PB2, PB1, PA, NP, M, NS, HA and NA, e.g., of the invention) are mixed with approximately 20 μl TransIT-LT1 and transfected into host cells. Optionally, serum-containing medium is replaced prior to transfection with serum-free medium, e.g., Opti-MEM I, and incubated for 4-6 hours.

Alternatively, electroporation can be employed to introduce such vectors incorporating influenza genome segments into host cells. For example, plasmid vectors incorporating an influenza A or influenza B virus are favorably introduced into Vero cells using electroporation according to the following procedure. In brief, approximately 5 x 10^6 Vero cells, e.g., grown in Modified Eagle's Medium (MEM) supplemented with 10% Fetal Bovine Serum (FBS) are resuspended in 0.4 ml OptiMEM and placed in an electroporation cuvette. Twenty micrograms of DNA in a volume of up to 25 μl is added to the cells in the cuvette, which is then mixed gently by tapping. Electroporation is performed according to the manufacturer's instructions (e.g., BioRad Gene Pulser II with Capacitance Extender Plus connected) at 300 volts, 950 microFarads with a time constant of between 28-33 msec. The cells are remixed by gently tapping and approximately 1-2 minutes following electroporation 0.7 ml MEM with 10% FBS is added directly to the cuvette. The cells are then transferred to two wells of a standard 6 well tissue culture dish containing 2 ml MEM, 10% FBS. The cuvette is washed to recover any remaining cells and the wash suspension is divided between the two wells. Final volume is approximately 3.5 mL. The cells are then incubated under conditions permissive for viral growth, e.g., at approximately 33°C for cold adapted strains.

In mammalian host cells, a number of expression systems, such as viral-based systems, can be utilized. In cases where an adenovirus is used as an expression vector, a coding sequence is optionally ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a nonessential E1 or E3 region of the viral genome will result in a viable virus capable of expressing the polypeptides of interest in infected host cells (Logan and Shenk (1984) Proc Natl Acad Sci 81:3655-3659). In addition, transcription enhancers, such as the rous sarcoma virus (RSV) enhancer, can be used to increase expression in mammalian host cells.

A host cell strain is optionally chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the protein include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation. Post-translational processing, which cleaves a precursor form into a mature form, of the protein is sometimes important for correct insertion, folding and/or function. Additionally proper location within a host cell (e.g., on the cell surface) is also important. Different host cells such as COS, CHO, BHK, MDCK, 293, 293T, COS7, etc. have specific cellular machinery and characteristic mechanisms for such post-translational activities and can be chosen to ensure the correct modification and processing of the current introduced, foreign protein.

For long-term, high-yield production of recombinant proteins encoded by, or having subsequences encoded by, the polynucleotides of the invention, stable expression systems are optionally used. For example, cell lines, stably expressing a polypeptide of the invention, are transfected using expression vectors that contain viral origins of replication or endogenous expression elements and a selectable marker gene. For example, following the introduction of the vector, cells are allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells that successfully express the introduced sequences. Thus, resistant clumps of stably transformed cells, e.g., derived from single cell type, can be proliferated using tissue culture techniques appropriate to the cell type.

Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The cells expressing said protein can be sorted, isolated and/or purified. The protein or fragment thereof produced by a recombinant cell can be secreted, membrane-bound, or retained intracellularly, depending on the sequence (e.g., depending upon fusion proteins encoding a membrane retention signal or the like) and/or the vector used.

Expression products corresponding to the nucleic acids of the invention can also be produced in non-animal cells such as plants, yeast, fungi, bacteria and the like. In addition to Sambrook, Berger and Ausubel, all *infra,* details regarding cell culture can be found in Payne et al. (1992) Plant Cell and Tissue Culture in Liquid Systems John Wiley &

Sons, Inc. New York, NY; Gamborg and Phillips (eds.) (1995) Plant Cell, Tissue and Organ Culture; Fundamental Methods Springer Lab Manual, Springer-Verlag (Berlin Heidelberg New York) and Atlas and Parks (eds.) The Handbook of Microbiological Media (1993) CRC Press, Boca Raton, FL.

In bacterial systems, a number of expression vectors can be selected depending upon the use intended for the expressed product. For example, when large quantities of a polypeptide or fragments thereof are needed for the production of antibodies, vectors that direct high-level expression of fusion proteins that are readily purified are favorably employed. Such vectors include, but are not limited to, multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the coding sequence of interest, e.g., sequences comprising those found herein, etc., can be ligated into the vector in-frame with sequences for the amino-terminal translation initiating methionine and the subsequent 7 residues of beta-galactosidase producing a catalytically active beta galactosidase fusion protein; pIN vectors (Van Heeke & Schuster (1989) J Biol Chem 264:5503-5509); pET vectors (Novagen, Madison WI); and the like. Similarly, in the yeast *Saccharomyces cerevisiae* a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase and PGH can be used for production of the desired expression products. For reviews, see Ausubel, *infra*, and Grant et al., (1987); Methods in Enzymology 153:516-544.

Cloning, Mutagenesis and Expression of Biomolecules of Interest

General texts which describe molecular biological techniques, which are applicable to the present invention, such as cloning, mutation, cell culture and the like, include Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA (Berger); Sambrook et al., Molecular Cloning - A Laboratory Manual (3rd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 2000 ("Sambrook") and 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., (supplemented through 2002) ("Ausubel")). These texts describe mutagenesis, the use of vectors, promoters and many other relevant topics related to, e.g., the generation of HA and/or NA molecules, etc.

Various types of mutagenesis are optionally used in the present invention, e.g., to produce and/or isolate, e.g., novel or newly isolated HA and/or NA molecules and/or to further modify/mutate the polypeptides (e.g., HA and NA molecules) of the invention. They include but are not limited to site-directed, random point mutagenesis, homologous recombination (DNA shuffling), mutagenesis using uracil containing templates, oligonucleotide-directed mutagenesis, phosphorothioate-modified DNA mutagenesis, mutagenesis using gapped duplex DNA or the like. Additional suitable methods include point mismatch repair, mutagenesis using repair-deficient host strains, restriction-selection and restriction-purification, deletion mutagenesis, mutagenesis by total gene synthesis, double-strand break repair, and the like. Mutagenesis, e.g., involving chimeric constructs, is also included in the present invention. In one embodiment, mutagenesis can be guided by known information of the naturally occurring molecule or altered or mutated naturally occurring molecule, e.g., sequence, sequence comparisons, physical properties, crystal structure or the like.

The above texts and examples found herein describe these procedures as well as the following publications (and references cited within): Sieber, et al., Nature Biotechnology, 19:456-460 (2001); Ling et al., *Approaches to DNA mutagenesis: an overview*, Anal Biochem 254(2): 157-178 (1997); Dale et al., *Oligonucleotide-directed random mutagenesis using the phosphorothioate method*, Methods Mol Biol 57:369-374 (1996); I. A. Lorimer, I. Pastan, Nucleic Acids Res 23, 3067-8 (1995); W. P. C. Stemmer, Nature 370, 389-91 (1994); Arnold, *Protein engineering for unusual environments*, Current Opinion in Biotechnology 4:450-455 (1993); Bass et al., *Mutant Trp repressors with new DNA-binding specificities*, Science 242:240-245 (1988); Fritz et al., *Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions in vitro*, Nucl Acids Res 16: 6987-6999 (1988); Kramer et al., *Improved enzymatic in vitro reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations*, Nucl Acids Res 16: 7207 (1988); Sakamar and Khorana, *Total synthesis and expression of a gene for the a-subunit of bovine rod outer segment guanine nucleotide-binding protein (transducin)*, Nucl Acids Res 14: 6361-6372 (1988); Sayers et al., *Y-T Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis*, Nucl Acids Res 16:791-802 (1988); Sayers et al., *Strand specific cleavage of phosphorothioate-containing DNA by reaction with restriction endonucleases in the presence of ethidium bromide*, (1988) Nucl Acids Res 16: 803-814; Carter, *Improved oligonucleotide-directed mutagenesis using M13 vectors*, Methods in Enzymol 154: 382-403 (1987); Kramer & Fritz *Oligonucleotide-directed construction of mutations via gapped* *duplex DNA*, Methods in Enzymol 154:350-367 (1987); Kunkel*, The efficiency of oligonucleotide directed mutagenesis*, in Nucleic Acids & Molecular Biology (Eckstein, F. and Lilley, D.M.J. eds., Springer Verlag, Berlin)) (1987); Kunkel et al., *Rapid and efficient site-specific mutagenesis without phenotypic selection*, Methods in Enzymol 154, 367-382 (1987); Zoller & Smith, *Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template*, Methods in Enzymol 154:329-350 (1987); Carter, *Site-directed mutagenesis*, Biochem J 237:1-7 (1986); Eghtedarzadeh & Henikoff, *Use of oligonucleotides to generate large deletions*, Nucl Acids Res 14: 5115 (1986); Mandecki, *Oligonucleotide-directed double-strand break repair in plasmids of Escherichia coli: a method for site-specific mutagenesis*, Proc Natl Acad Sci USA, 83:7177-7181 (1986); Nakamaye & Eckstein, *Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis*, Nucl Acids Res 14: 9679-9698 (1986); Wells et al., *Importance of hydrogen-bond formation in stabilizing the transition state of subtilisin*, Phil Trans R Soc Lond A 317: 415-423 (1986); Botstein & Shortle, *Strategies and applications of in vitro mutagenesis*, Science 229:1193-1201(1985); Carter et al., *Improved oligonucleotide site-directed mutagenesis using M13 vectors*, Nucl Acids Res 13: 4431-4443 (1985); Grundström et al., *Oligonucleotide-directed mutagenesis by microscale 'shot-gun' gene synthesis*, Nucl Acids Res 13: 3305-3316 (1985); Kunkel, *Rapid and efficient site-specific mutagenesis without phenotypic selection*, Proc Natl Acad Sci USA 82:488-492 (1985); Smith, *In vitro mutagenesis*, Ann Rev Genet 19:423-462(1985); Taylor et al., *The use of phosphorothioate-modified DNA in restriction enzyme reactions to prepare nicked DNA*, Nucl Acids Res 13: 8749-8764 (1985); Taylor et al., *The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA*, Nucl Acids Res 13: 8765-8787 (1985); Wells et al., *Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites*, Gene 34:315-323 (1985); Kramer et al., *The gapped duplex DNA approach to oligonucleotide-directed mutation construction*, Nucl Acids Res 12: 9441-9456 (1984); Kramer et al., *Point Mismatch Repair*, Cell 38:879-887 (1984); Nambiar et al., *Total synthesis and cloning of a gene coding for the ribonuclease S protein*, Science 223: 1299-1301 (1984); Zoller & Smith, *Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors*, Methods in Enzymol 100:468-500 (1983); and Zoller & Smith, *Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment*, Nucl Acids

Res 10:6487-6500 (1982). Additional details on many of the above methods can be found in Methods in Enzymol Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis, gene isolation, expression, and other methods.

Oligonucleotides, e.g., for use in mutagenesis of the present invention, e.g., mutating libraries of the HA and/or NA molecules of the invention, or altering such, are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers, Tetrahedron Letts 22(20):1859-1862, (1981) e.g., using an automated synthesizer, as described in Needham-VanDevanter et al., Nucleic Acids Res, 12:6159-6168 (1984).

In addition, essentially any nucleic acid can be custom or standard ordered from any of a variety of commercial sources Similarly, peptides and antibodies can be custom ordered from any of a variety of sources.

The present invention also relates to host cells and organisms comprising a HA and/or NA molecule or other polypeptide and/or nucleic acid of the invention or such HA and/or NA or other sequences within various vectors such as 6:2 reassortant influenza viruses, plasmids in plasmid rescue systems, etc. Host cells are genetically engineered (e.g., transformed, transduced or transfected) with the vectors of this invention, which can be, for example, a cloning vector or an expression vector. The vector can be, for example, in the form of a plasmid, a bacterium, a virus, a naked polynucleotide, or a conjugated polynucleotide. The vectors are introduced into cells and/or microorganisms by standard methods including electroporation (*see*, From et al., Proc Natl Acad Sci USA 82, 5824 (1985), infection by viral vectors, high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., Nature 327, 70-73 (1987)). Berger, Sambrook, and Ausubel provide a variety of appropriate transformation methods. *See*, above.

Several well-known methods of introducing target nucleic acids into bacterial cells are available, any of which can be used in the present invention. These include: fusion of the recipient cells with bacterial protoplasts containing the DNA, electroporation, projectile bombardment, and infection with viral vectors, etc. Bacterial cells can be used to amplify the number of plasmids containing DNA constructs of this invention. The bacteria are grown to log phase and the plasmids within the bacteria can be isolated by a variety of methods known in the art (*see*, for instance, Sambrook). In addition, a plethora of kits are commercially available for the purification of plasmids from bacteria, (*see*, e.g., EasyPrep™, FlexiPrep™, both from Pharmacia Biotech; StrataClean™, from Stratagene; and, QIAprep™ from Qiagen). The isolated and purified plasmids are then further manipulated to produce other plasmids, used to transfect cells or incorporated into related vectors to infect organisms. Typical vectors contain transcription and translation terminators, transcription and translation initiation sequences, and promoters useful for regulation of the expression of the particular target nucleic acid. The vectors optionally comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the cassette in eukaryotes, or prokaryotes, or both, (e.g., shuttle vectors) and selection markers for both prokaryotic and eukaryotic systems. Vectors are suitable for replication and integration in prokaryotes, eukaryotes, or preferably both. *See,* Giliman & Smith, Gene 8:81 (1979); Roberts, et al., Nature, 328:731 (1987); Schneider, B., et al., Protein Expr Purif 6435:10 (1995); Ausubel, Sambrook, Berger (*all supra*). A catalogue of Bacteria and Bacteriophages useful for cloning is provided, e.g., by the ATCC, e.g., The ATCC Catalogue of Bacteria and Bacteriophage (1992) Gherna et al. (eds.) published by the ATCC. Additional basic procedures for sequencing, cloning and other aspects of molecular biology and underlying theoretical considerations are also found in Watson et al. (1992) Recombinant DNA Second Edition Scientific American Books, NY. *See*, above.

POLYPEPTIDE PRODUCTION AND RECOVERY

In some embodiments, following transduction of a suitable host cell line or strain and growth of the host cells to an appropriate cell density, a selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. In some embodiments, a secreted polypeptide product, e.g., a HA and/or NA polypeptide as in a secreted fusion protein form, etc., is then recovered from the culture medium. In other embodiments, a virus particle containing one or more HA and/or NA polypeptide of the invention is produced from the cell. Alternatively, cells can be harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Eukaryotic or microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, or other methods, which are well know to those skilled in the art.

Additionally, cells expressing a HA and/or a NA polypeptide product of the invention can be utilized without separating the polypeptide from the cell. In such situations, the polypeptide of the invention is optionally expressed on the cell surface and is examined thus (e.g., by having HA and/or NA molecules, or fragments thereof, e.g., comprising fusion proteins or the like) on the cell surface bind antibodies, etc. Such cells are also features of the invention.

Expressed polypeptides can be recovered and purified from recombinant cell cultures by any of a number of methods well known in the art, including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography (e.g., using any of the tagging systems known to those skilled in the art), hydroxylapatite chromatography, and lectin chromatography. Protein refolding steps can be used, as desired, in completing configuration of the mature protein. Also, high performance liquid chromatography (HPLC) can be employed in the final purification steps. In addition to the references noted herein, a variety of purification methods are well known in the art, including, e.g., those set forth in Sandana (1997) Bioseparation of Proteins, Academic Press, Inc.; and Bollag et al. (1996) Protein Methods, 2nd Edition Wiley-Liss, NY; Walker (1996) The Protein Protocols Handbook Humana Press, NJ, Harris and Angal (1990) Protein Purification Applications: A Practical Approach IRL Press at Oxford, Oxford, England; Harris and Angal Protein Purification Methods: A Practical Approach IRL Press at Oxford, Oxford, England; Scopes (1993) Protein Purification: Principles and Practice 3rd Edition Springer Verlag, NY; Janson and Ryden (1998) Protein Purification: Principles, High Resolution Methods and Applications, Second Edition Wiley-VCH, NY; and Walker (1998) Protein Protocols on CD-ROM Humana Press, NJ.

When the expressed polypeptides of the invention are produced in viruses, the viruses are typically recovered from the culture medium, in which infected (transfected) cells have been grown. Typically, crude medium is clarified prior to concentration of influenza viruses. Common methods include ultrafiltration, adsorption on barium sulfate and elution, and centrifugation. For example, crude medium from infected cultures can first be clarified by centrifugation at, e.g., 1000-2000 x g for a time sufficient to remove cell debris and other large particulate matter, e.g., between 10 and 30 minutes. Optionally, the clarified medium supernatant is then centrifuged to pellet the influenza viruses, e.g., at 15,000 x g, for approximately 3-5 hours. Following resuspension of the virus pellet in an appropriate buffer, such as STE (0.01 M Tris-HCl; 0.15 M NaCl; 0.0001 M EDTA) or phosphate buffered saline (PBS) at pH 7.4, the virus is concentrated by density gradient centrifugation on sucrose (60%-12%) or potassium tartrate (50%-10%). Either continuous or step gradients, e.g., a sucrose gradient between 12% and 60% in four 12% steps, are suitable. The gradients are centrifuged at a speed, and for a time, sufficient for the viruses to concentrate into a visible band for recovery. Alternatively, and for most large-scale commercial applications, virus is elutriated from density gradients using a zonal-centrifuge rotor operating in continuous mode. Additional details sufficient to guide one of skill through the preparation of influenza viruses from tissue culture are provided, e.g., in Furminger. *Vaccine Production*, in Nicholson et al. (eds.) Textbook of Influenza pp. 324-332; Merten et al. (1996) *Production of influenza virus in cell cultures for vaccine preparation*, in Cohen & Shafferman (eds.) Novel Strategies in Design and Production of Vaccines pp. 141-151, and United States Patent No. 5,690,937. If desired, the recovered viruses can be stored at -80°C in the presence of sucrose-phosphate-glutamate (SPG) as a stabilizer

Modified Amino Acids

Expressed polypeptides of the invention can contain one or more modified amino acids. The presence of modified amino acids can be advantageous in, for example, (a) increasing polypeptide serum half-life, (b) reducing/increasing polypeptide antigenicity, (c) increasing polypeptide storage stability, etc. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production (e.g., N-linked glycosylation at N-X-S/T motifs during expression in mammalian cells) or modified by synthetic means (e.g., via PEGylation).

Non-limiting examples of a modified amino acid include a glycosylated amino acid, a sulfated amino acid, a prenlyated (e.g., farnesylated, geranylgeranylated) amino acid, an acetylated amino acid, an acylated amino acid, a PEG-ylated amino acid, a biotinylated amino acid, a carboxylated amino acid, a phosphorylated amino acid, and the like, as well as amino acids modified by conjugation to, e.g., lipid moieties or other organic derivatizing agents. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature. Example protocols are found in Walker (1998) Protein Protocols on CD-ROM Human Press, Towata, NJ.

Fusion Proteins

The present invention also provides fusion proteins comprising fusions of the sequences of the invention (e.g., encoding HA and/or NA polypeptides) or fragments thereof with, e.g., immunoglobulins (or portions thereof), sequences encoding, e.g., GFP (green fluorescent protein), or other similar markers, etc. Nucleotide sequences encoding such fusion proteins are another aspect of the invention. Fusion proteins of the invention are optionally used for, e.g., similar applications (including, e.g., therapeutic, prophylactic, diagnostic, experimental, etc. applications as described herein) as the non-fusion proteins of the invention. In addition to fusion with immunoglobulin sequences and marker sequences, the proteins of the invention are also optionally fused with, e.g., sequences which allow sorting of the fusion proteins and/or targeting of the fusion proteins to specific cell types, regions, etc.

Antibodies

The polypeptides of the invention can be used to produce antibodies specific for the polypeptides given herein and/or polypeptides encoded by the polynucleotides of the invention, e.g., those shown herein, and conservative variants thereof. Antibodies specific for the above mentioned polypeptides are useful, e.g., for diagnostic and therapeutic purposes, e.g., related to the activity, distribution, and expression of target polypeptides. For example, such antibodies can optionally be utilized to define other viruses within the same strain(s) as the HA/NA sequences herein.

Antibodies specific for the polypeptides of the invention can be generated by methods well known in the art. Such antibodies can include, but are not limited to, polyclonal, monoclonal, chimeric, humanized, single chain, Fab fragments and fragments produced by an Fab expression library.

Polypeptides do not require biological activity for antibody production (e.g., full length functional hemagglutinin or neuraminidase is not required). However, the polypeptide or oligopeptide must be antigenic. Peptides used to induce specific antibodies typically have an amino acid sequence of at least about 4 amino acids, and often at least 5 or 10 amino acids. Short stretches of a polypeptide can be fused with another protein, such as keyhole limpet hemocyanin, and antibody produced against the chimeric molecule.

Numerous methods for producing polyclonal and monoclonal antibodies are known to those of skill in the art, and can be adapted to produce antibodies specific for the polypeptides of the invention, and/or encoded by the polynucleotide sequences of the invention, etc. *See,* e.g., Coligan (1991) Current Protocols in Immunology Wiley/Greene, NY; Paul (ed.) (1998) Fundamental Immunology, Fourth Edition, Lippincott-Raven, Lippincott Williams & Wilkins; Harlow and Lane (1989) Antibodies: A Laboratory Manual Cold Spring Harbor Press, NY; Stites et al. (eds.) Basic and Clinical Immunology (4th ed.) Lange Medical Publications, Los Altos, CA, and references cited therein; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press, New York, NY; and Kohler and Milstein (1975) Nature 256: 495-497. Other suitable techniques for antibody preparation include selection of libraries of recombinant antibodies in phage or similar vectors. *See*, Huse et al. (1989) Science 246: 1275-1281; and Ward, et al. (1989) Nature 341: 544-546. Specific monoclonal and polyclonal antibodies and antisera will usually bind with a K_D of, e.g., at least about 0.1 μM, at least about 0.01 μM or better, and, typically and at least about 0.001 μM or better.

For certain therapeutic applications, humanized antibodies are desirable. Detailed methods for preparation of chimeric (humanized) antibodies can be found in U.S. Patent 5,482,856. Additional details on humanization and other antibody production and engineering techniques can be found in Borrebaeck (ed.) (1995) Antibody Engineering, 2nd Edition Freeman and Company, NY (Borrebaeck); McCafferty et al. (1996) Antibody Engineering, A Practical Approach IRL at Oxford Press, Oxford, England (McCafferty), and Paul (1995) Antibody Engineering Protocols Humana Press, Towata, NJ (Paul). Additional details regarding specific procedures can be found, e.g., in Ostberg et al. (1983), Hybridoma 2: 361-367, Ostberg, U.S. Pat. No. 4,634,664, and Engelman et al., U.S. Pat. No. 4,634,666.

NUCLEIC ACID AND POLYPEPTIDE SEQUENCE VARIANTS

As described herein, the invention provides for nucleic acid polynucleotide sequences and polypeptide amino acid sequences, e.g., hemagglutinin and neuraminidase sequences, and, e.g., compositions and methods comprising said sequences. Examples of said sequences are disclosed herein. However, one of skill in the art will appreciate that the invention is not necessarily limited to those sequences disclosed herein and that the present invention also provides many related and unrelated sequences with the functions described herein, e.g., encoding a HA and/or a NA molecule.

One of skill will also appreciate that many variants of the disclosed sequences are included in the invention. For example, conservative variations of the disclosed sequences that yield a functionally identical sequence are included in the invention. Variants of the nucleic acid polynucleotide sequences, wherein the variants hybridize to at least one disclosed sequence, are considered to be included in the invention. Unique subsequences of the sequences disclosed herein, as determined by, e.g., standard sequence comparison techniques, are also included in the invention.

Silent Variations

Due to the degeneracy of the genetic code, any of a variety of nucleic acid sequences encoding polypeptides and/or viruses of the invention are optionally produced, some which can bear lower levels of sequence identity to the HA and NA nucleic acid and polypeptide sequences herein. The following provides a typical codon table specifying the genetic code, found in many biology and biochemistry texts.

Table 1

Codon Table

Amino acids			Codon					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

The codon table shows that many amino acids are encoded by more than one codon. For example, the codons AGA, AGG, CGA, CGC, CGG, and CGU all encode the amino acid arginine. Thus, at every position in the nucleic acids of the invention where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described above without altering the encoded polypeptide. It is understood that U in an RNA sequence corresponds to T in a DNA sequence.

Such "silent variations" are one species of "conservatively modified variations," discussed below. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine, and TTG, which is ordinarily the only codon for tryptophan) can be modified by standard techniques to encode a functionally identical polypeptide. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in any described sequence. The invention, therefore, explicitly provides each and every possible variation of a nucleic acid sequence encoding a polypeptide of the invention that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code (e.g., as set forth in Table 1, or as is commonly available in the art) as applied to the nucleic acid sequence encoding a hemagglutinin or a neuraminidase polypeptide of the invention. All such variations of every nucleic acid herein are specifically provided and described by consideration of the sequence in combination with the genetic code. One of skill is fully able to make these silent substitutions using the methods herein.

Conservative variations

Owing to the degeneracy of the genetic code, "silent substitutions" (i.e., substitutions in a nucleic acid sequence which do not result in an alteration in an encoded polypeptide) are an implied feature of every nucleic acid sequence of the invention which encodes an amino acid. Similarly, "conservative amino acid substitutions," in one or a few amino acids in an amino acid sequence are substituted with different amino acids with highly similar properties, are also readily identified as being highly similar to a disclosed construct such as those herein. Such conservative variations of each disclosed sequence are a feature of the present invention.

"Conservative variation" of a particular nucleic acid sequence refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or, where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences, *see*, Table 2 below. One of skill will recognize that individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 4%, 3%, 2% or 1%) in an encoded sequence are “conservatively modified variations” where the alterations result in the deletion of an amino acid, addition of an amino acid, or substitution of an amino acid with a chemically similar amino acid. Thus, “conservative variations” of a listed polypeptide sequence of the present invention include substitutions of a small percentage, typically less than 5%, more typically less than 4%, 3%, 2% or 1%, of the amino acids of the polypeptide sequence, with a conservatively selected amino acid of the same conservative substitution group. Finally, the addition of sequences which do not alter the encoded activity of a nucleic acid molecule, such as the addition of a non-functional sequence, is a conservative variation of the basic nucleic acid.

Table 2. -- Conservative Substitution Groups

1	Alanine (A)	Serine (S)	Threonine (T)	
2	Aspartic acid (D)	Glutamic acid (E)		
3	Asparagine (N)	Glutamine (Q)		
4	Arginine (R)	Lysine (K)		
5	Isoleucine (I)	Leucine (L)	Methionine (M)	Valine (V)
6	Phenylalanine (F)	Tyrosine (Y)	Tryptophan (W)	

Sequence comparison, identity, and homology

The terms “identical” or percent “identity,” in the context of two or more nucleic acid or polypeptide sequences, 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 sequence comparison algorithms described below (or other algorithms available to persons of skill) or by visual inspection.

The phrase “substantially identical,” in the context of two nucleic acids or polypeptides (e.g., DNAs and/or RNAs encoding a HA or NA molecule, or the amino acid sequence of a HA or NA molecule) refers to two or more sequences or subsequences that have at least about 90%, preferably 91%, most preferably 92%, 93%, 94%, 95%, 96%, 97%, 98%, 98.5%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9% or more nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using a sequence comparison algorithm or by visual inspection. Such “substantially identical” sequences are typically considered to be “homologous,” without reference to actual ancestry. Preferably, “substantial identity” exists over a region of the amino acid sequences that is at least about 200 residues in length, more preferably over a region of at least about 250 residues, and most preferably the sequences are substantially identical over at least about 300 residues, 350 residues, 400 residues, 425 residues, 450 residues, 475 residues, 480 residues, 490 residues, 495 residues, 499 residues, 500 residues, 502 residues, 559 residues, 565 residues, or 566 residues, or over the full length of the two sequences to be compared when the amino acids are hemagglutinin or hemagglutinin fragments or which is substantially identical over at least about 350 amino acids; over at least about 400 amino acids; over at least about over at least about 436 amino acids, over at least about 450 amino acids; over at least about 451 amino acids; over at least about 465 amino acids; over at least about 466 amino acids; over at least about 469 amino acids; over at least about 470 amino acids; or over at least about 566 amino acids contiguous when the amino acid is neuraminidase or a neuraminidase fragment.

For sequence comparison and homology determination, 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 Natl Acad Sci USA 85:2444 (1988), by computerized implementations of algorithms such as 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*, Ausubel et al., *supra*).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J Mol Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/). 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 (*see*, 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, a cutoff of 100, 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 (1989) Proc Natl Acad Sci USA 89:10915).

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 Natl 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.

Another example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle (1987) J. Mol. Evol. 35:351-360. The method used is similar to the method described by Higgins & Sharp (1989) *CABIOS*5:151-153. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster can then be aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences can be aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program can also be used to plot a dendogram or tree representation of clustering relationships. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison.

An additional example of an algorithm that is suitable for multiple nucleic acid, or amino acid, sequence alignments is the CLUSTALW program (Thompson, J. D. et al. (1994) Nucl. Acids. Res. 22: 4673-4680). CLUSTALW performs multiple pairwise comparisons between groups of sequences and assembles them into a multiple alignment based on homology. Gap open and Gap extension penalties can be, e.g., 10 and 0.05 respectively. For amino acid alignments, the BLOSUM algorithm can be used as a protein weight matrix. *See*, e.g., Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919.

DIGITAL SYSTEMS

The present invention provides digital systems, e.g., computers, computer readable media and integrated systems comprising character strings corresponding to the sequence information herein for the nucleic acids and isolated or recombinant polypeptides herein, including, e.g., the sequences shown herein, and the various silent substitutions and conservative substitutions thereof. Integrated systems can further include, e.g., gene synthesis equipment for making genes corresponding to the character strings.

Various methods known in the art can be used to detect homology or similarity between different character strings, or can be used to perform other desirable functions such as to control output files, provide the basis for making presentations of information including the sequences and the like. Examples include BLAST, discussed *supra*. Computer systems of the invention can include such programs, e.g., in conjunction with one or more data file or data base comprising a sequence as noted herein.

Thus, different types of homology and similarity of various stringency and length between various HA or NA sequences or fragments, etc. can be detected and recognized in the integrated systems herein. For example, many homology determination methods have been designed for comparative analysis of sequences of biopolymers, for spell-checking in word processing, and for data retrieval from various databases. With an understanding of double-helix pair-wise complement interactions among four principal nucleobases in natural polynucleotides, models that simulate annealing of complementary homologous polynucleotide strings can also be used as a foundation of sequence alignment or other operations typically performed on the character strings corresponding to the sequences herein (e.g., word-processing manipulations, construction of figures comprising sequence or subsequence character strings, output tables, etc.).

Thus, standard desktop applications such as word processing software (e.g., Microsoft Word™ or Corel WordPerfect™) and database software (e.g., spreadsheet software such as Microsoft Excel™, Corel Quattro Pro™, or database programs such as Microsoft Access™, Paradox™, GeneWorks™, or MacVector™ or other similar programs) can be adapted to the present invention by inputting a character string corresponding to one or more polynucleotides and polypeptides of the invention (either nucleic acids or proteins, or both). For example, a system of the invention can include the foregoing software having the appropriate character string information, e.g., used in conjunction with a user interface (e.g., a GUI in a standard operating system such as a Windows, Macintosh or LINUX system) to manipulate strings of characters corresponding to the sequences herein. As noted, specialized alignment programs such as BLAST can also be incorporated into the systems of the invention for alignment of nucleic acids or proteins (or corresponding character strings).

Systems in the present invention typically include a digital computer with data sets entered into the software system comprising any of the sequences herein. The computer can be, e.g., a PC (Intel x86 or Pentium chip- compatible DOS™, OS2™ WINDOWS™ WINDOWSNT™, WINDOWS95™, WINDOWS2000™, WINDOWS98™, LINUX based machine, a MACINTOSH™, Power PC, or a UNIX based (e.g., SUN™ work station) machine) or other commercially available computer that is known to one of skill. Software for aligning or otherwise manipulating sequences is available, or can easily be constructed by one of skill using a standard programming language such as Visualbasic, PERL, Fortran, Basic, Java, or the like.

Any controller or computer optionally includes a monitor which is often a cathode ray tube (“CRT”) display, a flat panel display (e.g., active matrix liquid crystal display, liquid crystal display), or others. Computer circuitry is often placed in a box which includes numerous integrated circuit chips, such as a microprocessor, memory, interface circuits, and others. The box also optionally includes a hard disk drive, a floppy disk drive, a high capacity removable drive such as a writeable CD-ROM, and other common peripheral elements. Inputting devices such as a keyboard or mouse optionally provide for input from a user and for user selection of sequences to be compared or otherwise manipulated in the relevant computer system.

The computer typically includes appropriate software for receiving user instructions, either in the form of user input into a set parameter fields, e.g., in a GUI, or in the form of preprogrammed instructions, e.g., preprogrammed for a variety of different specific operations. The software then converts these instructions to appropriate language for instructing the operation, e.g., of appropriate mechanisms or transport controllers to carry out the desired operation. The software can also include output elements for controlling nucleic acid synthesis (e.g., based upon a sequence or an alignment of sequences herein), comparisons of samples for differential gene expression, or other operations.

KITS AND REAGENTS

The present invention is optionally provided to a user as a kit. For example, a kit of the invention contains one or more nucleic acid, polypeptide, antibody, or cell line described herein (e.g., comprising, or with, a HA and/or NA molecule of the invention). The kit can contain a diagnostic nucleic acid or polypeptide, e.g., antibody, probe set, e.g., as a cDNA micro-array packaged in a suitable container, or other nucleic acid such as one or more expression vector. The kit typically further comprises, one or more additional reagents, e.g., substrates, labels, primers, for labeling expression products, tubes and/or other accessories, reagents for collecting samples, buffers, hybridization chambers, cover slips, etc. The kit optionally further comprises an instruction set or user manual detailing preferred methods of using the kit components for discovery or application of diagnostic sets, etc.

When used according to the instructions, the kit can be used, e.g., for evaluating a disease state or condition, for evaluating effects of a pharmaceutical agent or other treatment intervention on progression of a disease state or condition in a cell or organism, or for use as a vaccine, etc.

In an additional aspect, the present invention provides system kits embodying the methods, composition, systems and apparatus herein. System kits of the invention optionally comprise one or more of the following: (1) an apparatus, system, system component or apparatus component; (2) instructions for practicing methods described herein, and/or for operating the apparatus or apparatus components herein and/or for using the compositions herein. In a further aspect, the present invention provides for the use of any apparatus, apparatus component, composition or kit herein, for the practice of any method or assay herein, and/or for the use of any apparatus or kit to practice any assay or method herein.

Additionally, the kits can include one or more translation system as noted above (e.g., a cell) with appropriate packaging material, containers for holding the components of the kit, instructional materials for practicing the methods herein and/or the like. Similarly, products of the translation systems (e.g., proteins such as HA and/or NA molecules) can be provided in kit form, e.g., with containers for holding the components of the kit, instructional materials for practicing the methods herein and/or the like. Furthermore, the kits can comprise various vaccines (e.g., produced through plasmid rescue protocols) such as live attenuated vaccine (e.g., FluMist) comprising the HA and/or NA sequences herein.

To facilitate use of the methods and compositions of the invention, any of the vaccine components and/or compositions, e.g., reassorted virus in allantoic fluid, etc., and additional components, such as, buffer, cells, culture medium, useful for packaging and infection of influenza viruses for experimental or therapeutic vaccine purposes, can be packaged in the form of a kit. Typically, the kit contains, in addition to the above components, additional materials which can include, e.g., instructions for performing the methods of the invention, packaging material, and a container.

EXAMPLES

The invention is now described with reference to the following examples. These examples are provided for the purpose of illustration only and the invention should in no way be construed as being limited to these examples but rather should be construed to encompass any and all variations which become evident as a result of the teachings provided herein.

Materials and Methods

Generation of recombinant viruses: Wild type (wt) influenza A H1N1 viruses, A/CA/4/09 isolated from MDCK cells and A/CA/7/09 isolated from eggs, were received from Centers for Disease Control and Prevention (CDC). A/CA/4/09 egg adapted viral RNA was provided by Dr. Ziping Ye of Food and Drug Administration (FDA). The HA and NA gene segments of A/CA/4/09 and A/CA/7/09 were amplified by RT-PCR using primers that are universal to the HA and NA gene end sequences and cloned into the plasmid vector pAD3000 (Hoffman (2000) PNAS 97:6108-6113). Site-directed mutagenesis was performed to introduce specific changes into the HA genes using the QuikChange® Site-Directed Mutagenesis kit (Stratagene) and the HA sequence was confirmed by sequencing analyses. The 6:2 reassortant vaccine strains were generated by co-transfecting 8 cDNA plasmids encoding the HA and NA of the H1N1 virus and the 6 internal gene segments of cold adapted (ca) A/Ann Arbor/6/60 (MDV-A, master donor virus for type A influenza virus) into co-cultured 293T and MDCK cells. The vaccine strains used for manufacture are produced in serum-free Vero/CEK cells by electroporation. Viruses were propagated in the allantoic cavities of 10- to 11-day-old embryonated chicken eggs. The HA and NA sequences of the rescued viruses were verified by sequencing of RT-PCR cDNAs amplified from vRNA.

Virus titration: Virus titers were measured by the fluorescence focus assay and expressed as log10FFU (fluorescent focus units Unit)/ml (Forrest et al. (2008) *Clin Vaccine Immunol* **15:**1042-1053). Virus plaque morphology was examined by plaque assay as previously described (Jin et al., (2003) *Virology* **306,** 18-24).

Receptor-binding assay: Chicken red blood cells (cRBCs) (HEMA Resource and Supply, Inc.) were desialylated and re-sialylated as previously described (). 100 μl of 10% cRBCs was incubated with 50 mU Vibrio cholerae neuraminidase (Sigma, St. Louis, MO) at 37°C for 1 h to remove sialic acid. After three washes with 1 ml PBS, cells were resuspended in 1 ml PBS containing 1% bovine serum albumin (BSA), incubated with 2.5 mU of α2,3(N)-sialyltransferase (Calbiochem, La Jolla, CA) or 2 mU of α2,6(N) sialyltransferase (Calbiochem, La Jolla, CA) for 1.5 h at 37°C, plus 1.5 mM CMP-SA (Sigma, St. Louis, MO). The resialylated cRBCs were resuspended as 0.5% (v/v) in PBS after washing three times with PBS. Haemagglutination assays (HA) were carried out in V-bottomed 96 well microtiter plates for the binding activity. 50 µl of two-fold serially diluted viruses were incubated with 50 µl of 0.5% cRBC, α2,3, or α2,6 resialylated cRBC at room temperature for 60 min. The HA titer was defined as the highest dilution that hemagglutinate the RBCs.

Ferret studies: 8-10 weeks old male and female ferrets from Simonson (Gilroy, CA) in groups of 3 were used to assess virus replication in the respiratory tracts and for vaccine immunogenicity. Ferrets were housed individually and inoculated intranasally with 7.0 log10FFU of virus per 0.2 ml dose. Three days after infection, ferrets were euthanized, and the lungs and nasal turbinates (NT) were harvested. Virus titers in the lung and NT were determined by the EID50 assay and expressed as 50% egg infectious dose per gram of tissue (log10EID50/g). Ferrets that were assigned for immunogenicity studies were bled on days 14, 21 and 28 days postinfection and sera were assayed for antibody titers by HAI.

Serum antibody detection by HAI assay: H1N1-specific antibody level in post-infected ferret sera against homologous and heterologous viruses was determined by HAI assay. Prior to serologic analysis, ferret sera were treated with receptor-destroying enzyme (RDE) (Denka Seiken, Tokyo, Japan) that was reconstituted in 10 mL of 0.9 % NaCl per vial. 0.1 mL serum was mixed with 0.15 mL RDE and incubated at 37°C for 18 hr and adjusted to a final 1:4 dilution by adding 0.15 mL of 0.9 % sodium citrate followed by incubation at 56 °C for 45 min. Strain-specific serum HAI titers were determined using 0.5% tRBC and the HAI titers are presented as the reciprocal value of the highest serum dilution that inhibited hemagglutination.

Results

Generation of reassortant candidate vaccine strains

The HA and NA gene segments from wt A/CA/4/09 were cloned from infected MDCK cell RNA following RT-PCR amplification. A total of 12 cDNA clones from each HA or NA were found to be identical by nucleotide sequence analysis. Plasmids representing this HA sequence and the NA sequence of wt A/CA/4/09 were transfected into 293/MDCK cells together with plasmids representing the six internal protein gene segments of MDV-A, however, no viable reassortant progeny could be recovered either on MDCK cells or eggs. The HA cDNAs cloned from the wt A/CA/4/09 egg isolate were heterogeneous at two amino acid positions (Table 3). From 12 clones analyzed, the following changes were observed: 42% L191I, 50% Q223R, one (8%) had both L191I and Q223 R. Plasmids representing these different HA sequences were combined and transfected into 293/MDCK cells with the MDV-A internal protein genes and reassortant viruses were readily rescued.

The HA plasmid cloned from A/CA/7/09 that did not have amino acid change at residues of 222 or 223 could be rescued to produce progeny virus. This indicated that T197A change in CA/7/09 was responsible for the efficient rescue of A/CA/7/09. Other A/CA/7/09 clones had changes of either D222G or Q223R, viruses containing D222G or Q223R in HA were also rescued. Due to the high degree of similarity between the HAs of A/CA/4/09 and A/CA/7/09 and since the NA sequences were identical between these two strains, the variants derived from A/CA/7/09 were developed further.

Table 3. HA sequences and virus titers of novel H1N1 variants

Virus	wt virus Passage History	Amino acid at position					% clones	Virus titer in eggs* (log_{10}FFU/ml± SE)
		H1#	191	197	222	223		
		H3#	194	200	225	226		
A/CA/04/09	MDCK 2x	swt	L	T	D	Q	NA	NA
		variant 1	L	T	D	Q	100	Not rescued
	Egg 2x	variant 2	I	T	D	Q	42	7.4 ± 0.09
		variant 3	L	T	D	R	50	7.8 ± 0.15
		variant 7	I	T	D	R	8	7.8 ± 0.40
A/CA/07/09	Egg 2x	swt	L	A	D/G	Q/R	NA	NA
		variant 4	L	A	D	Q	45	7.8 ± 0.27
		variant 5	L	A	G	Q	34	7.4 ± 0.14
		variant 6	L	A	D	R	21	7.7 ± 0.14

*Virus titers are mean titers from at least three virus stocks; NA: not applicable

Selection of vaccine strains with better growth in embryonated chicken eggs.

As shown in Table 3, the rescued A/CA/4/09 and A/CA/7/09 reassortant vaccine strains replicated in chicken embryonated eggs at titers of 7.4 to 7.8 log_{10}FFU/ml, which was lower than the seasonal H1N1 vaccine strains by at least 10-fold. Further, the recovered A/CA/7/09 reassortant vaccine candidates formed very small plaques in MDCK cells. To improve the vaccine virus growth in MDCK cells and eggs, A/CA/7/09 candidates (V5 and V6) were passaged twice in MDCK cells at moi of 4.0, 0.4 and 0.04, then the viruses present in the supernatants were examined by plaque assay. All the MDCK-passaged viruses contained plaques that were much larger (2-4 mm) than the parental viruses (Fig.1). The HA gene segment of twelve plaques from MDCK passaged V5 and V6 vaccine candidates were sequenced. The HA of each of the large plaque morphology isolates had single amino acid changes at one of the following positions: K119N or K119E, K153E, K154E derived from V5 and A186D from V6.

The HA sequence of A/CA/7/09 was also compared with two earlier H1N1 viruses that were originated from swine, A/swine/Iowa/1/1976 and A/swine/1931, and a recent human H1N1 virus, A/South Dakota/6/07 (A/SD/07). As shown in Fig. 2, K119, K153 and K154 are highly conserved among the swine H1N1 viruses. A/SD/6/07 also contained K119 and K154 residues. The amino acids at 186 are more diverse among the four viruses shown in Fig. 2. A previous study (Both et al. (1983) *Proc Natl Acad Sci U S A* **80:**6996-7000) showed that the G155E change is responsible for the high growth of the virus in eggs. These data indicate that the negatively charged E residue in the 153-155 region is preferred for virus replication in MDCK cells and eggs. To examine if the G155E change previously reported for A/NJ/76 virus could also improve virus replication of A/CA/7/09 in eggs, G155E was introduced into V5 and V6. In addition, to confirm that the amino acids identified in the large plaques conferred virus growth advantage in eggs, each of the identified mutation was introduced into the HA and reassortant vaccine candidate strains were rescued. Moreover, the A186D change identified in V6 was also introduced into V5 and V5-119E. Similarly, the 119N mutation found in V5 was also introduced into V6 and V6-186D to evaluate the influence of single and double amino acid change on virus replication in eggs. Similarly, the 119N mutation found in V5 was also introduced into V6 and V6-186D to evaluate the influence of single and double amino acid changes on virus replication in eggs. HA sequence analysis also showed that A/CA/09 strains contained a unique glycosylation site at residue 278 (Fig. 2). To evaluate if this additional glycosylation site affected virus growth, a T278K change was introduced into V5 and V6, respectively.

The rescued viruses were examined for their growth in eggs. As shown in Table 4, most of the variants containing the introduced HA mutations grew significantly better than V5 and V6. V5-278K and V6-278K had titers of 7.6 and 7.7 Log_{10}FFU/ml that were similar to V5 and V6. Thus, removal of the 278 glycosylation site had minimal impact on virus titers in eggs. The changes at the 119, 186, 153, 154, 155 and 186 sites increased virus titers by 0.2 to 1.2 log_{10}FFU/ml. The combined 119E and 186D change in V5 resulted in a slightly higher titer than either 119E or 186D on their own.

Table 4. A/CA/07/09 HA variants identified from MDCK cells and introduced by reverse genetics. Amino acid residue numbers of H1 HA are shown in row 2; corresponding amino acid residue numbers in H3 HA are shown in row 3.

	Amino acid at residue (H1# and H3#)								Virus titer in eggs (log_{10}FFU/ ml± SE)
	119	153	154	155	186	222	223	278	
Virus	122	156	157	158	189	225	226	280	
V5	K	K	K	G	A	G	Q	T	7.4 ± 0.14
V6							R		7.7 ± 0.14
V5-119N	N					G			8.3 ± 0.06
V5-119E	E					G			8.3 ± 0.07
V5-153E		E				G			8.3 ± 0.05
V5-154E			E			G			8.6 ± 0.05
V6-186D					D		R		8.4 ± 0.06
V5-186D					D	G			8.3 ± 0.15
V5-119E/186D	E				D	G			8.5 ± 0.06
V6-119N	N						R		7.9 ± 0.20
V6-119N/186D	N				D		R		8.1 ± 0.09
V5-155E				E		G			8.4 ± 0.11
V5-278K						G		K	7.6 ± 0.19
V6-155E				E			R		8.4 ± 0.19
V6-278K							R	K	7.7 ± 0.27

*Virus titers are mean titers from at least three virus stocks

Evaluation of vaccine variants for their antigenicity

To determine if any of the amino acid changes introduced into the H1 HA affected virus antigenicity, A/CA/7/09 variants were evaluated for their reactivity with different postinfection ferret sera using the HAI assay (Table 5). The cold adapted (ca) viruses, A/CA/4/07 with 223R residue (V3), A/CA/7/09 with 222G residue (V5) and A/CA/7/09 with 223R residue (V6), reacted similarly to the 4 reference sera from ferrets immunized with wt A/CA/4/09, ca A/CA/4/09 (V3), ca A/CA/7/09 (V5) and ca A/CA/07/09 (V6). The variants with amino acid changes introduced into V5 at positions 119 and 186 had antigenicity similar to V5. However, the viruses with the changes at 153, 154 and 155 positions had much lower reactivity with these sera, a titer reduction of greater than 4-fold was detected. Thus, these data demonstrate that the mutations at residues 153-154 should not be present in the vaccine strain. Changes at the 119 and 186 positions could be introduced into the vaccine strain without affecting virus antigenicity.

Table 5. Antigenicity of A/CA/7/09 HA variants. HAI assay was performed with turkey RBC.

Virus	Post infection ferret serum			
	A/CA/4/09 wt	A/CA/4/09 ca 223R (V3)	ACA/7/09 222G (V5)	A/CA/7/09 223R (V6)
CA04 V3	8192	**1024**	2048	1024
CA07 V5	8192	1024	**1024**	1024
CA07 V6	4096	1024	1024	**512**
V5-119N	8192	512	2048	1024
V5-119E	4096	512	1024	512
V5-153E	256	<32	128	64
V5-154E	512	<32	128	128
V5-155E	256	<32	128	128
V5-186D	8192	1024	2048	1024
V5-278K	4096	512	1024	512
V5-119E/186D	8192	1024	2048	1024

A/CA/7/09 vaccine candidates are attenuated but immunogenic in ferrets

To evaluate A/CA/7/09 vaccine variants for their attenuated phenotype and their ability to induce antibody responses, ferrets were inoculated with 7.0 log_{10}FFU of virus intranasally in 0.2 ml of dose volume and virus replication in the upper and lower respiratory tracts of ferrets was determined by EID_{50} assay. As shown in Table 6, all A/CA/7/09 variants replicated efficiently in the NT tissues, but no virus was detected in the lungs. These data confirmed that these viruses were attenuated in ferrets, a characteristic phenotype conferred by the six internal protein gene segments of MDV-A.

Ferret post-infection serum was collected on day 14 after intranasal inoculation and antibody titers were evaluated by HAI assay (Table 6). All V5 variants were very immunogenic and induced H1N1-specific antibody responses, with the HAI titers ranging from 256 to 1024. Several V6 variants were also evaluated for their immunogenicity and were found to be less immunogenic than V5 (data not shown). The variants with the mutations at residues 119 and 186 maintained antigenicity similar to wt virus and did not react well with 154E and 155E variants. Sera from ferrets infected with the 154E and 155E variants infected ferret sera also did not react well with wt virus, V5, and V5 variants with 119E and 186D changes; their titer differences were within 2-fold. V5-154E and 155E postinfected ferret sera had homologous HAI titers more than 4-fold higher than the other variants. Interestingly, the mutation at 186D resulted in a greater reduction in reactivity with 154E and 155E variants. These data demonstrate that the 119 and 186 HA variants of A/CA/07/09 (H1N1) conferred high growth in eggs without altering virus antigenicity or immunogenicity, making them potential vaccine candidates for the swine-origin H1N1 virus.

Table 6. Replication of A/CA/7/09 HA variants in the respiratory tracts of ferrets and their immunogenicity. Ferret serum was collected on day 14 of postinfection and HAI assay was performed with turkey RBC.

Virus	Virus titer ($log_{10}EID_{50}$/g ± SE)		GMT of HAI antibody to the indicated antigen						
	NT	lung	V5	119E	119N	186D	119E 186D	154E	155E
V5	4.0 ± 0.23	<1.5	**512**	406	406	323	323	64	256
V5-119E	4.2 ± 0.33	<1.5	813	**645**	645	323	406	64	256
V5-119N	4.5 ± 0.33	<1.5	256	203	**256**	256	323	64	161

V5-186D	4.9 ± 0.20	<1.5	813	645	645	**645**	645	128	256
V5-119E/186D	4.7 ± 0.29	<1.5	512	406	512	512	**645**	64	256
V5-154E	5.7 ± 0.29	<1.5	161	323	323	64	81	**512**	1024
V5-155E	5.0 ± 0.20	<1.5	128	203	161	51	64	203	**1024**
A/CA/7/09 wt	NA	NA	512	512	645	645	406	102	323

Receptor binding specificity of A/CA/7/09 variants

Growth of wild type A/CA/4/09 and A/CA/7/09 viruses in eggs resulted in amino acid change in the HA receptor binding site, D222G and Q223R. These positions have been previously identified in other H1N1 strains following egg passages and are responsible for the HA receptor binding specificity. To determine whether the vaccine virus variants have different receptor binding specificity, V5, V6 and V5-119 and V5-186 variants were evaluated for their receptor binding specificity by the RBC binding assay (Table 7). V4 (without 222 and 223 change) preferred to bind to α2-6 SA than α2-3 SA. V5 (D222G) bound to α2-3 and α2-6 SA resialylated RBC equally well. However, V6 (Q223R) could only bind to α2-3 SA resialylated RBC, confirming that these two residues affected virus receptor binding specificity. The V5-119E/N and V5-186D viruses had similar binding specificity as V5. The double HA mutant V5-119E/186D preferred binding to α2-6 SA better than α2-3 SA. The 119E and 186D residues introduced into V6 could not restore their binding to α2-6 SA (data not shown). Thus, the change in the 119 and 186 residues do not significantly affect virus receptor binding specificity.

Table 7. Receptor binding specificity of A/CA/07/09 vaccine variants

Virus	Untreated	α2,3-SA	α2,6-SA	desialylated
V4	128	16	128	<2
V5	512	64	64	<2
V6	512	512	<2	<2
V5-119N	512	64	64	<2

V5-119E	512	128	128	<2
V5-186D	512	32	64	<2
V5-119E/186D	512	16	64	<2

Protein composition of A/CA/7/09 reassortants

13 ml allantoic fluid harvested from infected eggs was pelleted through 2ml of 30% sucrose cushion at 25k rpm for 1hr. Virus pellet was resuspended in 0.2ml PBS. 5 ul virus suspension was loaded on 4-20% polyacrylamide gel and stained with Coomassie blue. The order of samples was as follows:

Figure 3A

Lane 1. Recombinant HA A/NC/20/99 0.5 ug
Lane 2. Recombinant HA A/NC/20/99 2 ug
Lane 3. MDVA-V5-119E/186D (FFA 8.6)
Lane 4. MDVA-V6 (FFA 7.9)
Lane 5. MDVA-V6-186D (FFA 8.1)
Lane 6. PR8-V5-119E/186D (FFA 8.2)
Lane 7. PR8-V6 (FFA 7.8)
Lane 8. PR8-V6-186D (FFA 8.5)
Lane 9. NYMC X-179A (FFA 8.5)
Lane 10. PR8 South Dakota (FFA 8.7)

Figure 3B

Lane 1. NYMC X-179A (FFA 8.5)
Lane 2. MDVA-V5-119E/186D (FFA 8.6)
Lane 3. MDVA-V5-119E/186D/PA-S395N (FFA8.9)
Lane 4. South Dakota (FFA 8.7)

FFA and peak titer values were determined using standard methods. Reassortant viruses with “MDVA” in their designation comprise 6 internal genome segment of A/Ann Arbor/6/60. Reassortant viruses with “PR8” in their designation comprise 6 internal genome segment of PR8.

Comparison of HA protein yield of A/California/7/09 variants

6:2 reassortant influenza viruses comprising the 6 internal genome segments from PR8 and the HA and NA genome segments from A/CA/7/09 were generated.

Additional 6:2 reassortant viruses comprising the 6 internal genome segments from PR8, the NA genome segment from A/CA/7/09, and an HA genome segment encoding an H1 HA variant polypeptide described herein were generated. The 6:2 reassortant viruses comprising different A/CA/7/09 HA variants, along with A/Texas/5/2009 RG15 (A/TX/7/09 RG15) and A/California/07/09 NYMC X179A, were expanded in chicken embryonated eggs and their peak titers were determined by FFA. Virus strains assayed are shown in Table 8. 6:2 PR8-South Dakota is a 6:2 reassortant virus comprising the 6 internal genome segments from PR8 and the HA and NA genome segments from A/South Dakota/6/07. 6:2AA-V5-119E/186D is a 6:2 reassortant virus comprising the 6 internal genome segments from A/Ann Arbor/6/60, the NA genome segment from A/CA/7/09, and the V5-119E/186D variant HA genome segment. PR8 reassortant viruses comprising H1 HA variant genome segments described herein had comparable titers to X179A, the highest yield strain available for TIV manufacture.

Table 8. Peak titer of 6:2 reassortant H1N1 viruses in embryonated eggs.

Virus	Peak titer (log_{10} FFU/ml)
6:2 PR8-V6	8.1
6:2 PR8-V6-186D	8.5
6:2 PR8-V5-119E/186D	8.6
A/CA/7/09 X179A.	8.5
A/TX/7/09 RG15	6.6
6:2AA-V5-119E/186D	8.6
6:2 PR8-South Dakota	9.2

In addition to measuring peak titers, we also determined the HA protein yield of some of the reassortant viruses listed in Table 8. Selected viruses were amplified by infecting 50 eggs each with an MOI of 10^3 FFU/egg. Viruses were harvested after incubation at 33°C for 62 hrs. Equal amount of allantoic fluid (250ml) were then purified by sucrose gradient. Virus proteins were analyzed by SDS PAGE followed by Coomassie blue staining.

A representative sample of the results is shown in Figure 4. As shown in Figure 4A, the total protein yield of X179A, 6:2 PR8-V6-186D and 6:2AA-V5-119E/186D was 460, 300, and 350 ug respectively. 6:2 AA-V5-119E/186D had the highest HA protein yield, even though 6:2 AA-V5-119E/186D had a lower total protein yield than A/CA/7/09

X179A. The lower total protein yield observed for 6:2AA-V5-119E/186D in this experiment was likely due to assay variation. As shown in Figure 4B, the total protein yield of 6:2 PR8-V5-119E/186D and X179A was 780 and 720 ug respectively. The HA protein yield of 6:2 PR8-V5-119E/186D was also higher than that of A/CA/7/09 X179A.

Reassortant viruses comprising the PR8 backbone and a variant A/California/7/09 H1 polypeptide

Additional 6:2 reassortant influenza viruses comprising 6 internal genome segments from PR8, a variant of the A/CA/7/09 H1 HA genome segment, and the A/CA/7/09 NA genome segment were generated. The H1 HA amino acid variations are summarized in Table 9.

Table 9. Reassortant viruses comprising variant A/CA/7/09 H1 HA and the PR8 backbone.

Virus (HA)	H1 HA residue #						Antigenicity
	119	186	190	222	223	273	
PR8-A (V6-186D)	K	D	R	D	R	H	no change
PR8-B (V5-119E/186D/190R)	E	D	S	G	Q	H	reduced
PR8-C (V6-186D/273Y)	K	D	R	D	R	Y	no change
PR8-D (V5-119E/186D)	E	D	R	G	Q	H	no change

Out of the variant HAs tested, only changes in V5-119E/186D/190R reduced antigenicity (Table 9). The 6:2 reassortant viruses comprising different A/CA/7/09 HA variants were expanded in chicken embryonated eggs to determine the HA protein yield. Viruses were harvested after incubation at 33°C for 48 hrs (Figure 5A) or 60 hrs (Figure 5B). Viruses were then purified by sucrose gradient sedimentation. Protein composition of the purified viruses was analyzed by SDS-PAGE followed by Coomassie blue staining. Individual lanes were loaded with samples comprising either an equal amount of purified virus (Figure 5A) or the virus purified from an equal volume of harvested allantoic fluid (Figure 5B). Samples prepared from AA-V5-ED (comprising the V5-119E/186D variant HA and the A/Ann Arbor/6/60 backbone) and X179A viruses were included as controls. The PR8-C virus produced higher yield of the HA polypeptide than X179A.

The HA yield of PR8-C and AA-V5-ED relative to the HA yield of X179A was further measured using SDS-PAGE followed by Coomassie blue staining. Various volumes (10, 7.5, 5 and 2.5 microliter) of the PR8-C and AA-V5-ED samples and 10 microliter of the X179A sample were analyzed by SDS-PAGE. The relative amount of HA1 protein found in each sample was measured using image analysis software. The result of the measurement is shown in Figure 6. The AA-V5-ED and PR8-C viruses produce 1-1.5 times more HA protein than X179A.

While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be clear to one skilled in the art from a reading of this disclosure that various changes in form and detail can be made without departing from the true scope of the invention. For example, all the techniques and apparatus described above may be used in various combinations. All publications, patents, patent applications, or other documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, or other document were individually indicated to be incorporated by reference for all purposes. In particular, the following patent applications are incorporated by reference in their entirety for all purposes: US Provisional Application Numbers 61/220,426 filed June 25, 2009, 61/227,986 filed on July 23, 2009, and 61/234,021 filed on August 14, 2009.

What is claimed is:

1. An isolated or recombinant polypeptide, which polypeptide is selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:1;

b) a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D;

c) a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the K119E and A186D amino acid substitutions;

d) a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the K119N and A186D amino acid substitutions;

e) a polypeptide comprising an amino acid sequence of SEQ ID NO:1 comprising a D222G and/or Q223R substitution;

f) a polypeptide comprising an amino acid sequence of SEQ ID NO:1 (i) comprising a D222G and/or Q223R substitution, and (ii) further comprising at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D;

g) a polypeptide comprising an amino acid sequence of SEQ ID NO:1 (i) comprising a D222G and/or Q223R substitution, and (ii) further comprising the K119E and A186D amino acid substitutions;

h) a polypeptide comprising an amino acid sequence of SEQ ID NO:1 (i) comprising a D222G and/or Q223R substitution, and (ii) further comprising the K119N and A186D amino acid substitutions;

i) a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:1;

j) a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:1 comprising at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D;

k) a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:1 comprising the K119E and A186D amino acid substitutions;

l) a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:1 comprising the K119N and A186D amino acid substitutions;

m) a polypeptide comprising an amino acid sequence of residues 1-327 of SEQ ID NO:1 comprising a D222G and/or Q223R substitution;

n) a polypeptide comprising an amino acid sequence of residues 1-327 of SEQ ID NO:1 (i) comprising a D222G and/or Q223R substitution, and (ii) further comprising at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D;

o) a polypeptide comprising an amino acid sequence of residues 1-327 of SEQ ID NO:1 (i) comprising a D222G and/or Q223R substitution, and (ii) further comprising the K119E and A186D amino acid substitutions;

p) a polypeptide comprising an amino acid sequence of residues 1-327 of SEQ ID NO:1 (i) comprising a D222G and/or Q223R substitution, and (ii) further comprising the K119N and A186D amino acid substitutions;

q) a polypeptide comprising the amino acid sequence of SEQ ID NO:6;

r) a polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6;

s) a polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of the polypeptide of any one of (a) to (r);

t) a polypeptide comprising an amino acid sequence of the polypeptide of any one of (a) to (r) in which less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid residues were substituted, deleted or inserted;

u) a polypeptide comprising comprising an amino acid sequence of the polypeptide of any one of (a) to (r) and further comprising the H273Y substitution; and

v) a polypeptide comprising the amino acid sequence of SEQ ID NO:8.

2. The isolated or recombinant polypeptide of claim 1, wherein the polypeptide is immunogenic.

3. A sterile composition comprising the isolated or recombinant polypeptide of claim 1.

4. An antibody specific for the isolated or recombinant polypeptide of claim 1.

5. An immunogenic composition comprising an immunologically effective amount of the isolated or recombinant polypeptide of claim 1.

6. A reassortant influenza virus comprising a nucleic acid encoding the isolated or recombinant polypeptide of claim 1.

7. An isolated or recombinant nucleic acid comprising a nucleotide sequence encoding the polypeptide of claim 1.

8. The isolated or recombinant nucleic acid of claim 7 comprising the nucleotide sequence of SEQ ID NO 3 or SEQ ID NO:7.

9. The isolated or recombinant nucleic acid of claim 7, wherein the nucleic acid is DNA.

10. The isolated or recombinant nucleic acid of claim 7, wherein the nucleic acid is RNA.

11. The isolated or recombinant nucleic acid of claim 7, wherein the polynucleotide encodes an immunogenic polypeptide.

12. A composition comprising isolated or recombinant nucleic acid of claim 7.

13. An immunogenic composition comprising an immunologically effective amount of the isolated or recombinant nucleic acid of claim 7.

14. A reassortant influenza virus comprising the nucleic acid of claim 7.

15. A reassortant influenza virus comprising the nucleic acid of claim 8.

16. A reassortant influenza virus, wherein the reassortant influenza virus is a 6:2 reassortant virus comprising 6 internal genome segments from one or more donor

virus, a first genome segment encoding the polypeptide of claim 1 and a second genome segment encoding a neuramidinase polypeptide.

17. A reassortant influenza virus, wherein the reassortant influenza virus is a 7:1 reassortant virus comprising a first genome segment encoding the polypeptide of claim 1 and further comprising 6 internal genome segments and a second genome segment encoding a neuramidinase polypeptide from one or more donor virus.

18. The reassortant influenza virus of claim 16 or 17, wherein the donor virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

19. The reassortant influenza virus of any one of claims 16 to 18, wherein the donor virus is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

20. The reassortant influenza virus of any one of claims 16 to 19, wherein the virus is a live virus.

21. The reassortant influenza virus of any one of claims 16 to 20, wherein the first genome segment encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:1 having at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D.

22. The reassortant influenza virus of any one of claims claim 16 to 20, wherein the first genome segment encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the K119E and A186D amino acid substitutions.

23. The reassortant influenza virus of any one of claims claim 16 to 20, wherein the first genome segment encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the K119N and A186D amino acid substitutions.

24. The reassortant influenza virus of any one of claims claim 21 to 23, wherein the amino acid sequence of the first genome segment encoded polypeptide further comprises a D222G and/or Q223R substitution.

25. The reassortant influenza virus of any one of claims 16 to 24, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

26. The reassortant influenza virus of any one of claims 16 to 24, wherein the neuramidinase polypeptide is N1 neuramidinase.

27. The reassortant influenza virus of any one of claims 16 to 26, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

28. A method for producing reassortant influenza viruses in cell culture, the method comprising:

a) introducing a plurality of vectors comprising an influenza virus genome into a population of host cells, which plurality of vectors comprises 6 internal genome segments of a first influenza strain; a first genome segment encoding the polypeptide of claim 1 and a second genome segment encoding a neuramidinase polypeptide, and which population is capable of supporting replication of influenza virus;

b) culturing the population of host cells; and,

c) recovering a plurality of reassortant influenza viruses.

29. The method of claim 28, wherein the first genome segment encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:1 having at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D.

30. The method of claim 28, wherein the first genome segment encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:1 comprising the K119E and A186D amino acid substitutions.

31. The method of claim 28, wherein the first genome segment encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:1 comprising the K119N and A186D amino acid substitutions.

32. The method of claim 28, wherein the amino acid sequence of the first genome segment encoded polypeptide further comprises a D222G and/or Q223R substitution.

33. The method of any one of claims 28 to 32, wherein the second genome segment is a swine influenza virus genome segment.

34. The method of any one of claims 28 to 33, wherein the neuramidinase polypeptide is an N1 neuramidinase.

35. The method of any one of claims 28 to 34, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

36. The method of any one of claims 28 to 35, wherein the first influenza virus strain comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

37. The method of any one of claims 28 to 35, wherein the first influenza strain is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

38. The method of any one of claims 28 to 37, wherein the reassortant influenza viruses are suitable for administration in an intranasal vaccine formulation.

39. The method of any one of claims 28 to 38, wherein the plurality of vectors comprising the influenza virus genome comprise an influenza A virus genome.

40. The method of any one of claims 28 to 39, wherein the plurality of vectors is a plurality of plasmid vectors.

41. The method of any one of claims 28 to 40, wherein the population of host cells comprises one or more of: Vero cells, PerC6 cells, MDCK cells, 293T cells, or COS cells.

42. The method of any one of claims 28 to 41, wherein the method does not comprise use of a helper virus.

43. The method of any one of claims 28 to 42, wherein the plurality of vectors consists of eight vectors.

44. An immunogenic composition comprising the isolated or recombinant polypeptide of claim 1.

45. An immunogenic composition comprising the isolated or recombinant nucleic acid of claim7.

46. The composition of claim 44 or 45, further comprising an excipient.

47. The composition of claim 46, wherein the excipient is a pharmaceutically acceptable excipient.

48. An immunogenic composition comprising the reassortant influenza virus of any one of claims 14 to 27.

49. The composition of claim 48, further comprising one or more pharmaceutically acceptable excipient.

50. The composition of claim 48 or 49, wherein the composition is a live attenuated influenza vaccine.

51. A method of producing a reassortant influenza virus vaccine, the method comprising:

a) introducing a plurality of vectors comprising an influenza virus genome into a population of host cells, which plurality of vectors comprises at least 6 internal genome segments of a first influenza strain; a first genome segment encoding the polypeptide of claim 1 and a second genome segment encoding a neuramidinase polypeptide, and which population is capable of supporting replication of influenza virus;

b) culturing the population of host cells;

c) recovering a plurality of reassortant influenza viruses; and,

d) providing one or more pharmaceutically acceptable excipient.

52. The method of claim 51, wherein the first genome segment encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising at least one amino acid substitution selected from the group consisting of K119E, K119N and A186D.

53. The method of claim 51, wherein the first genome segment encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the K119E and A186D amino acid substitutions.

54. The method of claim 51, wherein the first genome segment encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the K119N and A186D amino acid substitutions.

55. The method of claim 51, wherein the amino acid sequence of the first genome segment encoded polypeptide further comprises a D222G and/or Q223R substitution.

56. The method of any one of claims 51 to 55, wherein the second genome segment is a swine influenza virus genome segment.

57. The method of any one of claims 51 to 55, wherein the neuramidinase polypeptide is an N1 neuramidinase.

58. The method of any one of claims 51 to 57, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

59. The method of any one of claims 51 to 58, wherein the first influenza virus strain comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

60. The method of any one of claims 51 to 59, wherein the reassortant influenza viruses are suitable for administration in an intranasal vaccine formulation.

61. The method of any one of claims 51 to 60, wherein the plurality of vectors comprising the influenza virus genome comprise an influenza A virus genome.

62. The method of any one of claims 51 to 61, wherein the first influenza strain is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

63. The method of any one of claims 51 to 62, wherein the reassortant viruses are suitable for administration in an intranasal vaccine formulation.

64. A reassortant influenza virus comprising the polypeptide of claim 1, in an amount effective to produce an immunogenic response against a viral infection in a subject for the prophylactic or therapeutic treatment of the viral infection.

65. The reassortant influenza virus of claim 64, wherein the subject is a mammal.

66. The reassortant influenza virus of claim 65, wherein the mammal is a human.

67. The reassortant influenza virus of any one of claims 64-66, wherein the viral infection is a viral influenza infection.

68. The reassortant influenza virus of any one of claims 64-67, wherein the reassortant influenza virus is to be administered in vivo to the subject or in vitro or ex vivo to one or more cells of the subject.

69. The reassortant influenza virus of any one of claims 64-68, wherein a composition comprising the reassortant influenza virus and a pharmaceutically acceptable

excipient is administered to the subject in an amount effect to prophylactically or therapeutically treat the viral infection.

70. A method for increasing the peak titer in embryonated eggs for a reassortant or recombinant influenza virus, comprising altering an amino acid residue of the hemagglutinin polypeptide at a position corresponding to the amino acid residue of position 119 or 186 of SEQ ID NO: 1, thereby increasing the peak titer in embryonated eggs for the influenza virus.

71. The method of claim 70, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered.

72. The method of claim 71, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be glutamic acid (E).

73. The method of claim 71, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be asparagine (N).

74. The method of claim 70, wherein the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered.

75. The method of claim 74, wherein the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered to be aspartic acid (D).

76. The method of claim 70, wherein the amino acid residues corresponding to the amino acid residues of position 119 and 186 of SEQ ID NO: 1 are altered.

77. The method of claim 76, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be glutamic acid (E), and the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered to be aspartic acid (D).

78. The method of claim 76, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be asparagine (N), and

the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered to be aspartic acid (D).

79. The method of any one of claims 70 to 78, wherein the hemagglutinin polypeptide is an H1 hemagglutinin polypeptide.

80. The method of any one of claims 70 to 78, wherein the hemagglutinin polypeptide is a swine influenza virus hemagglutinin polypeptide.

81. The method of any one of claims 70 to 80, wherein the hemagglutinin polypeptide comprises the amino acid sequence of SEQ ID NO: 1.

82. The method of claim 811, wherein the hemagglutinin polypeptide further comprises a D222G and/or Q223R substitution.

83. The method of any one of claims 70 to 82, wherein the reassortant influenza virus comprises at least 6 internal genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

84. The method of any one of claims 70 to 82, wherein the reassortant influenza virus comprises 7 genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

85. The method of any one of claims 70 to 83, wherein the reassortant or recombinant influenza virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

86. The method of claim 85, wherein the reassortant influenza virus comprises at least 6 internal genome segments of A/Ann Arbor/6/60 or B/Ann Arbor/1/66.

87. The method of claim 85, wherein the reassortant influenza virus comprises 7 genome segments of A/Ann Arbor/6/60 or B/Ann Arbor/1/66.

88. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 2-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

89. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 4-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

90. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 8-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

91. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 10-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

92. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 20-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

93. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 10-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

94. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 20-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

95. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 40-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

96. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 5-fold and 20-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

97. The method of any one of claims 70 to 87, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 5-fold and 40-fold relative to the same reassortant or recombinant influenza virus not comprising the amino acid alteration.

98. The method of any one of claims 70 to 87, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml in embryonated eggs.

99. The method of any one of claims 70 to 87, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8 $\log_{10}$ PFU/ml in embryonated eggs.

100. The method of any one of claims 70 to 87, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8.5 $\log_{10}$ PFU/ml in embryonated eggs.

101. The method of any one of claims 70 to 87, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9 $\log_{10}$ PFU/ml in embryonated eggs.

102. An immunogenic composition comprising the reassortant or recombinant influenza virus of any of claims 70 to 101.

103. An influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 70 to 101.

104. A live, cold-adapted, temperature-sensitive, attenuated influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 70 to 101.

105. A reassortant or recombinant influenza virus comprising an hemagglutinin polypeptide, wherein the hemagglutinin polypeptide comprises an altered amino acid residue at a position corresponding to the amino acid residue of position 119 or 186 of SEQ ID NO: 1.

106. The reassortant or recombinant influenza virus of claim 105, wherein the altered amino acid residue corresponds to the amino acid residue of position 119 of SEQ ID NO: 1.

107. The reassortant or recombinant influenza virus of claim 106, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be glutamic acid (E).

108. The reassortant or recombinant influenza virus of claim 106, wherein the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be asparagine (N).

109. The reassortant or recombinant influenza virus of claim 105, wherein the altered amino acid residue corresponds to the amino acid residue of position 186 of SEQ ID NO: 1.

110. The reassortant or recombinant influenza virus of claim 109, wherein the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered to be aspartic acid (D).

111. The reassortant or recombinant influenza virus of claim 105, comprising altered amino acid residues at the positions corresponding to the amino acid residues of position 119 and 186 of SEQ ID NO: 1.

112. The reassortant or recombinant influenza virus of claim 111, wherein the altered amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be glutamic acid (E), and the altered amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered to be aspartic acid (D).

113. The reassortant or recombinant influenza virus of claim 111, wherein the altered amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1 is altered to be asparagine (N), and the altered amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1 is altered to be aspartic acid (D).

114. The reassortant or recombinant influenza virus of any one of claims 105 to 113, wherein the hemagglutinin polypeptide is an H1 hemagglutinin polypeptide.

115. The reassortant or recombinant influenza virus of any one of claims 105 to 113, wherein the hemagglutinin polypeptide is a swine influenza virus hemagglutinin polypeptide.

116. The reassortant or recombinant influenza virus of any one of claims 105 to 115, wherein the hemagglutinin polypeptide comprises the amino acid sequence of SEQ ID NO: 1.

117. The reassortant or recombinant influenza virus of claim 116, wherein the hemagglutinin polypeptide further comprises a D222G and/or Q223R substitution.

118. The reassortant influenza virus of any one of claims 105 to 117 further comprising at least 6 internal genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

119. The reassortant influenza virus of any one of claims 105 to 117 further comprising 7 genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

120. The reassortant or recombinant influenza virus of any one of claims 105 to 119, wherein the reassortant or recombinant influenza virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

121. The reassortant influenza virus of claim 120, wherein the reassortant influenza virus comprises at least 6 internal genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

122. The reassortant influenza virus of claim 120, wherein the reassortant influenza virus comprises 7 genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

123. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 2-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

124. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 4-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

125. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 8-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

126. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 10-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

127. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 20-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

128. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 10-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

129. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 20-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

130. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 40-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

131. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 5-fold and 20-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

132. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 5-fold and 40-fold relative to the same reassortant or recombinant influenza virus not comprising the altered amino acid residue.

133. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml in embryonated eggs.

134. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8 log_{10} PFU/ml in embryonated eggs.

135. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8.5 log_{10} PFU/ml in embryonated eggs.

136. The reassortant or recombinant influenza virus of any one of claims 105 to 122, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9 log_{10} PFU/ml in embryonated eggs.

137. An immunogenic composition comprising the reassortant or recombinant influenza virus of any of claims 105 to 136.

138. An influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 105 to 136.

139. A live, cold-adapted, temperature-sensitive, attenuated influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 105 to 136.

140. A reassortant influenza virus comprising a genome segment encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:1 except that an amino acid E or N is at position 119 and an amino acid D is at position 186.

141. A reassortant influenza virus comprising an HA genome segment encoding a polypeptide comprising the amino acid sequence of an H1N1 swine flu virus except that an amino acid E or N is at position 119 and an amino acid D is at position 186.

142. A reassortant influenza virus comprising an HA genome segment encoding a polypeptide comprising the amino acid sequence of an H1N1 swine flu virus except that a non-naturally occurring amino acid is at position 119 and position 186.

143. An immunogenic composition comprising the reassortant influenza virus produced by the method of any one of claims 28 to 43.

144. The composition of claim 143, further comprising one or more pharmaceutically acceptable excipients.

145. The composition of claim 143 or 144, wherein the composition is a live attenuated influenza vaccine.

146. A reassortant or recombinant influenza virus comprising an hemagglutinin polypeptide, wherein the hemagglutinin polypeptide comprises a non naturally occurring amino acid at the position corresponding to amino acid residue position 119 of SEQ ID NO: 1 or the position corresponding to amino acid residue position 186 of SEQ ID NO: 1.

147. The reassortant or recombinant influenza virus of claim 146, wherein the hemagglutinin polypeptide comprises a non naturally occurring amino acid at the position corresponding to amino acid residue position 119 of SEQ ID NO: 1 and the position corresponding to amino acid residue position 186 of SEQ ID NO: 1.

148. The reassortant or recombinant influenza virus of claim 146, wherein the hemagglutinin polypeptide comprises at least one non naturally occurring amino acid selected from the group consisting of: glutamic acid (E) at the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1, asparagine (N) at the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1, and aspartic acid (D) at the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1.

149. The reassortant or recombinant influenza virus of claim 148, wherein the hemagglutinin polypeptide comprises a glutamic acid (E) at the amino acid residue

corresponding to the amino acid residue of position 119 of SEQ ID NO: 1, and an aspartic acid (D) at the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1.

150. The reassortant or recombinant influenza virus of claim 148, wherein the hemagglutinin polypeptide comprises an asparagine (N) at the amino acid residue corresponding to the amino acid residue of position 119 of SEQ ID NO: 1, and an aspartic acid (D) at the amino acid residue corresponding to the amino acid residue of position 186 of SEQ ID NO: 1.

151. The reassortant or recombinant influenza virus of any one of claims 146 to 150, wherein the hemagglutinin polypeptide is an H1 hemagglutinin polypeptide.

152. The reassortant or recombinant influenza virus of any one of claims 146 to 150, wherein the hemagglutinin polypeptide is a swine influenza virus hemagglutinin polypeptide.

153. The reassortant or recombinant influenza virus of any one of claims 146 to 152, wherein the hemagglutinin polypeptide comprises the amino acid sequence of SEQ ID NO: 1 having an amino acid substitution at position 119 and/or 186.

154. The reassortant or recombinant influenza virus of claim 153, wherein the hemagglutinin polypeptide further comprises a D222G and/or Q223R substitution.

155. The reassortant influenza virus of any one of claims 146 to 154 further comprising at least 6 internal genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

156. The reassortant influenza virus of any one of claims 146 to 154 further comprising 7 genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

157. The reassortant or recombinant influenza virus of any one of claims 146 to 156, wherein the reassortant or recombinant influenza virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

158. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 2-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

159. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 4-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

160. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 8-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

161. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 10-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

162. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased at least 20-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

163. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 10-fold relative to the same

reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

164. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 20-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

165. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 2-fold and 40-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

166. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 5-fold and 20-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

167. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the peak titer in embryonated eggs for the reassortant or recombinant influenza virus is increased between 5-fold and 40-fold relative to the same reassortant or recombinant influenza virus not comprising a non naturally occurring amino acid.

168. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml in embryonated eggs.

169. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8 $\log_{10}$ PFU/ml in embryonated eggs.

170. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8.5 log_{10} PFU/ml in embryonated eggs.

171. The reassortant or recombinant influenza virus of any one of claims 146 to 157, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9 log_{10} PFU/ml in embryonated eggs.

172. An immunogenic composition comprising the reassortant or recombinant influenza virus of any of claims 146 to 171.

173. An influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 146 to 171.

174. A live, cold-adapted, temperature-sensitive, attenuated influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 146 to 171.

175. A reassortant or recombinant influenza virus comprising a hemagglutinin polypeptide comprising the amino acid sequence of SEQ ID NO:6.

176. A reassortant or recombinant influenza virus comprising a hemagglutinin polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6.

177. A reassortant or recombinant influenza virus comprising a hemagglutinin polypeptide comprising an amino acid sequence of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

178. A reassortant or recombinant influenza virus comprising a hemagglutinin polypeptide comprising the amino acid sequence of residues 1-327 of SEQ ID NO:6.

179. A reassortant or recombinant influenza virus comprising a hemagglutinin polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6.

180. A reassortant or recombinant influenza virus comprising a hemagglutinin polypeptide comprising an amino acid sequence of residues 1-327 of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

181. The reassortant or recombinant influenza virus of any one of claims 175 to 180 further comprising at least 6 internal genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

182. The reassortant or recombinant influenza virus of any one of claims 175 to 180 further comprising at least 6 internal genome segments of A/Ann Arbor/6/60.

183. The reassortant or recombinant influenza virus of any one of claims 175 to 180 further comprising at least 6 internal genome segments of A/Puerto Rico/8/34.

184. The reassortant or recombinant influenza virus of any one of claims 175 to 180 further comprising 7 genome segments of a virus selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

185. The reassortant or recombinant influenza virus of any one of claims 175 to 180 further comprising 7 genome segments of A/Ann Arbor/6/60.

186. The reassortant or recombinant influenza virus of any one of claims 175 to 180 further comprising 7 genome segments of A/Puerto Rico/8/34.

187. The reassortant or recombinant influenza virus of any one of claims 175 to 186, wherein the reassortant or recombinant influenza virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

188. The reassortant or recombinant influenza virus of any one of claims 175 to 187, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml in embryonated eggs.

189. The reassortant or recombinant influenza virus of any one of claims 175 to 187, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8 $\log_{10}$ PFU/ml in embryonated eggs.

190. The reassortant or recombinant influenza virus of any one of claims 175 to 187, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8.5 $\log_{10}$ PFU/ml in embryonated eggs.

191. The reassortant or recombinant influenza virus of any one of claims 175 to 187, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9 $\log_{10}$ PFU/ml in embryonated eggs.

192. The reassortant or recombinant influenza virus of any one of claims 175 to 187, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9.5 $\log_{10}$ PFU/ml in embryonated eggs.

193. The reassortant or recombinant influenza virus of any one of claims 175 to 187, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 10 $\log_{10}$ PFU/ml in embryonated eggs.

194. An immunogenic composition comprising the reassortant or recombinant influenza virus of any of claims 175 to 193.

195. An influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 175 to 193.

196. A live, cold-adapted, temperature-sensitive, attenuated influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 175 to 193.

197. The reassortant recombinant influenza virus of any one of claims 105 to 196 further comprising a neuramidinase polypeptide.

198. The reassortant recombinant influenza virus of claim 197, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

199. The reassortant recombinant influenza virus of claim 197, wherein the neuramidinase polypeptide is N1 neuramidinase.

200. The reassortant recombinant influenza virus of claim 197, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

201. A reassortant or recombinant influenza virus comprising 6 internal genome segments of a donor virus, a first genome segment encoding a hemagglutinin polypeptide, and a second genome segment encoding a neuramidinase polypeptide.

202. The reassortant or recombinant influenza virus of claim 201, wherein the hemagglutinin polypeptide comprises the amino acid sequence of SEQ ID NO:6.

203. The reassortant or recombinant influenza virus of claim 201, wherein the hemagglutinin polypeptide comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6.

204. The reassortant or recombinant influenza virus of claim 201, wherein the hemagglutinin polypeptide comprises an amino acid sequence of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

205. The reassortant or recombinant influenza virus of claim 201, wherein the hemagglutinin polypeptide comprises the amino acid sequence of residues 1-327 of SEQ ID NO:6.

206. The reassortant or recombinant influenza virus of claim 201, wherein the hemagglutinin polypeptide comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6.

207. The reassortant or recombinant influenza virus of claim 201, wherein the hemagglutinin polypeptide comprises an amino acid sequence of residues 1-327 of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

208. The reassortant or recombinant influenza virus of any one of claims 201 to 207, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

209. The reassortant or recombinant influenza virus of any one of claims 201 to 207, wherein the neuramidinase polypeptide is N1 neuramidinase.

210. The reassortant or recombinant influenza virus of any one of claims 201 to 207, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

211. The reassortant or recombinant influenza virus of any one of claims 201 to 210, wherein the donor virus is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

212. The reassortant or recombinant influenza virus of any one of claims 201 to 210, wherein the donor virus is A/Ann Arbor/6/60.

213. The reassortant or recombinant influenza virus of any one of claims 201 to 210, wherein the donor virus is A/Puerto Rico/8/34.

214. The reassortant or recombinant influenza virus of any one of claims 201 to 213, wherein the reassortant or recombinant influenza virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

215. The reassortant or recombinant influenza virus of any one of claims 201 to 214, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 7.5 log_{10} PFU/ml in embryonated eggs.

216. The reassortant or recombinant influenza virus of any one of claims 201 to 214, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8 log_{10} PFU/ml in embryonated eggs.

217. The reassortant or recombinant influenza virus of any one of claims 201 to 214, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8.5 log_{10} PFU/ml in embryonated eggs.

218. The reassortant or recombinant influenza virus of any one of claims 201 to 214, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9 log_{10} PFU/ml in embryonated eggs.

219. The reassortant or recombinant influenza virus of any one of claims 201 to 214, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9.5 log_{10} PFU/ml in embryonated eggs.

220. The reassortant or recombinant influenza virus of any one of claims 201 to 214, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 10 log_{10} PFU/ml in embryonated eggs.

221. An immunogenic composition comprising the reassortant or recombinant influenza virus of any of claims 201 to 220.

222. An influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 201 to 220.

223. A live, cold-adapted, temperature-sensitive, attenuated influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 201 to 220.

224. A reassortant or recombinant influenza virus comprising 6 internal genome segments of a donor virus, a first genome segment encoding a hemagglutinin polypeptide, and a second genome segment encoding a neuramidinase polypeptide.

225. The reassortant or recombinant influenza virus of claim 224, wherein the first genome segment comprises the nucleotide sequence of SEQ ID NO:7.

226. The reassortant or recombinant influenza virus of claim 224, wherein the first genome segment comprises the nucleotide sequence of 84 to 1064 of SEQ ID NO:7.

227. The reassortant or recombinant influenza virus of any one of claims 224 to 226, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

228. The reassortant or recombinant influenza virus of any one of claims 224 to 226, wherein the neuramidinase polypeptide is N1 neuramidinase.

229. The reassortant or recombinant influenza virus of any one of claims 224 to 226, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

230. The reassortant or recombinant influenza virus of any one of claims 224 to 226, wherein the second genome segment comprises the nucleotide sequence of SEQ ID NO:5.

231. The reassortant or recombinant influenza virus of any one of claims 224 to 230, wherein the donor virus is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

232. The reassortant or recombinant influenza virus of any one of claims 224 to 230, wherein the donor virus is A/Ann Arbor/6/60.

233. The reassortant or recombinant influenza virus of any one of claims 224 to 230, wherein the donor virus is A/Puerto Rico/8/34.

234. The reassortant or recombinant influenza virus of any one of claims 224 to 233, wherein the reassortant or recombinant influenza virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

235. The reassortant or recombinant influenza virus of any one of claims 224 to 234, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 7.5 $\log_{10}$ PFU/ml in embryonated eggs.

236. The reassortant or recombinant influenza virus of any one of claims 224 to 234, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8 $\log_{10}$ PFU/ml in embryonated eggs.

237. The reassortant or recombinant influenza virus of any one of claims 224 to 234, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 8.5 $\log_{10}$ PFU/ml in embryonated eggs.

238. The reassortant or recombinant influenza virus of any one of claims 224 to 234, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9 $\log_{10}$ PFU/ml in embryonated eggs.

239. The reassortant or recombinant influenza virus of any one of claims 224 to 234, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 9.5 $\log_{10}$ PFU/ml in embryonated eggs.

240. The reassortant or recombinant influenza virus of any one of claims 224 to 234, wherein the reassortant or recombinant influenza virus grows to a titer of at least about 10 $\log_{10}$ PFU/ml in embryonated eggs.

241. An immunogenic composition comprising the reassortant or recombinant influenza virus of any of claims 224 to 240.

242. An influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 224 to 240.

243. A live, cold-adapted, temperature-sensitive, attenuated influenza vaccine comprising the reassortant or recombinant influenza virus of any of claims 224 to 240.

244. A reassortant influenza virus of any one of claims 14-27 or 140-142 in an amount effective to produce an immunogenic response against a viral infection in a subject for the prophylactic or therapeutic treatment of the viral infection.

245. The reassortant influenza virus of claim 244, wherein the subject is a mammal.

246. The reassortant influenza virus of claim 245, wherein the mammal is a human.

247. The reassortant influenza virus of any one of claims 244-246, wherein the viral infection is a viral influenza infection.

248. The reassortant influenza virus of any one of claims 244-247, wherein the reassortant influenza virus is to be administered in vivo to the subject or in vitro or ex vivo to one or more cells of the subject.

249. The reassortant influenza virus of any one of claims 244-248, wherein a composition comprising the reassortant influenza virus and a pharmaceutically acceptable excipient is administered to the subject in an amount effect to prophylactically or therapeutically treat the viral infection.

250. A reassortant or recombinant influenza virus of any one of claims 105-136, 146-171, 175-193, 197-220 or 224-240 in an amount effective to produce an immunogenic response against a viral infection in a subject for the prophylactic or therapeutic treatment of the viral infection.

251. The reassortant or recombinant influenza virus of claim 250, wherein the subject is a mammal.

252. The reassortant or recombinant influenza virus of claim 251, wherein the mammal is a human.

253. The reassortant or recombinant influenza virus of any one of claims 250-252, wherein the viral infection is a viral influenza infection.

254. The reassortant or recombinant influenza virus of any one of claims 250-253, wherein the reassortant influenza virus is to be administered in vivo to the subject or in vitro or ex vivo to one or more cells of the subject.

255. The reassortant or recombinant influenza virus of any one of claims 250-254, wherein a composition comprising the reassortant influenza virus and a pharmaceutically acceptable excipient is administered to the subject in an amount effect to prophylactically or therapeutically treat the viral infection.

256. A method of prophylactic or therapeutic treatment of a viral infection in a subject, the method comprising: administering to the subject, the reassortant influenza virus of any one of claims 14-27 or 140-142 in an amount effective to produce an immunogenic response against the viral infection.

257. The method of claim 256, wherein the subject is a mammal.

258. The method of claim 257, wherein the mammal is a human.

259. The method of any one of claims 256-258, wherein the viral infection is comprises a viral influenza infection.

260. The method of any one of claims 256-259, wherein the reassortant influenza virus is administered in vivo to the subject or in vitro or ex vivo to one or more cells of the subject.

261. The method of any one of claims 256-260, wherein a composition comprising the reassortant influenza virus and a pharmaceutically acceptable excipient is

administered to the subject in an amount effect to prophylactically or therapeutically treat the viral infection.

262. A method of prophylactic or therapeutic treatment of a viral infection in a subject, the method comprising: administering to the subject, the reassortant influenza virus of any one of claims 105-136, 146-171, 175-193, 197-220 or 224-240 in an amount effective to produce an immunogenic response against the viral infection.

263. The method of claim 262, wherein the subject is a mammal.

264. The method of claim 263, wherein the mammal is a human.

265. The method of any one of claims 262-264, wherein the viral infection is comprises a viral influenza infection.

266. The method of any one of claims 262-265, wherein the reassortant influenza virus is administered in vivo to the subject or in vitro or ex vivo to one or more cells of the subject.

267. The method of any one of claims 262-266, wherein a composition comprising the reassortant influenza virus and a pharmaceutically acceptable excipient is administered to the subject in an amount effect to prophylactically or therapeutically treat the viral infection.

268. A method for producing reassortant influenza viruses in cell culture, the method comprising:

a) introducing a plurality of vectors comprising an influenza virus genome into a population of host cells, which plurality of vectors comprises 6 internal genome segments of a first influenza strain; a first genome segment encoding a hemagglutinin polypeptide and a second genome segment encoding a neuramidinase polypeptide, and which population of host cells is capable of supporting replication of influenza viruses;
b) culturing the population of host cells; and,
c) recovering a plurality of reassortant influenza viruses.

269. The method of claim 268, wherein the hemagglutinin polypeptide comprises the amino acid sequence of SEQ ID NO:6.

270. The method of claim 268, wherein the hemagglutinin polypeptide comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6.

271. The method of claim 268, wherein the hemagglutinin polypeptide comprises an amino acid sequence of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

272. The method of claim 268, wherein the hemagglutinin polypeptide comprises the amino acid sequence of residues 1-327 of SEQ ID NO:6.

273. The method of claim 268, wherein the hemagglutinin polypeptide comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6.

274. The method of claim 268, wherein the hemagglutinin polypeptide comprises an amino acid sequence of residues 1-327 of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

275. The method of claim 268, wherein the first genome segment comprises the nucleotide sequence of SEQ ID NO:7.

276. The method of claim 268, wherein the first genome segment comprises the nucleotide sequence of 84 to 1064 of SEQ ID NO:7.

277. The method of any one of claims 268-276, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

278. The method of any one of claims 268-276, wherein the neuramidinase polypeptide is N1 neuramidinase.

279. The method of any one of claims 268-276, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

280. The method of any one of claims 268-276, wherein the second genome segment comprises the nucleotide sequence of SEQ ID NO:5.

281. The method of any one of claims 268 to 280, wherein the first influenza virus strain comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

282. The method of any one of claims 268 to 281, wherein the first influenza strain is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

283. The method of any one of claims 268 to 281, wherein the first influenza strain is A/Ann Arbor/6/60.

284. The method of any one of claims 268 to 281, wherein the first influenza strain is A/Puerto Rico/8/34.

285. The method of any one of claims 268 to 284, wherein the reassortant influenza viruses are suitable for administration in an intranasal vaccine formulation.

286. The method of any one of claims 268 to 285, wherein the plurality of vectors comprising the influenza virus genome comprise an influenza A virus genome.

287. The method of any one of claims 268 to 286, wherein the plurality of vectors is a plurality of plasmid vectors.

288. The method of any one of claims 268 to 287, wherein the population of host cells comprises one or more of: Vero cells, PerC6 cells, MDCK cells, 293T cells, or COS cells.

289. The method of any one of claims 268 to 288, wherein the method does not comprise use of a helper virus.

290. The method of any one of claims 268 to 289, wherein the plurality of vectors consists of eight vectors.

291. A method of producing a reassortant influenza virus vaccine, the method comprising:
   a) introducing a plurality of vectors comprising an influenza virus genome into a population of host cells, which plurality of vectors comprises at least 6 internal genome segments of a first influenza strain; a first genome segment encoding a hemagglutinin polypeptide and a second genome segment encoding a neuramidinase polypeptide, and which population of host cells is capable of supporting replication of influenza viruses;
   b) culturing the population of host cells;
   c) recovering a plurality of reassortant influenza viruses; and
   d) providing one or more pharmaceutically acceptable excipient.

292. The method of claim 291, wherein the hemagglutinin polypeptide comprises the amino acid sequence of SEQ ID NO:6.

293. The method of claim 291, wherein the hemagglutinin polypeptide comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of SEQ ID NO:6.

294. The method of claim 291, wherein the hemagglutinin polypeptide comprises an amino acid sequence of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

295. The method of claim 291, wherein the hemagglutinin polypeptide comprises the amino acid sequence of residues 1-327 of SEQ ID NO:6.

296. The method of claim 291, wherein the hemagglutinin polypeptide comprises an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of residues 1-327 of SEQ ID NO:6.

297. The method of claim 291, wherein the hemagglutinin polypeptide comprises an amino acid sequence of residues 1-327 of SEQ ID NO:6 comprising less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid substitutions, deletions or insertions.

298. The method of claim 291, wherein the first genome segment comprises the nucleotide sequence of SEQ ID NO:7.

299. The method of claim 291, wherein the first genome segment comprises the nucleotide sequence of 84 to 1064 of SEQ ID NO:7.

300. The method of any one of claims 291-299, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

301. The method of any one of claims 291-299, wherein the neuramidinase polypeptide is N1 neuramidinase.

302. The method of any one of claims 291-299, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

303. The method of any one of claims 291-299, wherein the second genome segment comprises the nucleotide sequence of SEQ ID NO:5.

304. The method of any one of claims 291 to 303, wherein the first influenza virus strain comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

305. The method of any one of claims 291 to 304, wherein the first influenza strain is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

306. The method of any one of claims 291 to 304, wherein the first influenza strain is A/Ann Arbor/6/60.

307. The method of any one of claims 291 to 304, wherein the first influenza strain is A/Puerto Rico/8/34.

308. The method of any one of claims 291 to 307, wherein the reassortant influenza viruses are suitable for administration in an intranasal vaccine formulation.

309. The method of any one of claims 291 to 308, wherein the plurality of vectors comprising the influenza virus genome comprise an influenza A virus genome.

310. The method of any one of claims 291 to 309, wherein the plurality of vectors is a plurality of plasmid vectors.

311. The method of any one of claims 291 to 310, wherein the population of host cells comprises one or more of: Vero cells, PerC6 cells, MDCK cells, 293T cells, or COS cells.

312. The method of any one of claims 291 to 311, wherein the method does not comprise use of a helper virus.

313. The method of any one of claims 291 to 312, wherein the plurality of vectors consists of eight vectors.

314. An isolated or recombinant polypeptide, which polypeptide is selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:1;

b) a polypeptide comprising the amino acid sequence of SEQ ID NO:1 comprising the H273Y amino acid substitution;

c) a polypeptide comprising the amino acid sequence of SEQ ID NO:8;

d) a polypeptide comprising an amino acid sequence having at least 95%, at least 98%, at least 98.5%, at least 99%, at least 99.2%, at least 99.4%, at least 99.6%, at least 99.8% or at least 99.9% sequence identity to the amino acid sequence of the polypeptide of any one of (a) to (c); and

e) a polypeptide comprising an amino acid sequence of the polypeptide of any one of (a) to (c) in which less than 3, less than 5, less then 10, less then 15, less than 20, less than 25, less than 30 amino acid residues were substituted, deleted or inserted.

315. The isolated or recombinant polypeptide of claim 314, wherein the polypeptide is immunogenic.

316. A sterile composition comprising the isolated or recombinant polypeptide of claim 314.

317. An antibody specific for the isolated or recombinant polypeptide of claim 314.

318. An immunogenic composition comprising an immunologically effective amount of the isolated or recombinant polypeptide of claim 314.

319. A reassortant influenza virus comprising a nucleic acid encoding the isolated or recombinant polypeptide of claim 314.

320. An isolated or recombinant nucleic acid comprising a nucleotide sequence encoding the polypeptide of claim 314.

321. The isolated or recombinant nucleic acid of claim 320, wherein the nucleic acid is DNA.

322. The isolated or recombinant nucleic acid of claim 320, wherein the nucleic acid is RNA.

323. The isolated or recombinant nucleic acid of claim 320, wherein the polynucleotide encodes an immunogenic polypeptide.

324. A composition comprising isolated or recombinant nucleic acid of claim 320.

325. An immunogenic composition comprising an immunologically effective amount of the isolated or recombinant nucleic acid of claim 320.

326. A reassortant influenza virus comprising the nucleic acid of claim 320.

327. A reassortant influenza virus comprising the nucleic acid of claim 321.

328. A reassortant influenza virus, wherein the reassortant influenza virus is a 6:2 reassortant virus comprising 6 internal genome segments from one or more donor virus, a first genome segment encoding the polypeptide of claim 314 and a second genome segment encoding a neuramidinase polypeptide.

329. A reassortant influenza virus, wherein the reassortant influenza virus is a 7:1 reassortant virus comprising a first genome segment encoding the polypeptide of claim 314 and further comprising 6 internal genome segments and a second genome segment encoding a neuramidinase polypeptide from one or more donor virus.

330. The reassortant influenza virus of claim 3146 or 17, wherein the donor virus comprises one or more phenotypic attributes selected from the group consisting of: attenuated, cold adapted and temperature sensitive.

331. The reassortant influenza virus of any one of claims 328 to330, wherein the donor virus is selected from the group consisting of A/Ann Arbor/6/60, A/Puerto Rico/8/34, A/Leningrad/134/17/57, and A/Leningrad/17.

332. The reassortant influenza virus of any one of claims 328 to 331, wherein the virus is a live virus.

333. The reassortant influenza virus of any one of claims 328 to 332, wherein the first genome segment encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:8.

334. The reassortant influenza virus of any one of claims 328 to 333, wherein the neuramidinase polypeptide is a swine influenza virus neuramidinase.

335. The reassortant influenza virus of any one of claims 328 to 333, wherein the neuramidinase polypeptide is N1 neuramidinase.

336. The reassortant influenza virus of any one of claims 328 to 333, wherein the neuramidinase polypeptide comprises the amino acid sequence of SEQ ID NO 4.

337. A method for producing reassortant influenza viruses in cell culture, the method comprising:

a) introducing a plurality of vectors comprising an influenza virus genome into a population of host cells, which plurality of vectors comprises 6 internal genome segments of a first influenza strain; a first genome segment encoding the polypeptide of claim 314 and a second genome segment encoding a neuramidinase polypeptide, and which population is capable of supporting replication of influenza virus;

b) culturing the population of host cells; and,

c) recovering a plurality of reassortant influenza viruses.

338. An immunogenic composition comprising the isolated or recombinant polypeptide of claim 314.

339. An immunogenic composition comprising the reassortant influenza virus of any one of claims 328 to 336.

340. A method of producing a reassortant influenza virus vaccine, the method comprising:

a) introducing a plurality of vectors comprising an influenza virus genome into a population of host cells, which plurality of vectors comprises at least 6 internal genome segments of a first influenza strain; a first genome segment encoding the polypeptide of claim 314 and a second genome segment encoding a neuramidinase polypeptide, and which population is capable of supporting replication of influenza virus;

b) culturing the population of host cells;

c) recovering a plurality of reassortant influenza viruses; and,

d) providing one or more pharmaceutically acceptable excipient.

341. A reassortant influenza virus comprising the polypeptide of claim 314, in an amount effective to produce an immunogenic response against a viral infection in a subject for the prophylactic or therapeutic treatment of the viral infection.

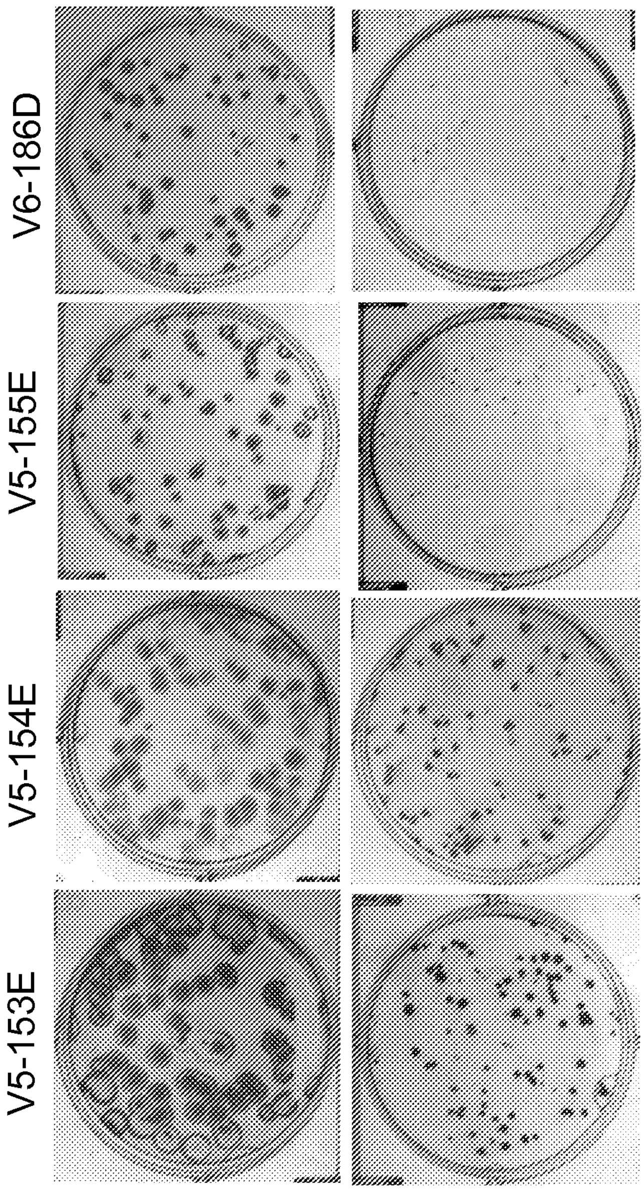

Fig. 1A

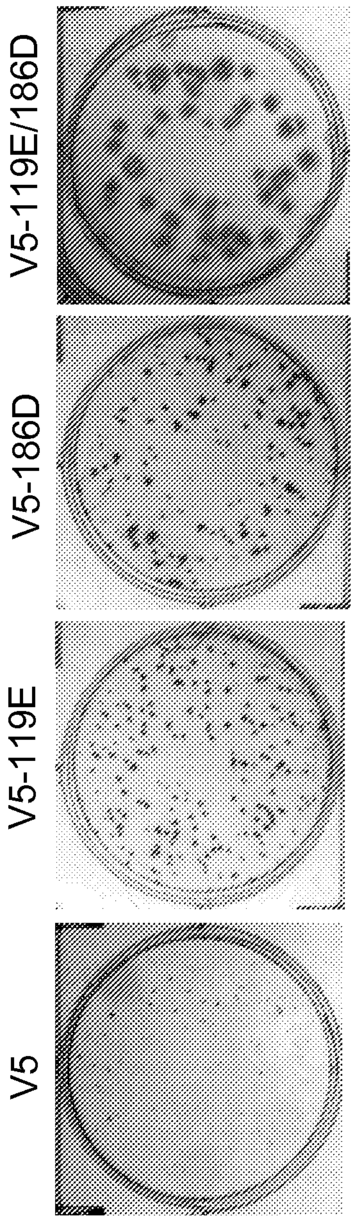

Fig. 1B

```
                       1                                                       50
A/California/7/09      DTLCIGYHAN NSTDTVDTVL EKNVTVTHSV NLLEDKHNGK LCKLRGVAPL
A/swine/Iowa/1/76      DTLCIGYHAN NSTDTVDTIL EKNVTVTHSV NLLEDRHNGK LCKLGGIAPL
A/Swine/31             DTLCIGYHAN NSTDTVDTVL EKNVTVTHSV NLLEDSHNGK LCRLGGIAPL
A/South Dakota/6/07    DTICIGYHAN NSTDTVDTVL EKNVTVTHSV NLLENSHNGR LCLLKGIAPL

                       51                                                     100
A/California/7/09      HLGKCNIAGW ILGNPECESL STASSWSYIV ETPSSDNGTC YPGDFIDYEE
A/swine/Iowa/1/1976    HLGKCNIAGW LLGNPECELL FTVSSWSYIV ETSNSDNGTC YPGDFINYEE
A/Swine/31             QLGKCNIAGW LLGNPECDLL LTVSSWSYIV ETSNSDNGTC YPGDFIDYEE
A/South Dakota/6/07    QLGNCSVAGW ILGNPECELL ISKESWSYIV EKPNPENGTC YPGHFADYEE

                       101              119                                   150
A/California/7/09      LREQLSSVSS FERFEIFPKT SSWPNHDSNK GVTAACPHAG AKSFYKNLIW
A/swine/Iowa/1/76      LREQLSSVSS FEKFEIFPKT SSWPNHETNR GVTAACPYAG ANSFYRNLIW
A/Swine/31             LREQLSSVSS FEKFEIFPKT SSWPNHETTR GVTAACPYAG ASSFYRNLLW
A/South Dakota/6/07    LREQLSSVSS LERFEIFPKE SSWPNHTVT. GVSASCSHNG ESSFYRNLLW

                       153-155                                186             200
A/California/7/09      LVKKGNSYPK LSKSYINDKG KEVLVLWGIH HPSTSADQQS LYQNADAYVF
A/swine/Iowa/1/76      LVKKGNSYPK LSKSYVNNKG KEVLVLWGIH HPPTSTDQQS LYQNADAYVF
A/Swine/31             LVKKENSYPK LSKSYVNNKG KEVLVLWGVH HPPTSTDQQS LYQNADAYVS
A/South Dakota/6/07    LTGKNGLYPN LSKSYANNKE KEVLVLWGVH HPPNIGNQKA LYHTENAYVS

                       201                                                    250
A/California/7/09      VGSSRYSKKF KPEIAIRPKV RXXEGRMNYY WTLVEPGDKI TFEATGNLVV
A/swine/Iowa/1/76      VGTSKYNRKF KPEIAARPKV RGQAGRMNYY WTLIESGDTI TFEATGNLVV
A/Swine/31             VGSSKYDRRF TPEIAARPKV RGQAGRMNYY WTLLEPGDTI TFEATGNLVA
A/South Dakota/6/07    VVSSHYSRKF TPEIAKRPKV RDQEGRINYY WTLLEPGDTI IFEANGNLIA

                       251                             278                    300
A/California/7/09      PRYAFAMERN AGSGIIISDT PVHDCNTTCQ TPKGAINTSL PFQNIHPITI
A/swine/Iowa/1/76      PRYAFAMNRG FGSGIIISDA PVHDCNTKCQ TPKGAINTSL PFQNIHPVTI
A/Swine/31             PRYAFALNRG SESGIITSDA PVHDCDTKCQ TPHGAINSSL PFQNIHPVTI
A/South Dakota/6/07    PRYAFALSRG FGSGIINSNA PMDKCDAKCQ TPQGAINSSL PFQNVHPVTI

                       301
A/California/7/09      GKCPKYVKST KLRLATGLRN IPSIQSR
A/swine/Iowa/1/76      GECPKYVKST KLRMATGLRN IPSIQSR
A/Swine/31             GECPKYVKST KLRMVTGLRN IPSIQSR
A/South Dakota/6/07    GECPKYVRSA KLRMVTGLRN IPSIQSR
```

Fig. 2

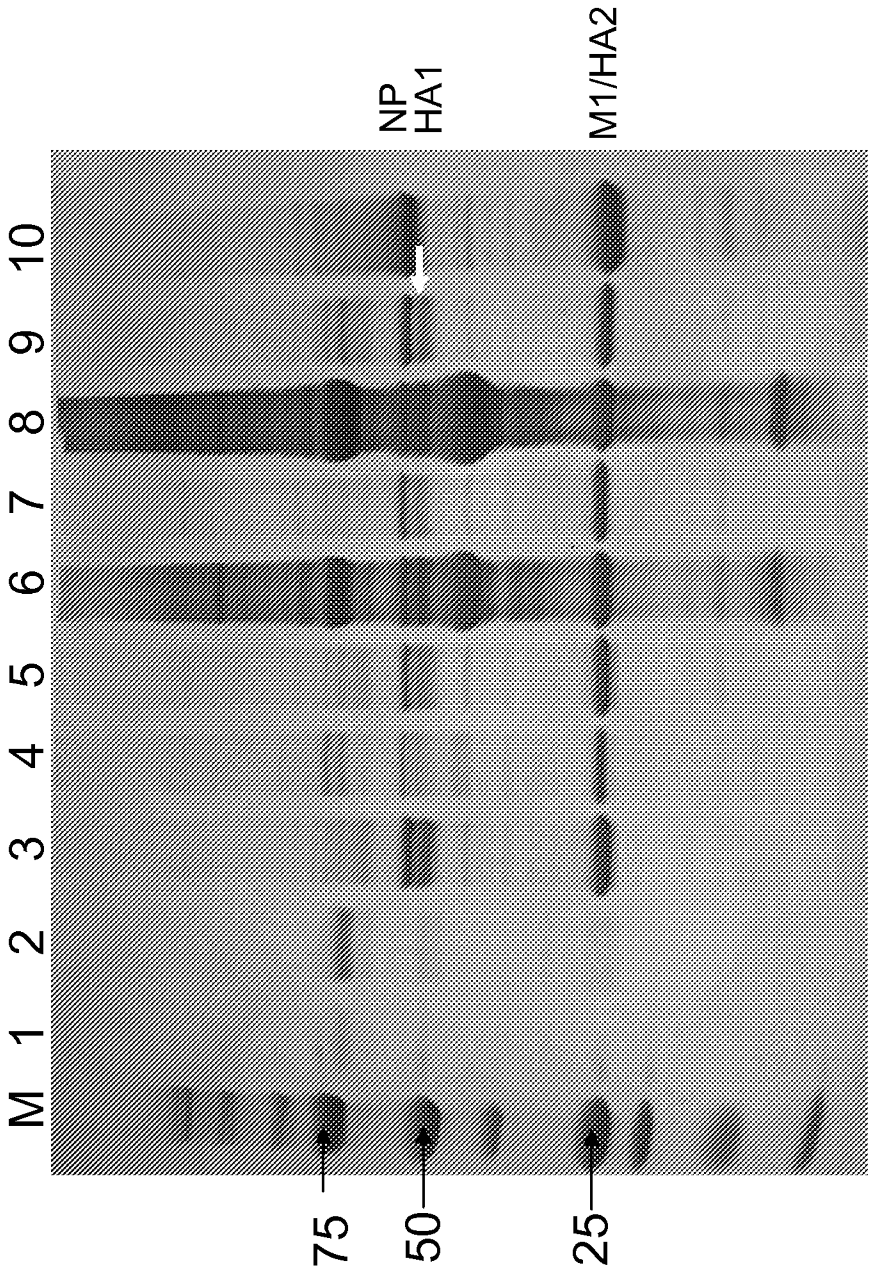

Fig. 3A

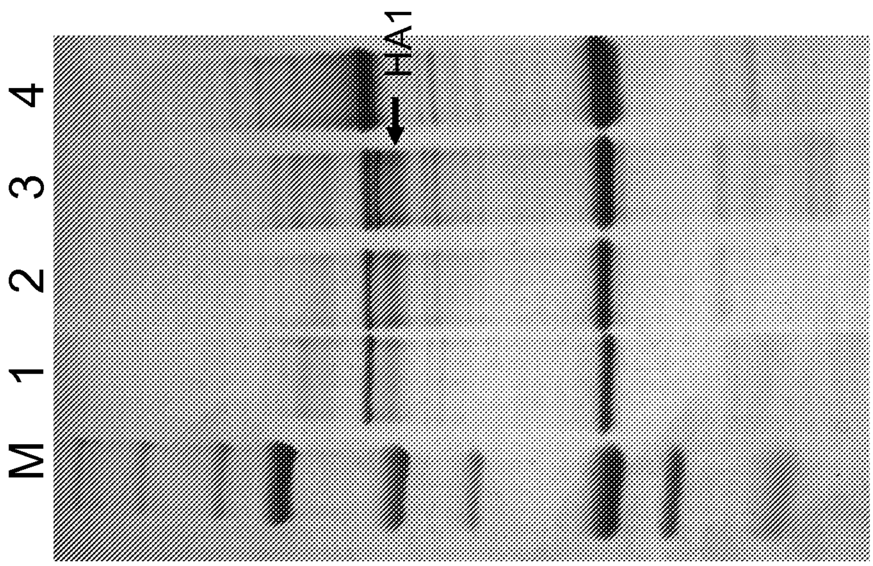

Fig. 3B

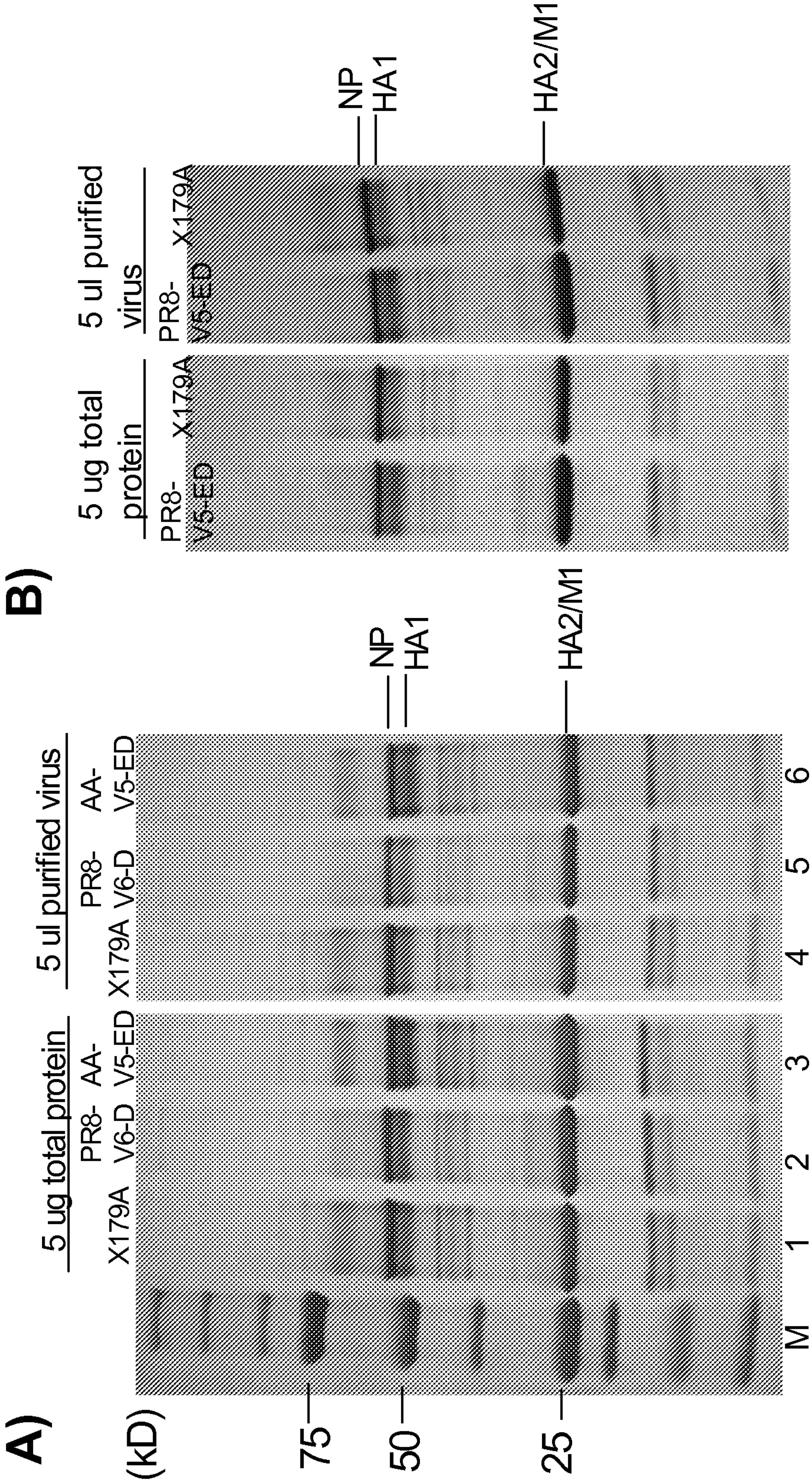
A)
(kD)
75
50
25
5 ug total protein
5 ul purified virus
X179A
PR8-
V6-D
AA-
V5-ED
X179A
PR8-
V6-D
AA-
V5-ED
M
1
2
3
4
5
6
NP
HA1
HA2/M1
B)
5 ug total protein
5 ul purified virus
PR8-
V5-ED
X179A
PR8-
V5-ED
X179A
NP
HA1
HA2/M1

Fig. 4

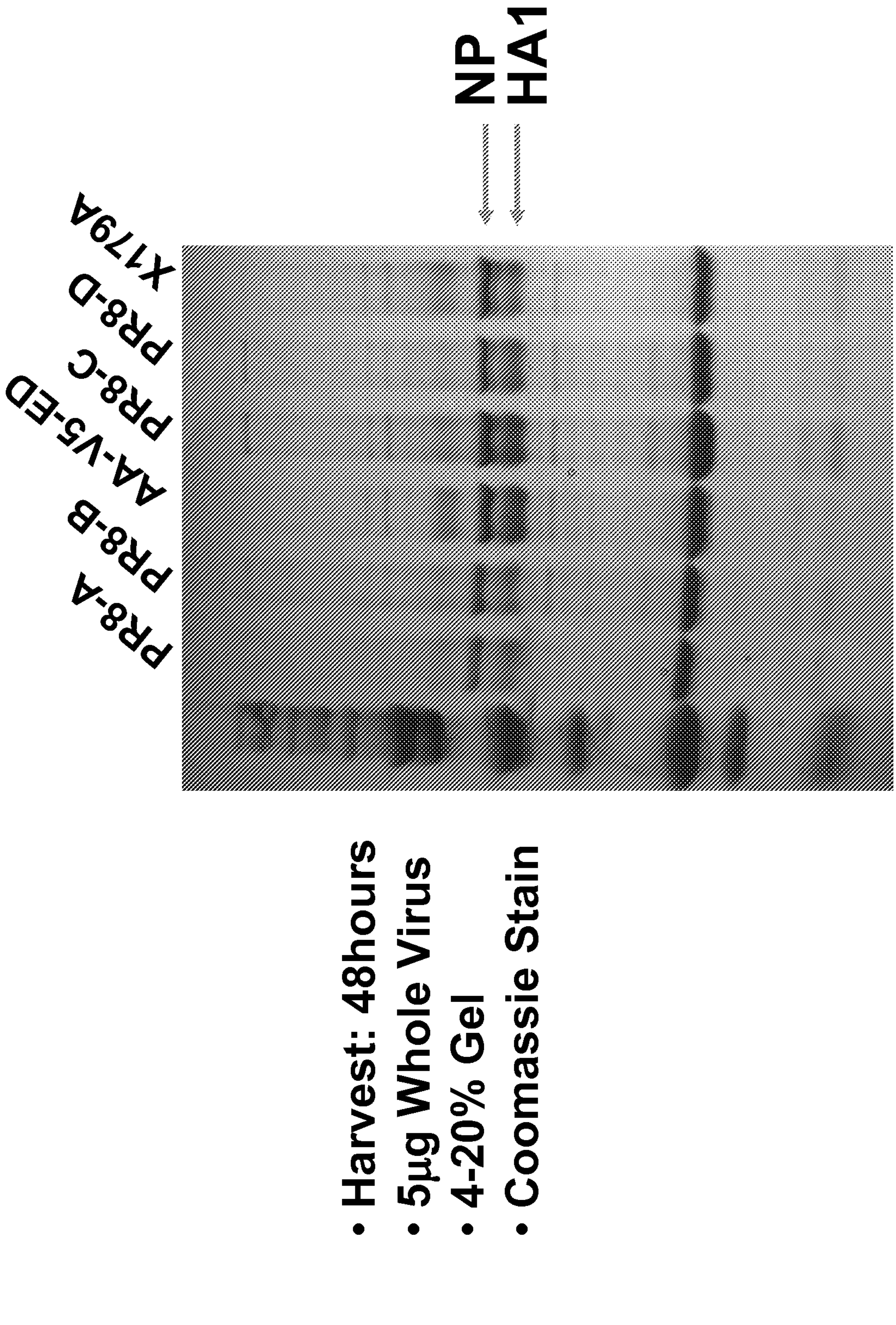
PR8-A
PR8-B
AA-V5-ED
PR8-C
PR8-D
X179A
NP
HA1
• Harvest: 48hours
• 5µg Whole Virus
• 4-20% Gel
• Coomassie Stain

Fig. 5A

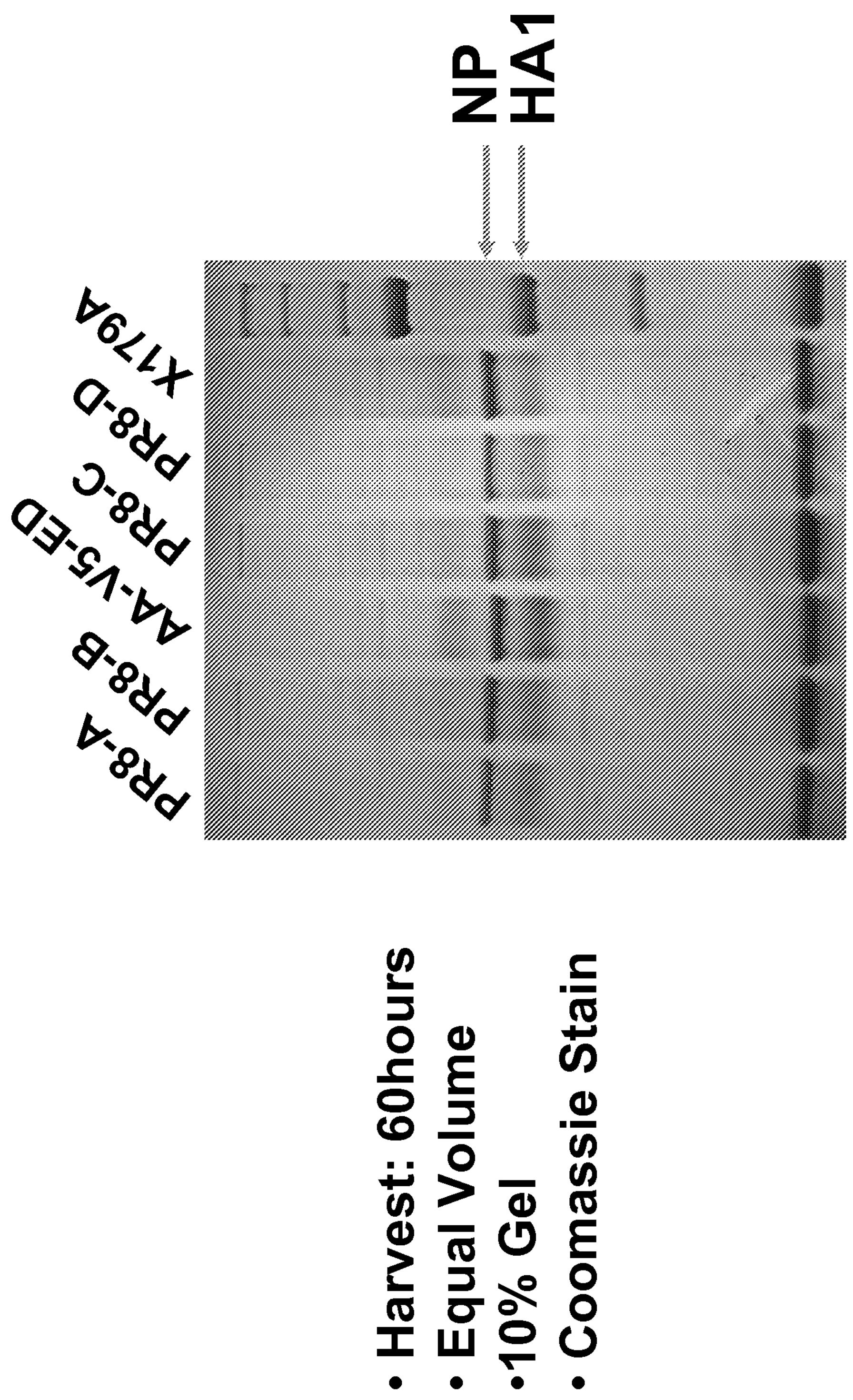
PR8-A
PR8-B
AA-V5-ED
PR8-C
PR8-D
X179A
NP
HA1
• Harvest: 60hours
• Equal Volume
•10% Gel
• Coomassie Stain

Fig. 5B

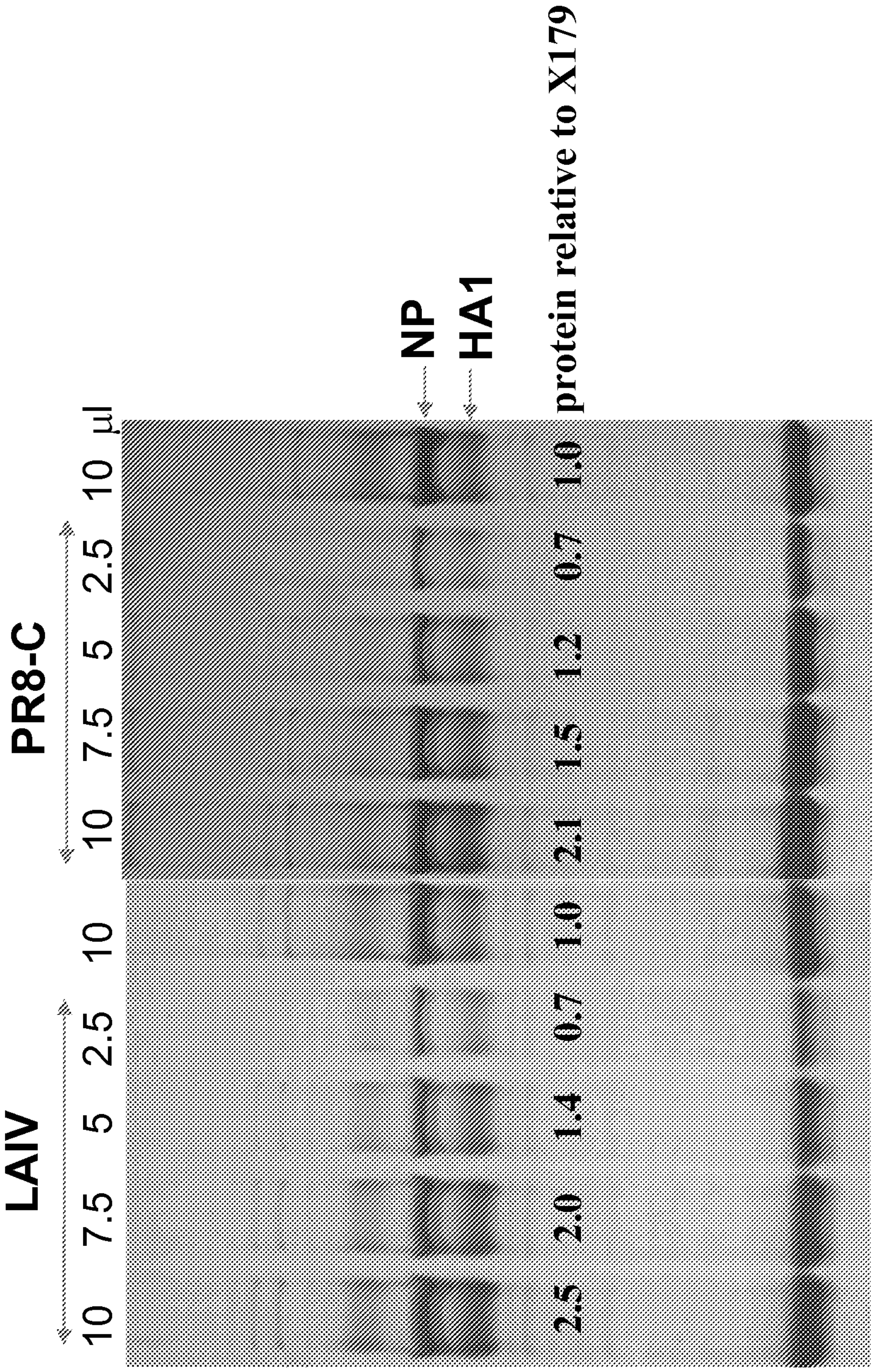
LAIV
PR8-C
10
7.5
5
2.5
10
10
7.5
5
2.5
10 µl
NP
HA1
protein relative to X179
2.5
2.0
1.4
0.7
1.0
2.1
1.5
1.2
0.7
1.0

Fig. 6

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 10/39826

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 39/145; C12N 7/00(2010.01)
USPC - 424/206.1; 435/235.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC(8) - A61K 39/145; C12N 7/00(2010.01)
USPC - 424/206.1; 435/235.1; 424/210.1; 530/350; 536/23.72

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
IPC(8) - A61K 39/145; C12N 7/00(2010.01) - see keyword below
USPC - 424/206.1; 435/235.1; 424/210.1; 530/350; 536/23.72 - see keyword below

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
PubWEST(USPT,PGPB,EPAB,JPAB); Medline, Google: H1N1, isolated, hemagglutinin, recombinant, polypeptide, influenza, sterile, antibody, immunogenic, vaccine, reassortant, 6:2, 7:1, attenuated, cold adapted, temperature sensitive, genome segment, producing, reassortant, swine, excipient, N1, neuramidinase, nucleic acid, DNA, RNA, A/Ann Arbor/6/60, A/

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2008/0069821 A1 (YANG et al.) 20 March 2008 (20.03.2008), Abstract, para [0006], [0008], [0009], [0010], [0013], [0016], [0017], [0018], [0053], [0056], [0067], [0073], [0074], [0076], [0087], [0088], [0095], [0162], [0172], [0180], [0233], and [0249]	1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56-57, 64-67, 314-331, 337-338, 340-341
Y	UniProtKB, C3W5X2_9INFA, Last modified 16 June 2009, Version 1 [online] [Retrieved on 2010.09.17]. Retrieved from the Internet: <URL: http://www.uniprot.org/uniprot/C3W5X2> entire document	1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56-57, 64-67, 314-331, 337-338, 340-341
Y	US 2008/0299151 A1 (Fomsgaard) 04 December 2008 (04.12.2008), Abstract, para [0007], [0011], and [0014]	33, 56
A	DUGAN et al. The Evolutionary Genetics and Emergence of Avian Influenza Viruses in Wild Birds. PLoS Pathog. 2008, vol. 4(5), p. e1000076.	1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56-57, 64-67, 314-331, 337-338, 340-341
A/P	GARTEN et al. Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. Science. 2009 Jul 10; Vol. 325(5937), p.197-201. Epub 2009 May 22.	1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56-57, 64-67, 314-331, 337-338, 340-341

☒ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
23 November 2010 (23.11.2010)	03 DEC 2010

Name and mailing address of the ISA/US	Authorized officer:
Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 10/39826

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	GenBank ID: FJ966974.1. (online) 1 June 2009 (Retrieved on 29 Nov 2010) Retrieved from the internet URL:< http://www.ncbi.nlm.nih.gov/nuccore/227831807?from=1&to=1701&report=gbwithparts>. See nucleic acid and amino acid sequences	1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56-57, 64-67, 314-331, 337-338, 340-341

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 10/39826

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

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

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

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

****

19-27, 34-43, 48-50, 58-63, 68, 69, 81-104, 116-139 , 143-145, 153-174, 187-200, 211-223, 231-267, 281-290, 304-313, 332-336, and 339

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

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

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to from a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I+: Claims 1-18, 28-33, 44-47, 51-57, 64-67, 70-80, 105-115, 140-142, 146-152, 175-186, 314-331, 337, 338, 340, and 341, drawn to an isolated or recombinant polypeptide, compositions comprising the polypeptide, nucleic acids encoding the peptide, viruses containing the nucleic acids, methods of producing the polypeptide and viruses containing the polypeptide, and methods of using the polypeptide. The first named invention (claims 1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56, 57, 64-67, 314-331, 337,-338, 340, and 341) is limited to a polypeptide comprising any of: a) SEQ ID NO: 1 (i.e. SEQ ID NO: 1 without mutations), i) residues1-327 of SEQ ID NO: 1, or s) a sequence having at least 90% identity to SEQ ID NO: 1 or residues 1-327 of SEQ ID NO: 1. Applicant may have one or more mutations (e.g. K119E) or mutational positions (e.g. position 119) and the sequences which contain the mutation(s) searched for an additional search fee per mutational position, with the exception of mutational positions 222 and 223, which may be searched together for a single additional search fee because they share a special technical features in that they are structurally related mutational positions. *****************************Continued in the extra sheet***

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7, 9-14, 16-18, 28, 33, 44-47, 51, 56, 57, 64-67, 314-331, 337,-338, 340, and 341, limited to a) SEQ ID NO: 1 (i.e. SEQ ID NO: 1 without mutations), i) residues1-327 of SEQ ID NO: 1, or s) a sequence having at least 90% identity to SEQ ID NO: 1 or residues 1-327 of SEQ ID NO: 1.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Continuation of:

Box No. III (unity of invention is lacking)

Group II: Claims 201-210, 224-230, 268-280, and 291-303 drawn to a reassortment virus and a method of producing a reassortment virus.

Note: The claims consistently use improper language to set forth limitations regarding mutations (e.g. claim 1). When a transitional phrase appears in a clause of the body of a claim, the limitation that follows the transitional phrase must further limit the element of the clause and therefore must be encompassed by the element. However, Applicant uses improper claim language to this regard. For example, the claims recite language such as "a polypeptide comprising the amino acid sequence of SEQ ID NO:l comprising the K119E and A186D amino acid substitutions." This language is improper because the K119E and A186D substitutions (and others) are not embraced by SEQ ID NO: 1. Accordingly, this claim language has been interpreted as "a polypeptide comprising the amino acid sequence produced by making K119E and A186D substations in SEQ ID NO:l."

The groups listed above do not relate to a single general inventive concept under PCT Rule 13.1 because under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons.

Groups share the technical feature of an influenza hemagglutin polypetide.

The inventions of Group I+ are drawn to different mutational variants of SEQ ID NO: 1. The mutations do not represent a special technical feature because they are not structurally related, i.e. they are spread accross a wide range of positions within SEQ ID NO: 1. The inventions do share a technical feature in that they are SEQ ID NO: 1 derivatives which are highly homologous (e.g. 99% identical) to SEQ ID NO: 1. However, this does not represent an improvement over the prior art. The UniProt entry C3W5X2_9INFA (16-JUN-2009; obtained from the URL:<http://www.uniprot.org/uniprot/C3W5X2>.) teaches an influenza hemagglutin polypetids comprising a equence that is 99.8% identical to SEQ ID NO: 1, with one mismatch.

Accordingly, unity of invention is lacking.

****
Continued from Item 4 of first sheet (unsearchable claims)

Claims 19-27, 34-43, 48-50, 58-63, 68, 69, 81-104, 116-139 , 143-145, 153-174, 187-200, 211-223, 231-267, 281-290, 304-313, 332-336, and 339 have been held unsearchable because they are multiple dependent claims and not drafted in accordance with PCT Rule 6.4(a).