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(12) **United States Patent**
Kawaoka et al.(10) **Patent No.:** **US 9,926,535 B2**
(45) **Date of Patent:** ***Mar. 27, 2018**(54) **HIGH TITER RECOMBINANT INFLUENZA VIRUSES FOR VACCINES**(71) Applicant: **Wisconsin Alumni Research Foundation (WARF)**, Madison, WI (US)(72) Inventors: **Yoshihiro Kawaoka**, Middleton, WI (US); **Taisuke Horimoto**, Bankyotan (JP); **Shin Murakami**, Mito (JP)(73) Assignee: **Wisconsin Alumni Research Foundation (WARF)**, Madison, WI (US)

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A61K 39/00 (2006.01)(52) **U.S. Cl.**CPC **C12N 7/00** (2013.01); **A61K 39/12** (2013.01); **A61K 39/145** (2013.01); **C07K 14/005** (2013.01); **C12N 9/2402** (2013.01); **C12N 15/85** (2013.01); **A61K 2039/525** (2013.01); **A61K 2039/5254** (2013.01); **C12N 2760/16051** (2013.01); **C12N 2760/16121** (2013.01); **C12N 2760/16134** (2013.01); **C12N 2760/16151** (2013.01); **C12N 2800/107** (2013.01); **C12Y 302/01018** (2013.01)(58) **Field of Classification Search**None
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Primary Examiner — Benjamin P Blumel(74) *Attorney, Agent, or Firm* — Schwegman Lundberg & Woessner, P.A.(57) **ABSTRACT**

The invention provides a composition useful to prepare high titer influenza viruses, e.g., in the absence of helper virus, which includes at least five internal genes from an influenza virus isolate that replicates to high titers in embryonated chicken eggs or MDCK cells.

23 Claims, 17 Drawing Sheets

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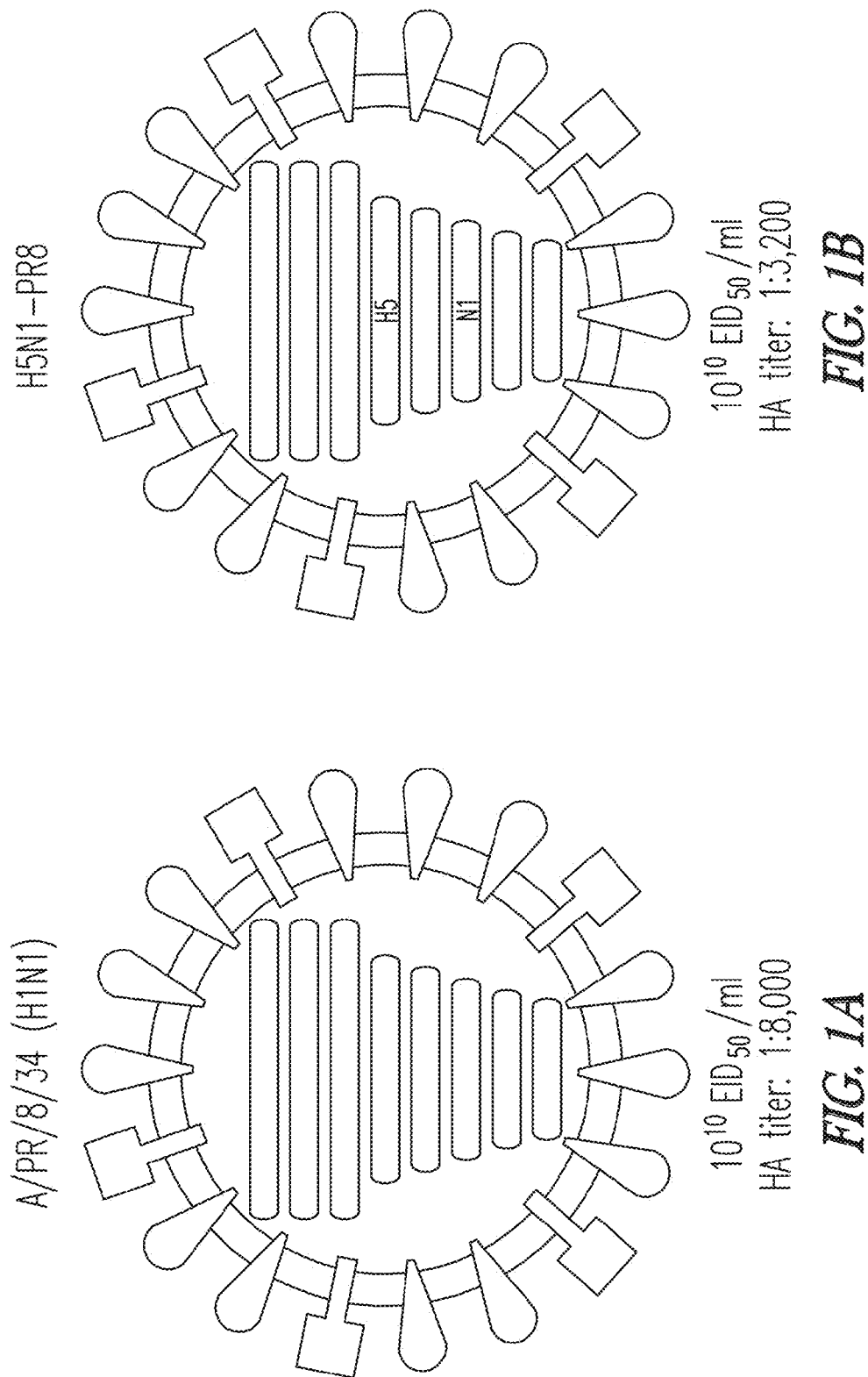
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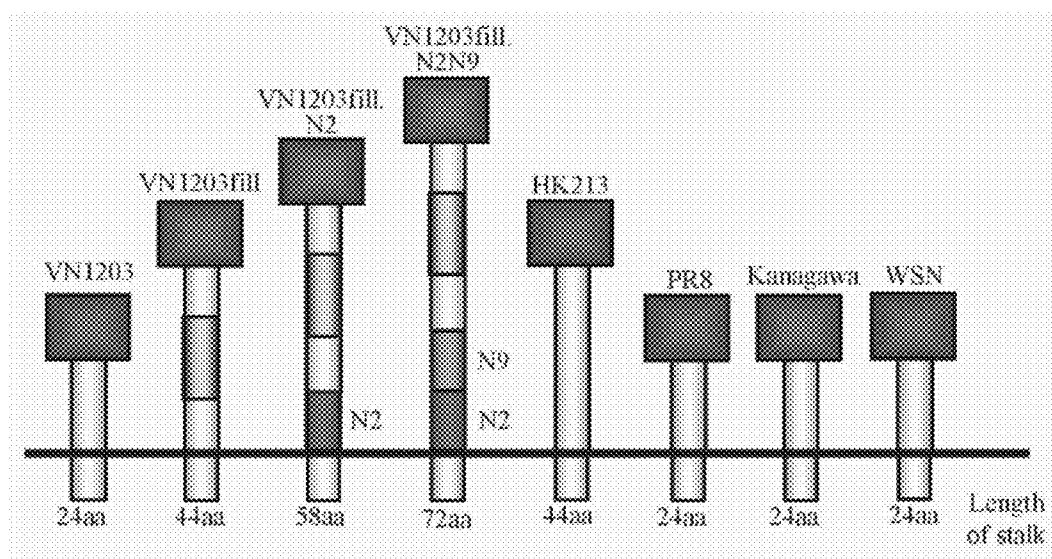
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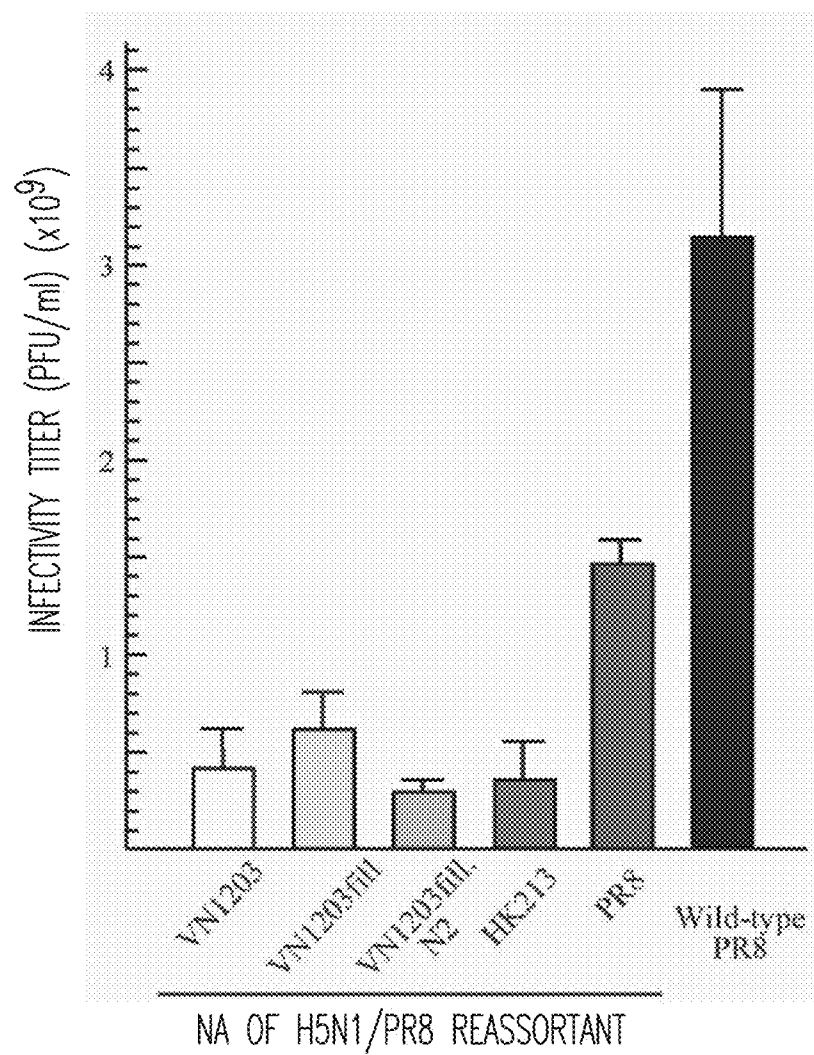
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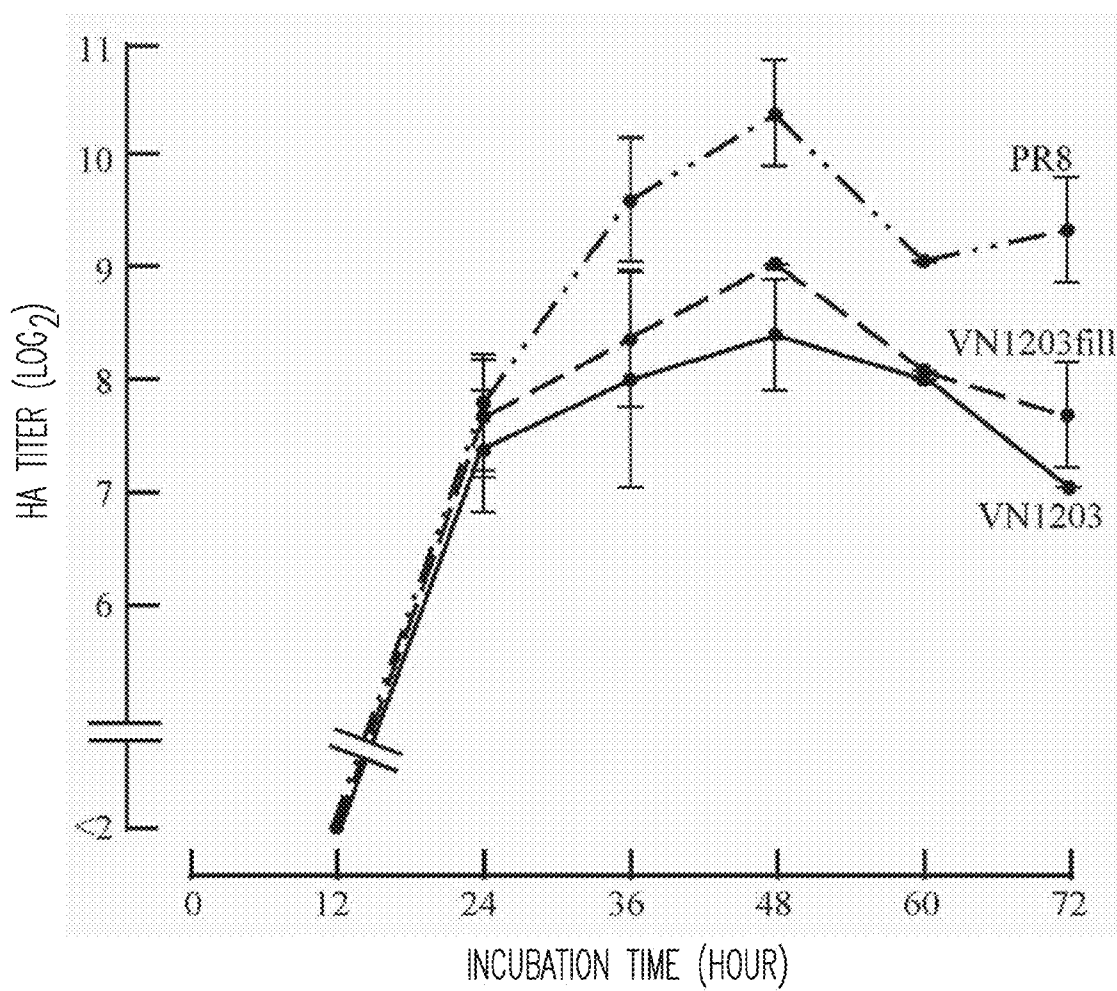
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*FIG. 2*

*FIG. 3*

**FIG. 4**

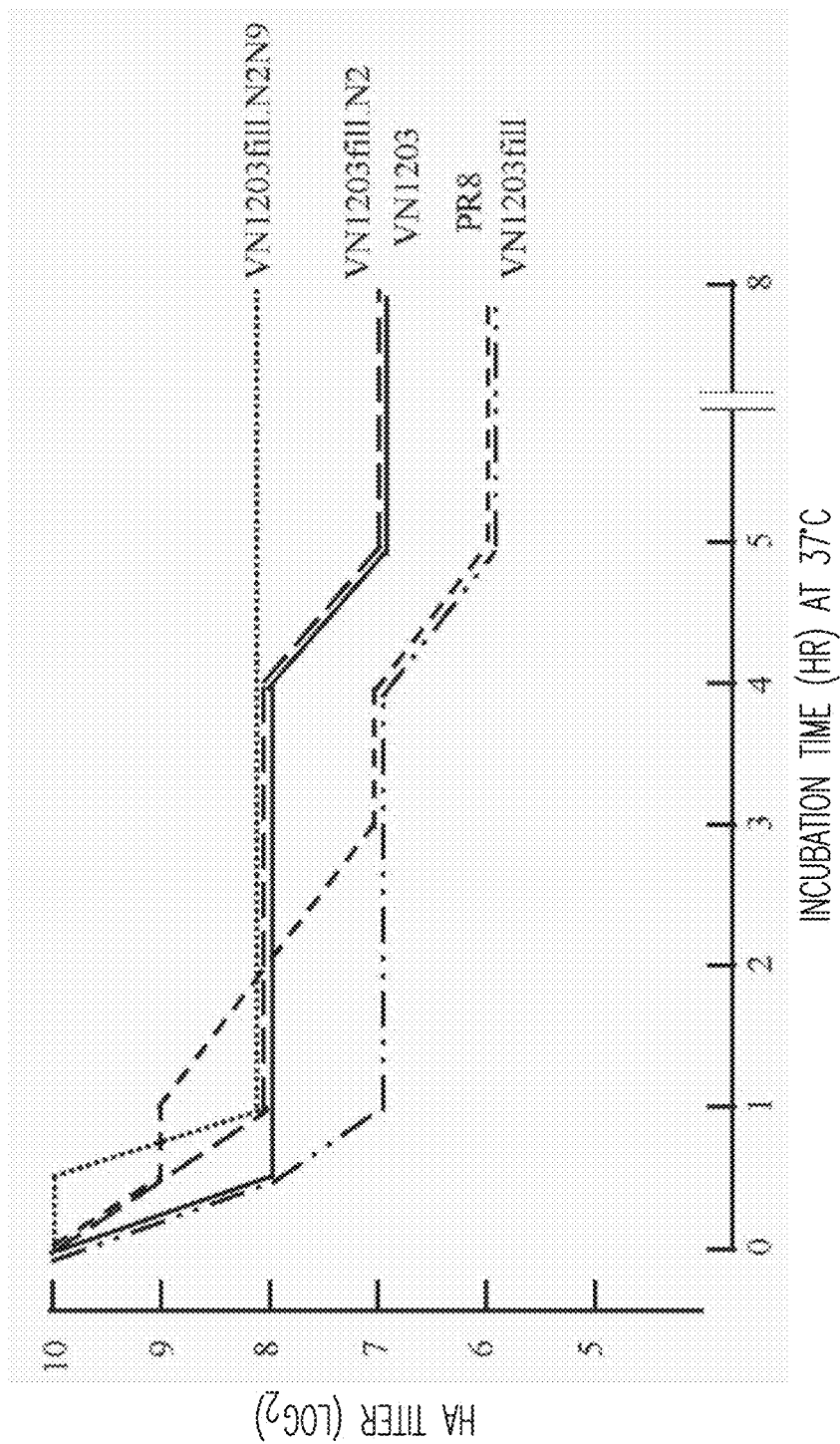
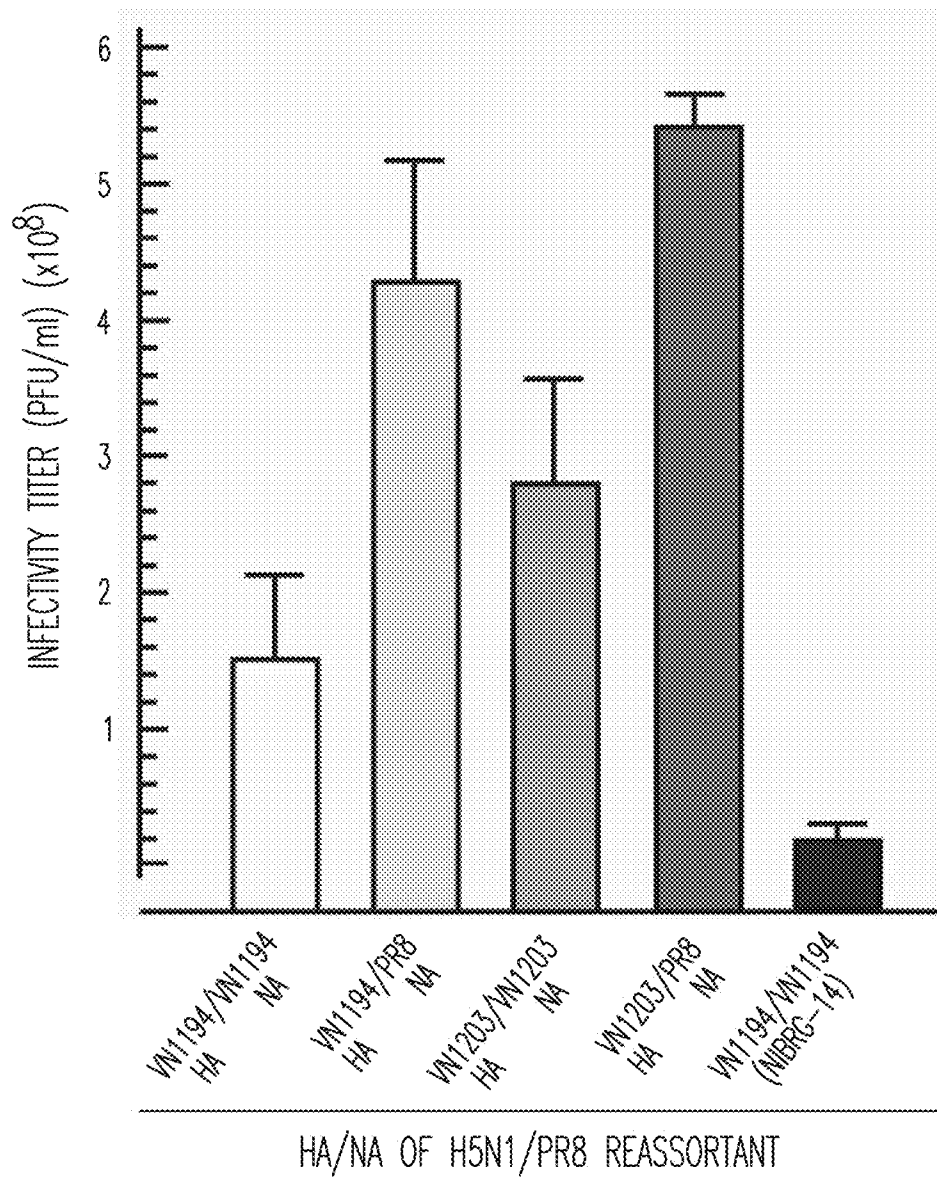


FIG. 5

*FIG. 6*

GROWTH OF REASSORTANT H5N1 VIRUSES POSSESSING PR8(UW)
OR PR8(CAMBRIDGE) INTERNAL GENES IN CHICKEN EMBRYONATED EGGS

	PA	PB1	PB2	HA	NP	NA	M	NS	LOG ₁₀ EID ₅₀ /ml
PR8(UW)/1194	R	R	R	G	R	G	R	R	9.07 ± 0.37
PR8(UW)/1194-CamPA	B	R	R	G	R	G	R	R	8.88 ± 0.25
PR8(UW)/1194-CamPB1	R	B	R	G	R	G	R	R	9.08 ± 0.38
PR8(UW)/1194-CamPB2	R	R	B	G	R	G	R	R	9.05 ± 0.40
PR8(UW)/1194-CamNP	R	R	R	G	B	G	R	R	9.00 ± 0.20
PR8(UW)/1194-CamPB12	R	B	B	G	R	G	R	R	8.75 ± 0.25
PR8(UW)/1194-CamP3	B	B	B	G	R	G	R	R	8.56 ± 0.13*
PR8(UW)/1194-CamP3NP	B	B	B	G	B	G	R	R	8.19 ± 0.31*
NIBRG-14	B	B	B	G	B	G	B	B	8.32 ± 0.20*

R	B	G
PR8(UW)	PR8(CAMBRIDGE)	A/VIETNAM/1194/2004

FIG. 7

THE EFFECT OF THE M AND NS GENES ON THE GROWTH OF
VIRUSES IN CHICKEN EMBRYONATED EGGS

	PA	PB1	PB2	HA	NP	NA	M	NS	$\times 10^8$ PFU/ml
PR8(UW)/1194	R	R	R	G	R	G	R	R	3.39 ± 1.42
PR8(UW)/1194-CamM	R	R	R	G	R	G	B	R	2.94 ± 0.28
PR8(UW)/1194-CamNS	R	R	R	G	R	G	R	B	$6.25 \pm 1.44^*$
NIBRG-14	B	B	B	G	B	G	B	B	0.73 ± 0.43

R	B	G
PR8(UW)	PR8(CAMBRIDGE)	A/VIETNAM/1194/2004

FIG. 8

Growth of PR8(UW)/1194 and NIBRG-14 virus in MDCK cells

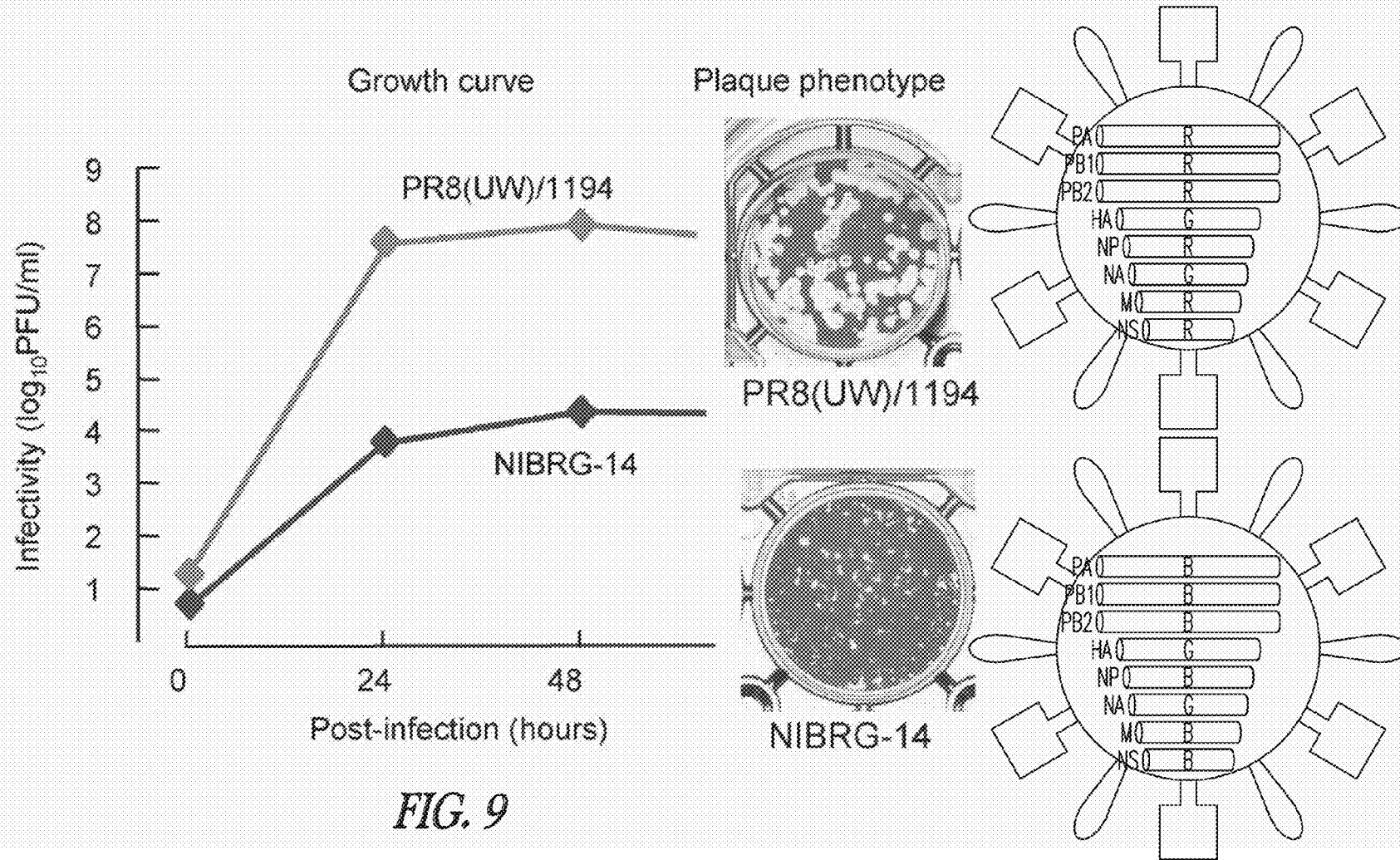
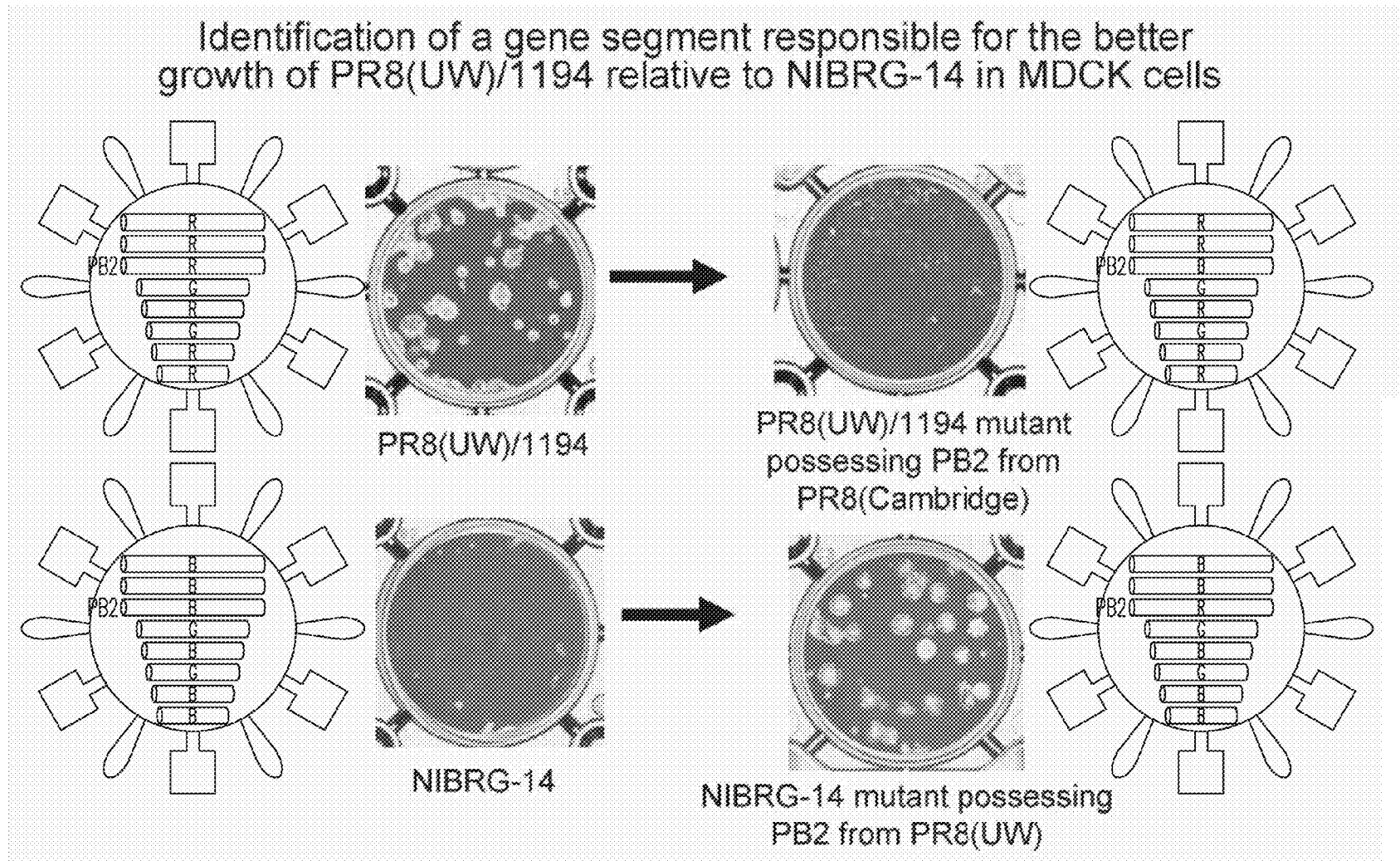


FIG. 9

*FIG. 10*

Identification of the amino acid in PB2 responsible for
the high growth rate of the vaccine seed virus in MDCK cells

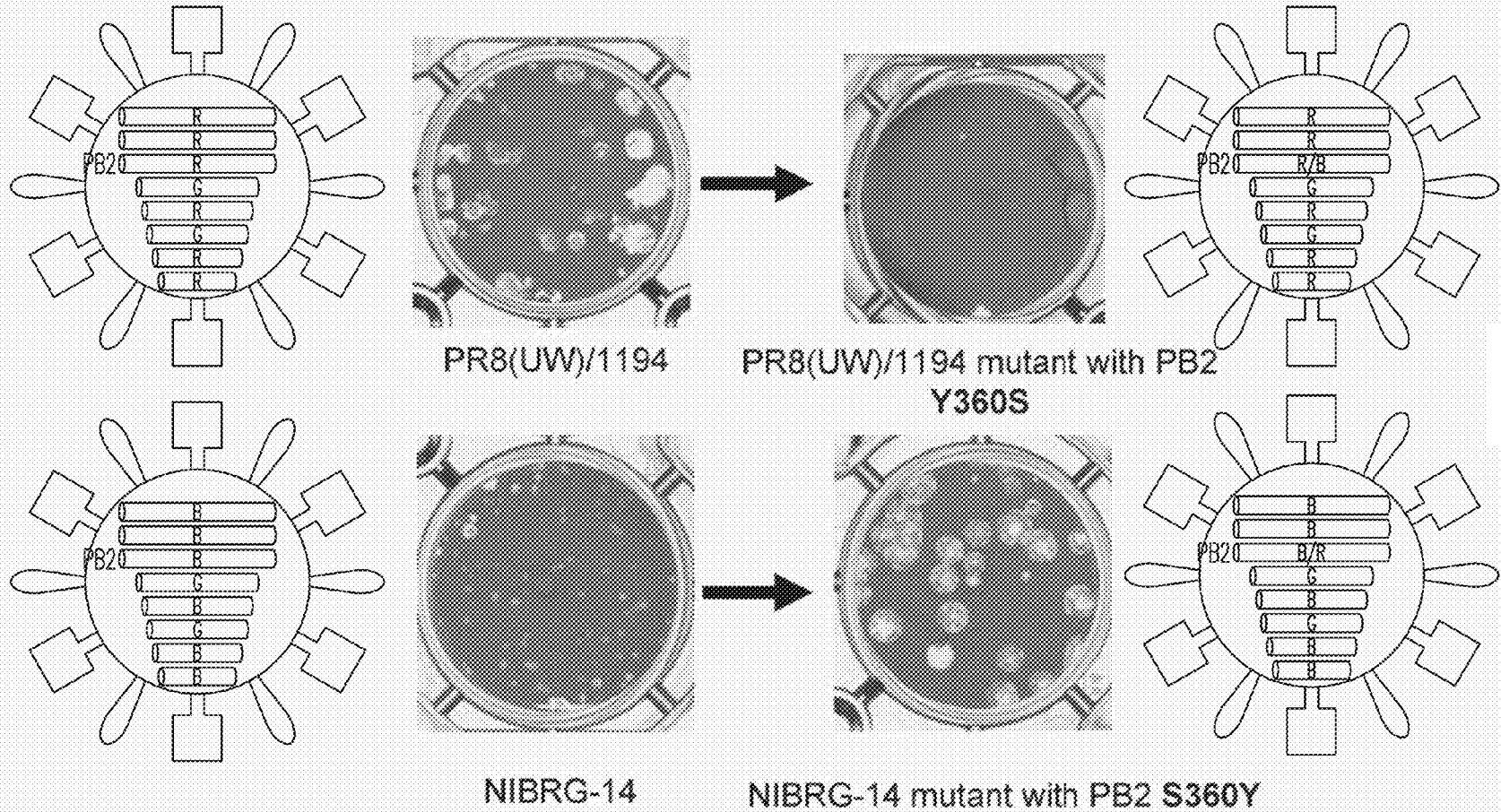


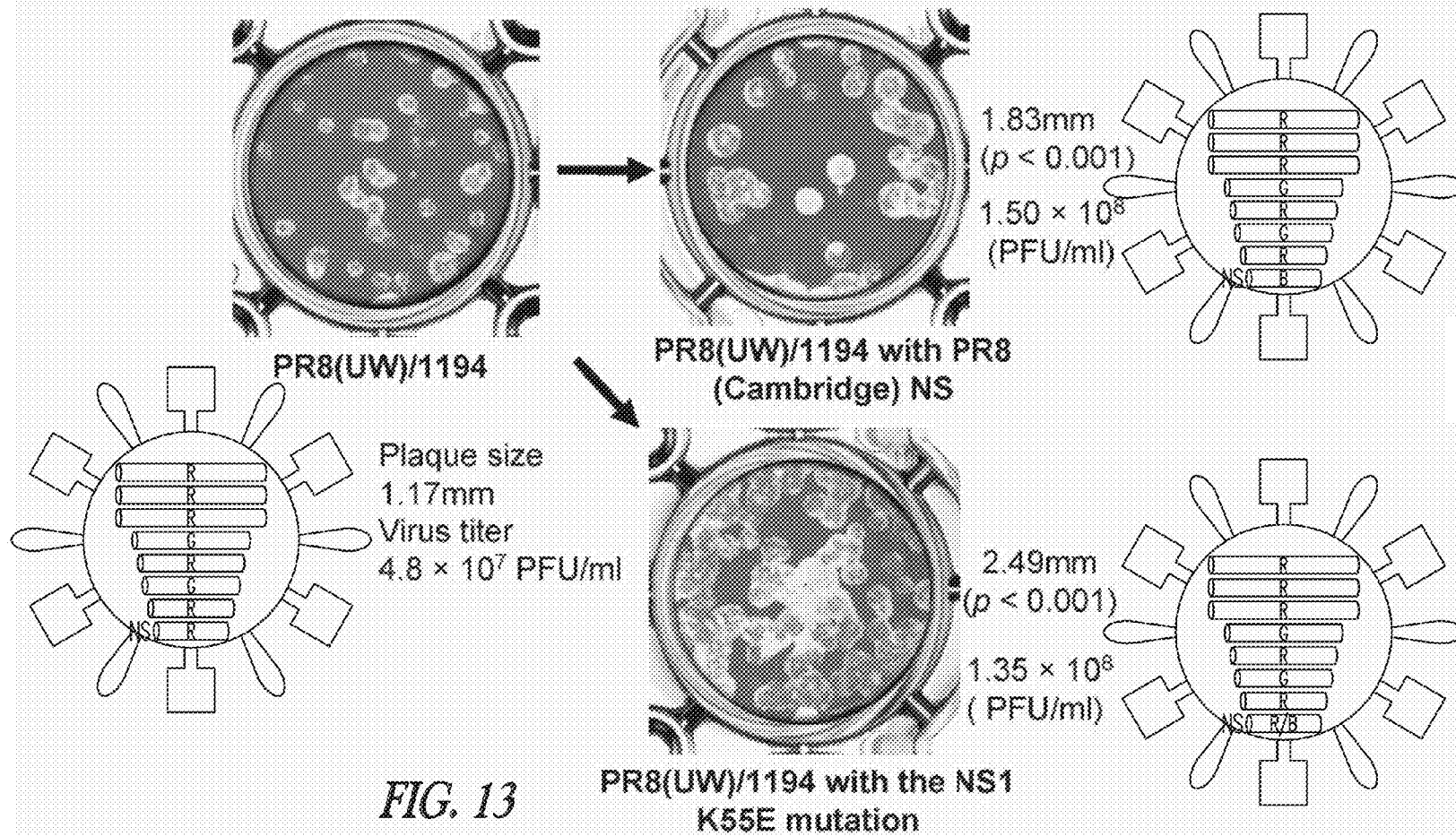
FIG. 11

GROWTH RATES IN MDCK CELL OF REASSORTANTS WITH DIFFERENT HA, NA, AND NS GENES

	PA	PB1	PB2	HA	NP	NA	M	NS	$\times 10^8$ PFU/ml
PR8(UW)/1194	R	R	R	G1	R	G1	R	R	0.39 ± 0.21
PR8(UW)/1203	R	R	R	G2	R	G2	R	R	0.40 ± 0.20
PR8(UW)/1203/03FILL	R	R	R	G2	R	Y	R	R	$1.26 \pm 0.47^*$
PR8(UW)/1203/HK213	R	R	R	G2	R	BR	R	R	$1.10 \pm 0.37^*$
PR8(UW)/1203/03FILL-CamNS	R	R	R	G2	R	Y	R	B	$2.33 \pm 0.27^{**}$
PR8(UW)/1203/HK213-CamNS	R	R	R	G2	R	BR	R	B	$2.35 \pm 0.21^{**}$
	R			B			33°C , 36 hpi, moi=0.01		
	PR8(UW)			PR8(CAMBRIDGE)					
	G1			G2					
	A/VIETNAM/1194/2004			A/VIETNAM/1203/2004 (1203)					
	Y			BR					
	VN1203FILL (1203 WITH LONGER STALK)			A/HONG KONG/213/203					

FIG. 12

Growth in MDCK cells of the H5N1 vaccine seed virus
containing an heterologous NS segment



THE GENOTYPE OF AN H5N1 VACCINE SEED VIRUS WITH
HIGH GROWTH CAPACITY IN CHICKEN EMBRYONATED EGGS OR MDCK CELLS

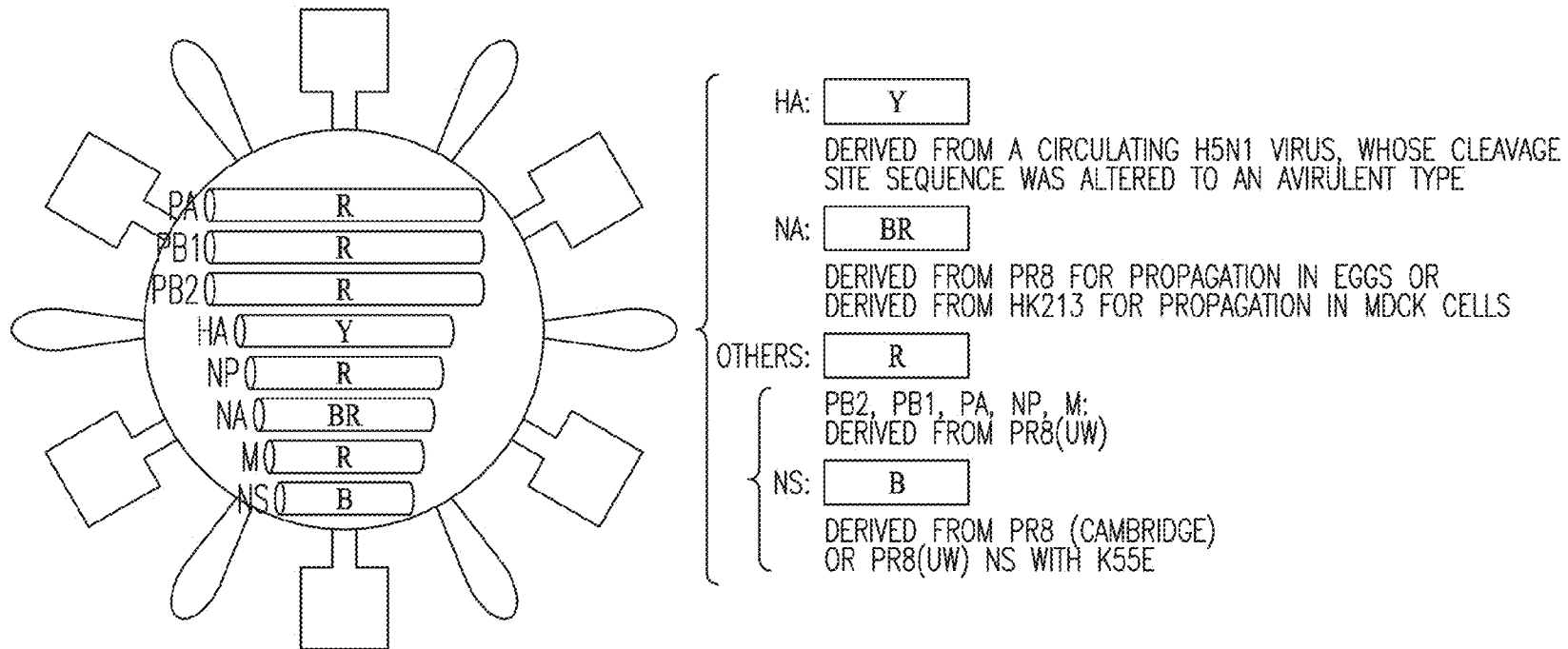


FIG. 14

PR8 (Cambridge)

PB2

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SEQ ID NO. 33

PB1

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SEQ ID NO. 34

FIG. 15A

PR8 (Cambridge)

PA

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TTACTTAATGCACTTTGTGCAAGCAATGGATGATTTCCAATTAATTTCCAATGATAAGCAAGTGTAGAAGTAAAGGAGGGAAGGCGA
AAGCCAACTTGATGGTTTCATCATAAAGGAAGATCCACTTAAGGAATGACACCGAGTGGTAACTTTGTGAGCATGGAG
TTTTCTCTCACTGACCAAGACTTGAACACACAATGGGAGAGTACTGTGTTCTTGAGATAGGAGATAGCTTCTAAGAAAT
GCCATAGGGCAGGTTTCAAGGCGCATGTTCTTGTATGTGAGGACAAATGGAACCTCAAAATTAATTAATGAAATGGGGAATGGAG
ATGAGCGCTTGTCTCTCCAGTCACTTCAACAAATTGAGAGTATGATTGAAGCTGAGTCTCTGTCAAAGAGAAAGACATGACC
AAAGAGTCTTTGAGAACAAATCAGAAACATGGCCATTGGAGAGTCTCCAAAGGAGTGGAGGAAAGTTCCATTGGGAAGGTC
TGCAGGACTTATATAGCAAGTGGTATTTAAGCAGTGTATGCACTCTCACAACTAGAAGGATTTTCAGCTGAATCAAGAAAA
CTGCTTCTTATCGTTCAGGCTCTTAGGGACAATCGAACTCGGACCTTGATCTTGGGGGCTATATGAAGCAATGAGGAG
TGCTAATTAATGATCCCTGGGTTTGTCTAATGCTTCTTGGTCAACTCTTCTTACACATGCAATTGAGTATGTTGTGGCAG
TGCTACTATTTGCTATCCATCTGTCCAAAAAGTACCTTGTCTACT

SEQ ID NO. 35

NP

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCCCAAGGCACCAACGGTCTTACGAACAGATG
GAGACTGATGAGAACGCCAGAAATGCCACTGAAATCAGAGCATCCGTCCGAAAAATGATTGGTGGAAATGGACGATTCATCTC
CAAAATGTGCACAGAACTTAACTCAGTGATTTAGGGGACGGTTGATCCAAAACAGCTTAACAAATAGAGAGAAATGGTGTCTCT
GCTTTTGAAGAAAGGAGAAATAAATACCTGGGAAGAACATCCAGTGGGGGAAAGATCCTAAGAAAACCTGGAGGACCTATATAC
AGAAGAGTAAACGGAAAGTGGATGAGAGAACTCATCTTTATGCAAGAAAGAAATAAGGCGAATCTGGCGCCAGCTAATAAT
GGTGACGATGCAACGGCTGGTCTGACTCACATGATGATTTGCGATTCCAATTTGAATGATGCAACTTATCAGAGGACAAAGGCT
CTTGTTCCGACCCGAATGGATCCAGGATGTGCTCTCTGATGCAAGGTTCAACTCTCCCTAGGAGGTCTGGAGCCGAGGTGCT
GCAGTCAAAGGAGTTGGAACAATGGTGTGGAATGGTCAGGATGATCAAACTGGGATCAATGATCGGAACCTCTGGAGGGT
GAGAATGGACGAAAAACAAGAAATGCTTATGAAGAAATGTGCAACATTCTCAAAGGGAATTTCAAACCTGTCACAAAAAGCA
ATGATGGATCAAGTGAGAGAGAGCCGGAACCCAGGGAATGCTGAGTTCGAAGATCTCACTTTCTAGCACGGTCTGCACTCATA
TTGAGAGGGTGGTGTCTACAAGTCTGCTGCTGCTGCTGTGTATGGACCTGCGCTAGCCAGTGGGTACGACTTTGAAAGA
GAGGGATACTCTCTAGTCCGAATAGACCCTTTCAGACTGCTTCAAAACAGCCAAGTGTACAGCTAATCAGACCAATGAGAAAT
CCAGCACACAAGAGTCAACTGGTGTGGATGGCATGCCATTTGCGCCCATTTGAAGATCTAAGAGTATTGAGCTTCATCAAGGG
ACGAAGGTGGTCCCAAGAGGGAAGCTTTCAGTACAGGAGTTCAATTTGCTTCCAATGAAAAATGGAGACTATGGAATCAAGT
ACACTTGAAGTGAAGGACGGTACTGGGCCATAAGGACCAGAAATGGAGGAAACCAATCAACAGAGGGCATCTGCGGCCAA
ATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAACACCGTTATGGCAGCACTTCACTGGGAATACA
GAGGGGAGAACATCTGACATGAGGACCGAAATCATAAGGATGATGGAAGTGAAGACCAGAGATGTGCTTTCCAGGGGCGG
GGAGTCTTCGAGCTCTCGGACGAAAGGCGAGCGAGCCGATCGGCTTCTTTGACATGAGTAATGAAGGATCTTATTTCTTC
GGAGACAATGCAAGGAGTACGACAATTAAGAAAAATACCTTGTCTACT

SEQ ID NO. 36

M

AGCAAAAGCAGGTAGATAATGAAAGATGAGTCTTCAACCGAGGTGAAACGTACGTTCTCTCTATCATCCGTCAGGCCCCCT
CAAAGCCGAGATCGACAGAGACTTGAAGATGTCTTTGACGGGAAGAACACCGATCTTGAGGTTCTCATGGAATGGCTAAAGAC
AAGACCAATCCTGTCACTCTGACTAAGGGGATTTAGGATTTGTGTTACGCTCACCGTGGCCAGTGAGGAGGAGGATGCAAGC
TAGACGCTTTGTCCAAATGCCCTTAATGGGAACGGGATCCAAATAACATGGACAAAGCAGTTAACTGTATAGGAAGCTCAA
GAGGGAGATAACATTCATGGGGCAAGAAATCTCACTCAGTTATTCTGCTGGTGCATTTGCCAGTTGTATGGGCTCATATA
CAACAGGATGGGGCTGTGACCACTGAAGTGGCATTTGGCTGGTATGTGCAACCTGTGAAACAGATTGCTGACTCCAGCATCG

FIG. 15B

PR8(Cambridge)

GTCTCATAGGCAAAATGGTGACAACAACCAACCCACTAATCAGACATGAGAACAGAAATGGTTTTAGCCAGCACTACAGCTAAGGC
TATGGAGCAAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGGCAAAATGGTGCAAGCCAT
GAGAACCATTGGGACTCATCTAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAAATTTGCAGGCCATCAGAAACGAAT
GGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCTATTGCCGCAAAATATCATTGGGATCTTGCACCTGATATTGTGGATTCT
TTGATCGTCTTTTTTCAAATGCATTTACCGTGGCTTTAAATACGGACTGAAGGGAGGGCTTCTACGGAAGGAGTGCCAAAGT
CTATGAGGGAAGAATATCGAAAGGAACAGCAGAGTGTGTGGATGCTGACGATGGTCATTTGTGAGCATAGAGCTGGAGTAAA
AAACTACCTTGTCTACT

SEQ ID NO. 37

NS

ACCAAAAGCAGGGTGACAAAGACATAATGGATCCAAACACTGTGTCAAGCTTTCAGGTAGATTGCTTTCTTTGGCATGTCCGCA
AACGAGTTGCAGACCAAGAACTAGGTGATGCCCCATTCTTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCA
GCACCTCTTGGTCTGGACATCGAGACAGCCACACGCTCTGGAAGCAGATAGTGGAGCGGATTCTGAAAGAAGAAATCCGATGAGG
CACTTAAATGACCATGGCCTCTGTACCTGCGTGGCTTACCTAACCGACATGACTCTTGAGGAAATGTCAAGGGAATGGTCCA
TGCTCATACCCAAGCAGAAAGTGGCAGGCCCTCTTTGTATCAGAAATGGACCAAGCGATCATGGATAAAAACATCATACTGAAAG
CGAACTTCAGTGTGATTTTGAACGGCTGGAGACTCTAATATTGCTAAGGGCTTTCAECGAAGAGGGAGCAATTGTTGGCGAAA
TTTCACCATTTGCCTTCTCTCCAGGACATACTGCTGAGGATGTCAAAAATGCAGTTGGAGTCTCATCGGAGGACTTGAATGGA
ATGATAACACAGTTGGAGTCTCTGAAACTCTACAGAGATTGCTTGGAGAGCAGTAATGAGAAATGGGAGACCTCCACTCACTC
CAAAACAGAAACGAGAAATGGCGGGAACAATTAGGTCAGAAAGTTGAGGAAATAAGATGTTGATTGAAGAAATGAGACACAAA
CTGAAGGTAACAGAGAAATAGTTTTGAGCAAAATAACATTTATGCAAGCCTTACATCTATTGCTTGAAGTGGAGCAAGAGATAAGA
ACTTTCTCATTTGAGCTTATTTAATAATAAAAAACACCTTGTCTACT

SEQ ID NO. 38

FIG. 15C

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HIGH TITER RECOMBINANT INFLUENZA VIRUSES FOR VACCINES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 11/729,557, filed Mar. 29, 2007, which claims the benefit of the filing date of U.S. Application Ser. No. 60/787,766, filed Mar. 31, 2006, the disclosures of which are incorporated by reference herein.

GOVERNMENT SUPPORT

This invention was made with government support under AI044386 awarded by the National Institutes of Health. The Government has certain rights in the invention.

BACKGROUND

Negative-sense RNA viruses are classified into seven families (Rhabdoviridae, Paramyxoviridae, Filoviridae, Bornaviridae, Orthomyxoviridae, Bunyaviridae, and Arenaviridae) which include common human pathogens, such as respiratory syncytial virus, influenza virus, measles virus, and Ebola virus, as well as animal viruses with major economic impact on the poultry and cattle industries (e.g., Newcastle disease virus and Rinderpest virus). The first four families are characterized by nonsegmented genomes, while the latter three have genomes comprised of six-to-eight, three, or two negative-sense RNA segments, respectively. The common feature of negative-sense RNA viruses is the negative polarity of their RNA genome; i.e., the viral RNA (vRNA) is complementary to mRNA and therefore is not infectious by itself. In order to initiate viral transcription and replication, the vRNA has to be transcribed into a plus-sense mRNA or cRNA, respectively, by the viral polymerase complex and the nucleoprotein; for influenza A viruses, the viral polymerase complex is comprised of the three polymerase proteins PB2, PB1, and PA. During viral replication, cRNA serves as a template for the synthesis of new vRNA molecules. For all negative-stranded RNA viruses, non-coding regions at both the 5' and 3' termini of the vRNA and cRNA are critical for transcription and replication of the viral genome. Unlike cellular or viral mRNA transcripts, both cRNA and vRNA are neither capped at the 5' end nor polyadenylated at the very 3' end.

The basic functions of many viral proteins have been elucidated biochemically and/or in the context of viral infection. However, reverse genetics systems have dramatically increased our knowledge of negative-stranded segmented and non-segmented RNA viruses with respect to their viral replication and pathogenicity, as well as to the development of live attenuated virus vaccines. Reverse genetics, as the term is used in molecular virology, is defined as the generation of virus possessing a genome derived from cloned cDNAs (for a review, see Neumann et al., 2002).

In order to initiate viral replication of negative-stranded RNA viruses, vRNA(s) or cRNA(s) must be coexpressed with the polymerase complex and the nucleoprotein. Rabies virus was the first non-segmented negative-sense RNA virus which was generated entirely from cloned cDNA: Schnell et al. (1994) generated recombinant rabies virus by cotransfection of a cDNA construct encoding the full-length cRNA and protein expression constructs for the L, P, and N proteins, all under control of the T7 RNA polymerase promoter. Infection with recombinant vaccinia virus, which

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provided T7 RNA polymerase, resulted in the generation of infectious rabies virus. In this T7 polymerase system, the primary transcription of the full length cRNA under control of the T7 RNA polymerase resulted in a non-capped cRNA transcript. However, three guanine nucleotides, which form the optimal initiation sequence for T7 RNA polymerase, were attached to the 5' end. In order to create an authentic 3' end of the cRNA transcript which is essential for a productive infective cycle, the hepatitis delta ribozyme (HDVRz) sequence was used for exact autocatalytic cleavage at the 3' end of the cRNA transcript.

Since the initial report by Schnell et al. (1994), reverse genetics systems using similar techniques led to the generation of many non-segmented negative strand RNA viruses (Conzelmann, 1996; Conzelmann, 1998; Conzelmann et al., 1996; Marriott et al., 1999; Munoz et al., 2000; Nagai, 1999; Neumann et al., 2002; Roberts et al., 1998; Rose, 1996). Refinements of the original rescue procedure included the expression of T7 RNA polymerase from stably transfected cell lines (Radecke et al., 1996) or from protein expression plasmids (Lawson et al., 1995), or heat shock procedures to increase rescue efficiencies (Parks et al., 1999). Based on the T7 polymerase system, Bridgen and Elliott (1996) created Bunyamwera virus (family Bunyaviridae) from cloned cDNAs and demonstrated the feasibility of artificially generating a segmented negative-sense RNA virus by the T7 polymerase system.

In 1999, a plasmid-based reverse genetics technique was generated based on the cellular RNA polymerase I for the generation of segmented influenza A virus entirely from cloned cDNAs (Fodor et al., 1999; Neumann and Kawaoka, 1999). RNA polymerase I, a nucleolar enzyme, synthesizes ribosomal RNA which, like influenza virus RNA, does not contain 5' cap or 3' polyA structures. The RNA polymerase I transcription of a construct containing an influenza viral cDNA, flanked by RNA polymerase I promoter and terminator sequences, resulted in influenza vRNA synthesis (Fodor et al., 1999; Neumann and Kawaoka, 1999; Neumann and Kawaoka, 2001; Pekosz et al., 1999). The system was highly efficient, producing more than 10⁸ infectious virus particles per ml of supernatant of plasmid-transfected cells 48 hours post-transfection.

What is needed is a method to prepare high titer orthomyxoviruses such as influenza A virus, entirely from cloned cDNAs.

SUMMARY OF THE INVENTION

The invention provides a composition comprising a plurality of influenza virus vectors of the invention, e.g., those useful to prepare reassortant viruses including 7:1 reassortants, 6:1:1 reassortants, 5:1:2 reassortants, and 5:1:1:1 reassortants. In one embodiment of the invention, the composition includes vectors for vRNA production selected from a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription

termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising an operably linked to an influenza virus NS cDNA linked to a transcription termination sequence. The composition also includes vectors for viral protein production selected from a vector encoding influenza virus PA, a vector encoding influenza virus PB1, a vector encoding influenza virus PB2, and a vector encoding influenza virus NP, and optionally one or more vectors encoding NP, NS, M, e.g., M1 and M2, HA or NA. Preferably, the vectors encoding viral proteins further comprise a transcription termination sequence.

In one embodiment, the cDNAs for PB1, PB2, PA, NP, M, and NS, and optionally NA, have sequences for PB1, PB2, PA, NP, M, and NS, and optionally NA, from an influenza virus that replicates to high titers in embryonated eggs, and the cDNA for HA has sequences from a different strain of influenza virus (from a heterologous influenza virus isolate with the same or a different HA subtype, i.e., a heterologous HA). For HA from pathogenic H5N1 viruses which do not grow to high titers in embryonated eggs, the cDNA for at least NA has sequences from a N1 influenza virus that replicates to high titers in embryonated eggs.

In one embodiment, the cDNAs for PB1, PB2, PA, NP, M, and NS include a nucleic acid molecule corresponding to a sequence (polynucleotide) encoding at least one of the proteins of a high titer, e.g., titers greater than 10^8 EID₅₀/mL, e.g., 10^9 EID₅₀/mL, 10^{10} EID₅₀/mL, or more, influenza virus. Reassortants within the scope of the invention that have high titers in embryonated eggs have titers of at least about 10^9 EID₅₀/mL for 5:1:1:1 reassortants (with NS K55), 5:1:2 reassortants (with NS K55) and 6:1:1 reassortants (with NS K55) and at least 4×10^8 PFU/mL for 5:1:1:1 reassortants (with NS K55E) or 5:1:2 reassortants (with NS K55E). Reassortants within the scope of the invention that have high titers in MDCK cells have titers of at least 0.75×10^8 PFU/mL, e.g., at least 2.0×10^8 PFU/mL, for 5:1:1:1 or 6:1:1.

In one embodiment, the invention includes a composition comprising a plurality of influenza virus vectors for a 5:1:2 or a 6:1:1 reassortant. The composition includes a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence. The cDNAs for PB1, PB2, PA, NP, and M have sequences that are from one or more influenza viruses that replicate to high titers in embryonated eggs, wherein the cDNA for NS is from the one or more influenza viruses that replicate to high titers in embryonated eggs, and the cDNA for NA is from the one or more influenza viruses that replicate to high titers in embryonated eggs or has sequences for a heterologous NA. The cDNA for HA has sequences for a heterologous HA, which is heter-

ologous to at least the viral gene segments for PB1, PB2, PA, NP, and M. In one embodiment, the cDNA for NS has a Glu at position 55. The composition also includes a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NS2. In one embodiment, the cDNAs for PB1, PB2, PA, NP, M, and NS include a nucleic acid molecule corresponding to a sequence (polynucleotide) encoding at least one of the proteins of a high titer, e.g., titers greater than 10^8 EID₅₀/mL, e.g., 10^9 EID₅₀/mL, 10^{10} EID₅₀/mL, or more, influenza virus.

In one embodiment, a composition comprising a plurality of influenza virus vectors for a 5:1:1:1 or 6:1:1 reassortant. The composition includes comprising a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence. The cDNAs for PB1, PB2, PA, NP, and M have sequences from one or more influenza viruses that replicate to high titers in MDCK cells, wherein the cDNA for NS is from the one or more influenza viruses that replicate to high titers in MDCK cells, wherein the cDNA for NA may have sequences for a heterologous NA, and wherein the cDNA for HA has sequences for a heterologous HA. The composition also includes a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector comprising a promoter operably linked to a DNA segment encoding

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influenza virus NS2. In one embodiment, the cDNAs for PB1, PB2, PA, NP, M, and NS include a nucleic acid molecule corresponding to a sequence (polynucleotide) encoding at least one of the proteins of a high titer, e.g., titers greater than 10^8 EID₅₀/mL, e.g., 10^9 EID₅₀/mL, 10^{10} EID₅₀/mL, or more, influenza virus.

As described herein, recombinant (6:2 reassortant) viruses grow less well in eggs than does the wild-type PR8 strain, even though they possess the same PR8 "internal" genes (i.e., those other than the HA and NA). Since vigorous growth in eggs is an essential property of vaccine seed viruses used in the production of inactivated vaccines, H5N1 vaccine candidates were generated that grow as well as the PR8 donor strain in eggs. It was found that HA-NA balance and PB1 function are important growth determinants. With this knowledge, a series of H5N1 viruses was produced with altered HA-NA combinations, with the PR8 background, to assess their growth in eggs against more conventional 6:2 reassortants, including the WHO-recommended NIBRG-14 virus. A 7:1 reassortant virus and one of the 6:2 reassortants showed enhanced growth in eggs. Thus, for vaccine viruses that generally produce low titers in eggs, replacement of at least the NA of the vaccine virus with the NA of an influenza virus that grows well in eggs, or replacement of all but the HA and NA, or all but the HA, of the vaccine virus, with the other viral gene segments from an influenza virus that grows to high titers in eggs, can result in significantly higher viral titers. The titers of the reassortant viruses of the invention may be 2-fold, 3-fold, or greater, e.g., 7-fold or greater, than the corresponding nonreassortant vaccine virus. As also described herein, the internal genes responsible for the high growth rate of reassortants in eggs having genes from two different PR8 virus isolates was determined. The highest viral titers were those where the majority of internal genes were from PR8HG (PR8(UW)). In particular, 5:1:2 reassortants (PR8(UW) PB1, PB2, PA, NP and M; PR8(Cam) NS; and H5N1 HA and NA) and 6:1:1 reassortants (PR8(UW) NA, PB1, PB2, PA, NP and M; PR8(Cam) NS; and H5 HA) had high titers in eggs.

As also described herein, the viral genes responsible for a high growth rate in MDCK cells, cells likely to be approved as a source of vaccine virus, was assessed. The highest growth rate in MDCK cells was found with PB2 from PR8(UW), NS from PR8(Cam) or NS K55E from PR8(UW), and a NA with a long stalk, e.g., a stalk greater than 20 amino acids but less than about 100 amino acids, e.g., greater than about 40 and up to about 80 amino acids in length. Thus 5:1:1:1 and 6:1:1 reassortants with PR8(UW) PA, PB1, PB2, NP and M, and NS K55E from PR8(UW) or PR8(Cam), NA from PR8(UW) or a heterologous NA source, and a heterologous HA, grew to the highest titers in MDCK cells.

In one embodiment, the nucleic acid molecule corresponds to a sequence encoding PB1, PB2, PA, NP, M, and NS, and optionally NA, having substantially the same activity as a corresponding polypeptide encoded by one of SEQ ID NOs:1-6 or 8. As used herein, "substantially the same activity" includes an activity that is about 0.1%, 1%, 10%, 30%, 50%, 90%, e.g., up to 100% or more, or detectable protein level that is about 80%, 90% or more, the activity or protein level, respectively, of the corresponding full-length polypeptide. In one embodiment, the nucleic acid molecule corresponds to a sequence encoding a polypeptide which is substantially the same as, e.g., having at least 80%, e.g., 90%, 92%, 95%, 97% or 99%, contiguous amino acid sequence identity to, a polypeptide encoded by one of SEQ ID NOs:1-6 or 8. In one embodiment, the isolated and/or

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purified nucleic acid molecule comprises a nucleotide sequence which is substantially the same as, e.g., having at least 50%, e.g., 60%, 70%, 80% or 90% or more contiguous nucleic acid sequence identity to, one of SEQ ID NOs:1-6, 8, or 33 to 38 and, in one embodiment, also encodes a polypeptide having at least 80%, e.g., 90%, 92%, 95%, 97% or 99%, contiguous amino acid sequence identity to a polypeptide encoded by one of SEQ ID NOs:1-6, 8, or 33 to 38. In one embodiment, the isolated and/or purified nucleic acid molecule encodes a polypeptide with one or more, for instance, 2, 5, 10, 15, 20 or more, conservative amino acid substitutions, e.g., conservative substitutions of up to 10% or 20% of the residues, relative to a polypeptide encoded by one of SEQ ID NOs:1-6 or 8. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine and tryptophan; a group of amino acids having basic side chains is lysine, arginine and histidine; and a group of amino acids having sulfur-containing side chain is cysteine and methionine. In one embodiment, conservative amino acid substitution groups are: valine-leucine-isoleucine; phenylalanine-tyrosine; lysine-arginine; alanine-valine; glutamic-aspartic; and asparagine-glutamine. In one embodiment, the isolated and/or purified nucleic acid molecule encodes a polypeptide with one or more, for instance, 2, 3 or 4, nonconservative amino acid substitutions, relative to a polypeptide encoded by one of SEQ ID NOs:1-6 or 33-38. For instance, a K55E NS and a S360Y PB2 substitution are nonconservative substitutions.

In another embodiment, the nucleic acid molecule having PB1, PB2, PA, NP, M, and NS, and optionally NA, sequences, or the complement thereof, hybridizes to one of SEQ ID NOs:1-6, 8, or 33 to 38, the complement thereof, under low stringency, moderate stringency or stringent conditions. For example, the following conditions may be employed: 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50° C. with washing in 2×SSC, 0.1% SDS at 50° C. (low stringency), more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50° C. with washing in 1×SSC, 0.1% SDS at 50° C. (moderate stringency), more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50° C. with washing in 0.5×SSC, 0.1% SDS at 50° C. (stringent), preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50° C. with washing in 0.1×SSC, 0.1% SDS at 50° C. (more stringent), more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50° C. with washing in 0.1×SSC, 0.1% SDS at 65° C. (very stringent). In one embodiment, the nucleic acid molecule encodes a polypeptide which is substantially the same as, e.g., having at least 50%, e.g., 60%, 70%, 80% or 90% or more contiguous nucleic acid sequence identity to, one of SEQ ID NOs:1-6, or 33 to 38, and preferably has substantially the same activity as a corresponding full-length polypeptide encoded by one of SEQ ID NOs:1-6, 8 or 33 to 38. Those nucleic acid molecules, or nucleic acid molecules from other N1 strains that grow well in eggs, may be employed with nucleic acid for any HA, e.g., H5.

Thus, nucleic acid molecule may be employed to express influenza proteins, to prepare chimeric genes, e.g., with other viral genes including other influenza virus genes,

and/or to prepare recombinant virus. Thus, the invention also provides isolated polypeptides, recombinant virus, and host cells contacted with the nucleic acid molecules or recombinant virus of the invention.

The invention also provides a plurality of the following isolated and/or purified vectors: a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein at least one vector comprises sequences corresponding to those encoding PB1, PB2, PA, NP, M, NS, and optionally NA, or a portion thereof, having substantially the same activity as a corresponding polypeptide encoded by one of SEQ ID NOs:1-6 or 8, e.g., a sequence encoding a polypeptide with at least 80% amino acid identity to a polypeptide encoded by one of SEQ ID NOs:1-6, 8 or 33 to 38. Optionally, two vectors may be employed in place of the vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, e.g., a vector comprising a promoter operably linked to an influenza virus M1 cDNA linked to a transcription termination sequence and a vector comprising a promoter operably linked to an influenza virus M2 cDNA linked to a transcription termination sequence.

The invention includes the use of isolated and purified vectors or plasmids, which express or encode influenza virus proteins, or express or encode influenza vRNA, both native and recombinant vRNA. Preferably, the vectors comprise influenza cDNA, e.g., influenza A (e.g., any influenza A gene including any of the 15 HA or 9 NA subtypes), B or C DNA (see Chapters 45 and 46 of Fields *Virology* (Fields et al. (eds.), Lippincott-Raven Publ., Philadelphia, Pa. (1996), which are specifically incorporated by reference herein), although it is envisioned that the gene(s) of any organism may be employed in the vectors or methods of the invention. The cDNA may be in the sense or antisense orientation relative to the promoter. Thus, a vector of the invention may encode an influenza virus protein (sense) or vRNA (antisense). Any suitable promoter or transcription termination sequence may be employed to express a protein or peptide, e.g., a viral protein or peptide, a protein or peptide of a nonviral pathogen, or a therapeutic protein or peptide.

A composition of the invention may also comprise a gene or open reading frame of interest, e.g., a foreign gene encoding an immunogenic peptide or protein useful as a vaccine. Thus, another embodiment of the invention comprises a composition of the invention as described above in which one of the vectors is replaced with, or the composition further comprises, a vector comprising a promoter linked to 5' influenza virus sequences optionally including 5' influenza virus coding sequences or a portion thereof, linked to a desired nucleic acid sequence, e.g., a desired cDNA, linked to 3' influenza virus sequences optionally including 3' influ-

enza virus coding sequences or a portion thereof, linked to a transcription termination sequence. Preferably, the desired nucleic acid sequence such as a cDNA is in an antisense orientation. The introduction of such a composition to a host cell permissive for influenza virus replication results in recombinant virus comprising vRNA corresponding to sequences of the vector. The promoter in such a vector for vRNA production may be a RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T7 promoter, and a T3 promoter, and optionally the vector comprises a transcription termination sequence such as a RNA polymerase I transcription termination sequence, a RNA polymerase II transcription termination sequence, a RNA polymerase III transcription termination sequence, or a ribozyme. In one embodiment, the vector comprising the desired nucleic acid sequence comprises a cDNA of interest. The cDNA of interest, whether in a vector for vRNA or protein production, may encode an immunogenic epitope, such as an epitope useful in a cancer therapy or vaccine, or a peptide or polypeptide useful in gene therapy. When preparing virus, the vector or plasmid comprising the gene or cDNA of interest may substitute for a vector or plasmid for an influenza viral gene or may be in addition to vectors or plasmids for all influenza viral genes.

A plurality of the vectors of the invention may be physically linked or each vector may be present on an individual plasmid or other, e.g., linear, nucleic acid delivery vehicle.

The promoter or transcription termination sequence in a vRNA or virus protein expression vector may be the same or different relative to the promoter or any other vector. Preferably, the vector or plasmid which expresses influenza vRNA comprises a promoter suitable for expression in at least one particular host cell, e.g., avian or mammalian host cells such as canine, feline, equine, bovine, ovine, or primate cells including human cells, or preferably, for expression in more than one host.

In one embodiment, one or more vectors for vRNA production comprise a promoter including, but not limited to, a RNA polymerase I promoter, e.g., a human RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T7 promoter, or a T3 promoter. Preferred transcription termination sequences for the vRNA vectors include, but are not limited to, a RNA polymerase I transcription termination sequence, a RNA polymerase II transcription termination sequence, a RNA polymerase III transcription termination sequence, or a ribozyme. Ribozymes within the scope of the invention include, but are not limited to, tetrahymena ribozymes, RNase P, hammerhead ribozymes, hairpin ribozymes, hepatitis ribozyme, as well as synthetic ribozymes.

In one embodiment, at least one vector for vRNA comprises a RNA polymerase II promoter linked to a ribozyme sequence linked to viral coding sequences linked to another ribozyme sequences, optionally linked to a RNA polymerase II transcription termination sequence. In one embodiment, at least 2 and preferably more, e.g., 3, 4, 5, 6, 7 or 8, vectors for vRNA production comprise a RNA polymerase II promoter, a first ribozyme sequence, which is 5' to a sequence corresponding to viral sequences including viral coding sequences, which is 5' to a second ribozyme sequence, which is 5' to a transcription termination sequence. Each RNA polymerase II promoter in each vRNA vector may be the same or different as the RNA polymerase II promoter in any other vRNA vector. Similarly, each ribozyme sequence in each vRNA vector may be the same or different as the

ribozyme sequences in any other vRNA vector. In one embodiment, the ribozyme sequences in a single vector are not the same.

The invention also provides a method to prepare influenza virus. The method comprises contacting a cell with a plurality of the vectors of the invention, e.g., sequentially or simultaneously, for example, employing a composition of the invention, in an amount effective to yield infectious influenza virus. The invention also includes isolating virus from a cell contacted with the composition. Thus, the invention further provides isolated virus, as well as a host cell contacted with the composition or virus of the invention. In another embodiment, the invention includes contacting the cell with one or more vectors, either vRNA or protein production vectors, prior to other vectors, either vRNA or protein production vectors.

The methods of producing virus described herein, which do not require helper virus infection, are useful in viral mutagenesis studies, and in the production of vaccines (e.g., for AIDS, influenza, hepatitis B, hepatitis C, rhinovirus, filoviruses, malaria, herpes, and foot and mouth disease) and gene therapy vectors (e.g., for cancer, AIDS, adenosine deaminase, muscular dystrophy, ornithine transcarbamylase deficiency and central nervous system tumors). Thus, a virus for use in medical therapy (e.g., for a vaccine or gene therapy) is provided.

The invention also provides a method to immunize an individual against a pathogen, e.g., a bacteria, virus, or parasite, or a malignant tumor. The method comprises administering to the individual an amount of at least one isolated virus of the invention, optionally in combination with an adjuvant, effective to immunize the individual. The virus comprises vRNA comprising a polypeptide encoded by the pathogen or a tumor-specific polypeptide.

Also provided is a method to augment or increase the expression of an endogenous protein in a mammal having an indication or disease characterized by a decreased amount or a lack of the endogenous protein. The method comprises administering to the mammal an amount of an isolated virus of the invention effective to augment or increase the amount of the endogenous protein in the mammal. Preferably, the mammal is a human.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A and 1B. Titer of various influenza viruses.

FIG. 2. Schematic diagram of the N1 NAs used to generate H5N1/PR8 reassortant viruses by reverse genetics. VN1203fill contains a 20 amino acid (aa) insertion derived from the N1 of the H5N1 precursor strain, GsGd96. VN1203fill.N2 contains, in addition to 20 aa from GsGd96 NA, a 14-aa insertion from N2 NA, resulting in a 34-aa insertion into the stalk of VN1203 NA. VN1202fill.N2N9 contains, in addition to 20 aa from GsGd96 NA and 14 aa from N2 NA, a 14-aa insertion from N9 NA, resulting in a 48-aa insertion into the stalk of VN1203. The predicted total length of the stalk region of each NA is given beneath each molecule.

FIG. 3. Growth of H5N1/PR8 reassortant viruses in chicken embryonated eggs. The titers of the reassortant viruses containing avirulent-form VN1203 HA and either homologous NA (VN1203) or heterologous NAs (VN1203fill, VN1203fill.N2, HK213, or PR8) with a PR8 background were compared by plaque titration with MDCK cells. The titer of wild-type (egg-adapted) PR8 also is

included for comparison. The data are reported as mean titers and standard deviations for 3 eggs inoculated with each virus.

FIG. 4. Growth kinetics of H5N1 reassortant viruses in chicken embryonated eggs. We inoculated eggs with the same amounts (10^4 EID₅₀) of viruses containing PR8 NA (PR8), VN1203 NA (VN1203), or VN1203fill NA (VN1203fill). Mean HA titers and standard deviations for 3 eggs inoculated with each virus were determined at the indicated time points.

FIG. 5. Virus elution from chicken erythrocytes. Twofold dilutions of each virus (HA titers of 1:1024) containing VN1203 NA with a different stalk length, or PR8 NA, were incubated with chicken erythrocytes in a microtiter plate at 4° C. for 1 hour. The plate was then stored at 37° C. and reductions in the HA titer were recorded for 8 hours.

FIG. 6. Growth comparison of H5N1/PR8 reassortant viruses in chicken embryonated eggs. Viral titers of the 6:2 and 7:1 reassortant viruses, including the WHO-recommended NIBRG-14 strain (a VN1194/PR8 6:2 reassortant virus) were compared by plaque titration with MDCK cells. Mean titers and standard deviations of 3 eggs inoculated with each virus are shown. Thus, replacing just the NA of H5N1 viruses with the NA of PR8 may improve titers in eggs.

FIG. 7. Growth of reassortant H5N1 viruses possessing PR8(UW) or PR8(Cambridge) internal genes in chicken embryonated eggs. Asterisks indicate a significant ($p < 0.05$, Student t-test) reduction in infectivity compared to PR8(UW)/1194.

FIG. 8. The effect of the M and NS genes on the growth of viruses in chicken embryonated eggs. The asterisk indicates a significant ($p < 0.05$, Student t-test) increase in infectivity compared to PR8(UW)/1194.

FIG. 9. Growth of PR8(UW)/1194 and NBRG-14 virus in MDCK cells.

FIG. 10. Identification of a gene segment responsible for the enhanced growth of PR8(UW)/1194 relative to NIBRG-14 in MDCK cells.

FIG. 11. Identification of the amino acid in PB2 responsible for the high growth rate of the vaccine seed virus in MDCK cells.

FIG. 12. Growth rates in MDCK cells of reassortants with different HA, NA, and NS genes. The asterisk indicates significantly better virus growth compared to that of PR8(UW)/1194. Double asterisks indicate significantly better growth rates compared to viruses expressing PR8(UW) NS.

FIG. 13. Growth in MDCK cells of the H5N1 vaccine seed virus containing a heterologous NS segment.

FIG. 14. Schematic of the genotype of an H5N1 vaccine seed virus with high growth capacity in chicken embryonated eggs or MDCK cells.

FIG. 15A-15C. Nucleotide sequence for PR8(Cambridge) genes (SEQ ID NOs:33-38).

DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used herein, the terms "isolated and/or purified" refer to in vitro preparation, isolation and/or purification of a vector, plasmid or virus of the invention, so that it is not associated with in vivo substances, or is substantially purified from in vitro substances. An isolated virus preparation

is generally obtained by in vitro culture and propagation, and/or via passage in eggs, and is substantially free from other infectious agents.

As used herein, "substantially free" means below the level of detection for a particular infectious agent using standard detection methods for that agent.

A "recombinant" virus is one which has been manipulated in vitro, e.g., using recombinant DNA techniques, to introduce changes to the viral genome. Reassortant viruses can be prepared by recombinant or nonrecombinant techniques.

As used herein, the term "recombinant nucleic acid" or "recombinant DNA sequence or segment" refers to a nucleic acid, e.g., to DNA, that has been derived or isolated from a source, that may be subsequently chemically altered in vitro, so that its sequence is not naturally occurring, or corresponds to naturally occurring sequences that are not positioned as they would be positioned in the native genome. An example of DNA "derived" from a source, would be a DNA sequence that is identified as a useful fragment, and which is then chemically synthesized in essentially pure form. An example of such DNA "isolated" from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering.

As used herein, a "heterologous" influenza virus gene or gene segment is from an influenza virus source that is different than a majority of the other influenza viral genes or gene segments in a reassortant influenza virus.

Influenza Virus Replication

Influenza A viruses possess a genome of eight single-stranded negative-sense viral RNAs (vRNAs) that encode a total of ten proteins. The influenza virus life cycle begins with binding of the hemagglutinin (HA) to sialic acid-containing receptors on the surface of the host cell, followed by receptor-mediated endocytosis. The low pH in late endosomes triggers a conformational shift in the HA, thereby exposing the N-terminus of the HA2 subunit (the so-called fusion peptide). The fusion peptide initiates the fusion of the viral and endosomal membrane, and the matrix protein (M1) and RNP complexes are released into the cytoplasm. RNPs consist of the nucleoprotein (NP), which encapsidates vRNA, and the viral polymerase complex, which is formed by the PA, PB1, and PB2 proteins. RNPs are transported into the nucleus, where transcription and replication take place. The RNA polymerase complex catalyzes three different reactions: synthesis of an mRNA with a 5' cap and 3' polyA structure, of a full-length complementary RNA (cRNA), and of genomic vRNA using the cDNA as a template. Newly synthesized vRNAs, NP, and polymerase proteins are then assembled into RNPs, exported from the nucleus, and transported to the plasma membrane, where budding of progeny virus particles occurs. The neuraminidase (NA) protein plays a crucial role late in infection by removing sialic acid from sialyloligosaccharides, thus releasing newly assembled virions from the cell surface and preventing the self aggregation of virus particles. Although virus assembly involves protein-protein and protein-vRNA interactions, the nature of these interactions is largely unknown.

Although influenza B and C viruses are structurally and functionally similar to influenza A virus, there are some differences. For example, influenza B virus does not have a M2 protein. Similarly, influenza C virus does not have a M2 protein.

Cell Lines and Influenza Viruses that can be Used in the Present Invention

According to the present invention, any cell which supports efficient replication of influenza virus can be employed in the invention, including mutant cells which express reduced or decreased levels of one or more sialic acids which are receptors for influenza virus. Viruses obtained by the methods can be made into a reassortant virus.

Preferably, the cells are WHO certified, or certifiable, continuous cell lines. The requirements for certifying such cell lines include characterization with respect to at least one of genealogy, growth characteristics, immunological markers, virus susceptibility tumorigenicity and storage conditions, as well as by testing in animals, eggs, and cell culture. Such characterization is used to confirm that the cells are free from detectable adventitious agents. In some countries, karyology may also be required. In addition, tumorigenicity is preferably tested in cells that are at the same passage level as those used for vaccine production. The virus is preferably purified by a process that has been shown to give consistent results, before being inactivated or attenuated for vaccine production (see, e.g., World Health Organization, 1982).

It is preferred to establish a complete characterization of the cell lines to be used, so that appropriate tests for purity of the final product can be included. Data that can be used for the characterization of a cell to be used in the present invention includes (a) information on its origin, derivation, and passage history; (b) information on its growth and morphological characteristics; (c) results of tests of adventitious agents; (d) distinguishing features, such as biochemical, immunological, and cytogenetic patterns which allow the cells to be clearly recognized among other cell lines; and (e) results of tests for tumorigenicity. Preferably, the passage level, or population doubling, of the host cell used is as low as possible.

It is preferred that the virus produced in the cell is highly purified prior to vaccine or gene therapy formulation. Generally, the purification procedures will result in the extensive removal of cellular DNA, other cellular components, and adventitious agents. Procedures that extensively degrade or denature DNA can also be used. See, e.g., Mizrahi, 1990.

Vaccines

A vaccine of the invention may comprise immunogenic proteins including glycoproteins of any pathogen, e.g., an immunogenic protein from one or more bacteria, viruses, yeast or fungi. Thus, in one embodiment, the influenza viruses of the invention may be vaccine vectors for influenza virus or other viral pathogens including but not limited to lentiviruses such as HIV, hepatitis B virus, hepatitis C virus, herpes viruses such as CMV or HSV or foot and mouth disease virus.

A complete virion vaccine is concentrated by ultrafiltration and then purified by zonal centrifugation or by chromatography. It is inactivated before or after purification using formalin or beta-propiolactone, for instance.

A subunit vaccine comprises purified glycoproteins. Such a vaccine may be prepared as follows: using viral suspensions fragmented by treatment with detergent, the surface antigens are purified, by ultracentrifugation for example. The subunit vaccines thus contain mainly HA protein, and also NA. The detergent used may be cationic detergent for example, such as hexadecyl trimethyl ammonium bromide (Bachmeyer, 1975), an anionic detergent such as ammonium deoxycholate (Laver & Webster, 1976); or a nonionic detergent such as that commercialized under the name TRITON X100. The hemagglutinin may also be isolated after treat-

ment of the virions with a protease such as bromelin, then purified by a method such as that described by Grand and Skehel (1972).

A split vaccine comprises virions which have been subjected to treatment with agents that dissolve lipids. A split vaccine can be prepared as follows: an aqueous suspension of the purified virus obtained as above, inactivated or not, is treated, under stirring, by lipid solvents such as ethyl ether or chloroform, associated with detergents. The dissolution of the viral envelope lipids results in fragmentation of the viral particles. The aqueous phase is recuperated containing the split vaccine, constituted mainly of hemagglutinin and neuraminidase with their original lipid environment removed, and the core or its degradation products. Then the residual infectious particles are inactivated if this has not already been done.

Inactivated Vaccines.

Inactivated influenza virus vaccines of the invention are provided by inactivating replicated virus of the invention using known methods, such as, but not limited to, formalin or β -propiolactone treatment. Inactivated vaccine types that can be used in the invention can include whole-virus (WV) vaccines or subvirion (SV) (split) vaccines. The WV vaccine contains intact, inactivated virus, while the SV vaccine contains purified virus disrupted with detergents that solubilize the lipid-containing viral envelope, followed by chemical inactivation of residual virus.

In addition, vaccines that can be used include those containing the isolated HA and NA surface proteins, which are referred to as surface antigen or subunit vaccines. In general, the responses to SV and surface antigen (i.e., purified HA or NA) vaccines are similar. An experimental inactivated WV vaccine containing an NA antigen immunologically related to the epidemic virus and an unrelated HA appears to be less effective than conventional vaccines (Ogra et al., 1977). Inactivated vaccines containing both relevant surface antigens are preferred.

Live Attenuated Virus Vaccines.

Live, attenuated influenza virus vaccines, can also be used for preventing or treating influenza virus infection, according to known method steps. Attenuation is preferably achieved in a single step by transfer of attenuated genes from an attenuated donor virus to a replicated isolate or reassorted virus according to known methods (see, e.g., Murphy, 1993). Since resistance to influenza A virus is mediated by the development of an immune response to the HA and NA glycoproteins, the genes coding for these surface antigens must come from the reassorted viruses or high growth clinical isolates. The attenuated genes are derived from the attenuated parent. In this approach, genes that confer attenuation preferably do not code for the HA and NA glycoproteins. Otherwise, these genes could not be transferred to reassortants bearing the surface antigens of the clinical virus isolate.

Many donor viruses have been evaluated for their ability to reproducibly attenuate influenza viruses. As a non-limiting example, the A/Ann Arbor(AA)/6/60 (H2N2) cold adapted (ca) donor virus can be used for attenuated vaccine production (see, e.g., Edwards, 1994; Murphy, 1993). Additionally, live, attenuated reassortant virus vaccines can be generated by mating the ca donor virus with a virulent replicated virus of the invention. Reassortant progeny are then selected at 25° C., (restrictive for replication of virulent virus), in the presence of an H2N2 antiserum, which inhibits replication of the viruses bearing the surface antigens of the attenuated A/AA/6/60 (H2N2) ca donor virus.

A large series of H1N1 and H3N2 reassortants have been evaluated in humans and found to be satisfactorily: (a) infectious, (b) attenuated for seronegative children and immunologically primed adults, (c) immunogenic and (d) genetically stable. The immunogenicity of the ca reassortants parallels their level of replication. Thus, the acquisition of the six transferable genes of the ca donor virus by new wild-type viruses has reproducibly attenuated these viruses for use in vaccinating susceptible adults and children.

Other attenuating mutations can be introduced into influenza virus genes by site-directed mutagenesis to rescue infectious viruses bearing these mutant genes. Attenuating mutations can be introduced into non-coding regions of the genome, as well as into coding regions. Such attenuating mutations can also be introduced into genes other than the HA or NA, e.g., the PB2 polymerase gene (Subbarao et al., 1993). Thus, new donor viruses can also be generated bearing attenuating mutations introduced by site-directed mutagenesis, and such new donor viruses can be used in the reduction of live attenuated reassortants H1N1 and H3N2 vaccine candidates in a manner analogous to that described above for the A/AA/6/60 ca donor virus. Similarly, other known and suitable attenuated donor strains can be reassorted with influenza virus of the invention to obtain attenuated vaccines suitable for use in the vaccination of mammals (Enami et al., 1990; Muster et al., 1991; Subbarao et al., 1993).

It is preferred that such attenuated viruses maintain the genes from the virus that encode antigenic determinants substantially similar to those of the original clinical isolates. This is because the purpose of the attenuated vaccine is to provide substantially the same antigenicity as the original clinical isolate of the virus, while at the same time lacking infectivity to the degree that the vaccine causes minimal change of inducing a serious pathogenic condition in the vaccinated mammal.

The virus can thus be attenuated or inactivated, formulated and administered, according to known methods, as a vaccine to induce an immune response in an animal, e.g., a mammal. Methods are well-known in the art for determining whether such attenuated or inactivated vaccines have maintained similar antigenicity to that of the clinical isolate or high growth strain derived therefrom. Such known methods include the use of antisera or antibodies to eliminate viruses expressing antigenic determinants of the donor virus; chemical selection (e.g., amantadine or rimantidine); HA and NA activity and inhibition; and DNA screening (such as probe hybridization or PCR) to confirm that donor genes encoding the antigenic determinants (e.g., HA or NA genes) are not present in the attenuated viruses. See, e.g., Robertson et al., 1988; Kilbourne, 1969; Aymard-Henry et al., 1985; Robertson et al., 1992.

Pharmaceutical Compositions

Pharmaceutical compositions of the present invention, suitable for inoculation or for parenteral or oral administration, comprise attenuated or inactivated influenza viruses, optionally further comprising sterile aqueous or non-aqueous solutions, suspensions, and emulsions. The compositions can further comprise auxiliary agents or excipients, as known in the art. See, e.g., Berkow et al., 1987; *Avery's Drug Treatment*, 1987; Osol, 1980; Katzung, 1992. The composition of the invention is generally presented in the form of individual doses (unit doses).

Conventional vaccines generally contain about 0.1 to 200 μ g, preferably 10 to 15 μ g, of hemagglutinin from each of the strains entering into their composition. The vaccine forming the main constituent of the vaccine composition of

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the invention may comprise a virus of type A, B or C, or any combination thereof, for example, at least two of the three types, at least two of different subtypes, at least two of the same type, at least two of the same subtype, or a different isolate(s) or reassortant(s). Human influenza virus type A includes H1N1, H2N2 and H3N2 subtypes.

Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and/or emulsions, which may contain auxiliary agents or excipients known in the art. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents. See, e.g., Berkow et al., 1992; Avery's, 1987; Osol, 1980; and Katzung, 1992.

When a composition of the present invention is used for administration to an individual, it can further comprise salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. For vaccines, adjuvants, substances which can augment a specific immune response, can be used. Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the organism being immunized. Examples of materials suitable for use in vaccine compositions are provided in Osol (1980).

Heterogeneity in a vaccine may be provided by mixing replicated influenza viruses for at least two influenza virus strains, such as 2-50 strains or any range or value therein. Influenza A or B virus strains having a modern antigenic composition are preferred. According to the present invention, vaccines can be provided for variations in a single strain of an influenza virus, using techniques known in the art.

A pharmaceutical composition according to the present invention may further or additionally comprise at least one chemotherapeutic compound, for example, for gene therapy, immunosuppressants, anti-inflammatory agents or immune enhancers, and for vaccines, chemotherapeutics including, but not limited to, gamma globulin, amantadine, guanidine, hydroxybenzimidazole, interferon- α , interferon- β , interferon- γ , tumor necrosis factor-alpha, thiosemicarbazones, methisazone, rifampin, ribavirin, a pyrimidine analog, a purine analog, foscarnet, phosphonoacetic acid, acyclovir, dideoxynucleosides, a protease inhibitor, or ganciclovir. See, e.g., Katzung (1992), and the references cited therein on pages 798-800 and 680-681, respectively.

The composition can also contain variable but small quantities of endotoxin-free formaldehyde, and preservatives, which have been found safe and not contributing to undesirable effects in the organism to which the composition is administered.

Pharmaceutical Purposes

The administration of the composition (or the antisera that it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compositions of the invention which are vaccines, are provided before any symptom of a pathogen infection becomes manifest. The prophylactic administration of the composition serves to

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prevent or attenuate any subsequent infection. When provided prophylactically, the gene therapy compositions of the invention, are provided before any symptom of a disease becomes manifest. The prophylactic administration of the composition serves to prevent or attenuate one or more symptoms associated with the disease.

When provided therapeutically, an attenuated or inactivated viral vaccine is provided upon the detection of a symptom of actual infection. The therapeutic administration of the compound(s) serves to attenuate any actual infection. See, e.g., Berkow et al., 1992; Avery, 1987; and Katzung, 1992. When provided therapeutically, a gene therapy composition is provided upon the detection of a symptom or indication of the disease. The therapeutic administration of the compound(s) serves to attenuate a symptom or indication of that disease.

Thus, an attenuated or inactivated vaccine composition of the present invention may thus be provided either before the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection. Similarly, for gene therapy, the composition may be provided before any symptom of a disorder or disease is manifested or after one or more symptoms are detected.

A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. A composition of the present invention is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient, e.g., enhances at least one primary or secondary humoral or cellular immune response against at least one strain of an infectious influenza virus.

The "protection" provided need not be absolute, i.e., the influenza infection need not be totally prevented or eradicated, if there is a statistically significant improvement compared with a control population or set of patients. Protection may be limited to mitigating the severity or rapidity of onset of symptoms of the influenza virus infection.

Pharmaceutical Administration

A composition of the present invention may confer resistance to one or more pathogens, e.g., one or more influenza virus strains, by either passive immunization or active immunization. In active immunization, an inactivated or attenuated live vaccine composition is administered prophylactically to a host (e.g., a mammal), and the host's immune response to the administration protects against infection and/or disease. For passive immunization, the elicited antisera can be recovered and administered to a recipient suspected of having an infection caused by at least one influenza virus strain. A gene therapy composition of the present invention may yield prophylactic or therapeutic levels of the desired gene product by active immunization.

In one embodiment, the vaccine is provided to a mammalian female (at or prior to pregnancy or parturition), under conditions of time and amount sufficient to cause the production of an immune response which serves to protect both the female and the fetus or newborn (via passive incorporation of the antibodies across the placenta or in the mother's milk).

The present invention thus includes methods for preventing or attenuating a disorder or disease, e.g., an infection by at least one strain of pathogen. As used herein, a vaccine is said to prevent or attenuate a disease if its administration results either in the total or partial attenuation (i.e., suppression) of a symptom or condition of the disease, or in the total

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or partial immunity of the individual to the disease. As used herein, a gene therapy composition is said to prevent or attenuate a disease if its administration results either in the total or partial attenuation (i.e., suppression) of a symptom or condition of the disease, or in the total or partial immunity of the individual to the disease.

At least one inactivated or attenuated influenza virus, or composition thereof, of the present invention may be administered by any means that achieve the intended purposes, using a pharmaceutical composition as previously described.

For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, oral or transdermal routes. Parenteral administration can be by bolus injection or by gradual perfusion over time. A preferred mode of using a pharmaceutical composition of the present invention is by intramuscular or subcutaneous application. See, e.g., Berkow et al., 1992; Avery, 1987; and Katzung, 1992.

A typical regimen for preventing, suppressing, or treating an influenza virus related pathology, comprises administration of an effective amount of a vaccine composition as described herein, administered as a single treatment, or repeated as enhancing or booster dosages, over a period up to and including between one week and about 24 months, or any range or value therein.

According to the present invention, an "effective amount" of a composition is one that is sufficient to achieve a desired biological effect. It is understood that the effective dosage will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect wanted. The ranges of effective doses provided below are not intended to limit the invention and represent preferred dose ranges. However, the most preferred dosage will be tailored to the individual subject, as is understood and determinable by one of skill in the art. See, e.g., Berkow et al., 1992; Avery's, 1987; and Katzung, 1992.

The dosage of an attenuated virus vaccine for a mammalian (e.g., human) or avian adult organism can be from about 10^3 - 10^7 plaque forming units (PFU)/kg, or any range or value therein. The dose of inactivated vaccine can range from about 0.1 to 200, e.g., 50 µg of hemagglutinin protein. However, the dosage should be a safe and effective amount as determined by conventional methods, using existing vaccines as a starting point.

The dosage of immunoreactive HA in each dose of replicated virus vaccine can be standardized to contain a suitable amount, e.g., 1-50 µg or any range or value therein, or the amount recommended by the U.S. Public Health Service (PHS), which is usually 15 µg, per component for older children \geq 3 years of age, and 7.5 µg per component for older children $<$ 3 years of age. The quantity of NA can also be standardized, however, this glycoprotein can be labile during the processor purification and storage (Kendal et al., 1980). Each 0.5-ml dose of vaccine preferably contains approximately 1-50 billion virus particles, and preferably 10 billion particles.

The invention will be further described by the following nonlimiting examples.

Example 1

To develop a reverse genetics system for influenza A/Puerto Rico/8/34, viral RNA was extracted from the allantoic fluid of A/Puerto Rico/8/34 (H1N1), Madison high grower variant (PR8HG), using RNeasy Mini kit (Qiagen)

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according to the manufacturer's protocol. cDNA was synthesized using MMLV-RTase (Promega) and Uni12 primer. The cDNAs were amplified overnight by PCR using the following:

Primer Sets

PB1:

Ba PB1-1 and PB1-1735R (front fragment) and PB1-903 and Ba-PB1-2341R (rear fragment)

Ba-PB 1-1

(SEQ ID NO: 9)

CACACACGGTCTCCGGGAGCGAAAGCAGGCA

173PB1-1735R

(SEQ ID NO: 28)

GGGTTTGTATTTGTGTGCACC

233PB1-903

(SEQ ID NO: 10)

CCAGGACACTGAAATTTCTTTCAC

Ba-PB1-2341R

(SEQ ID NO: 11)

CACACAGGTCTCCTATTAGTAGAAACAAGGCATTT

PB2:

Ba PB2-1 and B2 1260R (front fragment) and WSN PB2 seq-2 and Ba-PB2-2341R (rear fragment)

Ba-PB2-1

(SEQ ID NO: 12)

CACACAGGTCTCCGGGAGCGAAAGCAGGTC

B2 1260R

(SEQ ID NO: 13)

CACACACGTCTCCATCATACAATCCTCTTG

WSN PB2 seq-2

(SEQ ID NO: 14)

CTCCTCTGATGGTGGCATACT

Ba-PB2-2341R

(SEQ ID NO: 15)

CACACAGGTCTCCTATTAGTAGAAACAAGGTCGTTT

PA:

Bm-PA-1

(SEQ ID NO: 16)

CACACACGTCTCCGGGAGCGAAAGCAGGTAC

Bm-PA-2233R

(SEQ ID NO: 17)

CACACACGTCTCCTATTAGTAGAAACAAGGTACTT

HA:

Bm-HA-1:

(SEQ ID NO: 18)

CACACACGTCTCCGGGAGCGAAAGCAGGGG

Bm-NS-890R:

(SEQ ID NO: 19)

CACACACGTCTCCTATTAGTAGAAACAAGGGTGTITT

NP:

Bm-NP-1

(SEQ ID NO: 20)

CACACACGTCTCCGGGAGCGAAAGCAGGGTA

Bm-NP-1565R

(SEQ ID NO: 21)

CACACACGTCTCCTATTAGTAGAAACAAGGGTATTTT

NA:

Ba-NA-1:

(SEQ ID NO: 22)

CACACAGGTCTCCGGGAGCGAAAGCAGGAGT

Ba-NA-1413R:

(SEQ ID NO: 23)

CACACAGGTCTGGTATTAGTAGAAACAAGGATTTTTT

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M:
Bm-M-1 (SEQ ID NO: 24)
CACACACGTCCTCCGGGAGCAAAAGCAGGTAG

Bm-M-1027R (SEQ ID NO: 25)
CACACACGTCCTCTATTAGTAGAAACAAGGTAGTTTT

NS:
Bm-NS-1 (SEQ ID NO: 26)
CACACACGTCCTCCGGGAGCAAAAGCAGGGTG

Bm-NS-890R (SEQ ID NO: 27)
CACACACGTCCTCTATTAGTAGAAACAAGGGTGT
DNA polymerase: pfu Native DNA
polymerase (Stratagene)

The PCR products were separated by gel electrophoresis and extracted from the agarose gel using a gel extraction kit (Qiagen). The extracted genes were ligated into pT7Blue blunt vector (Novagen) using a Takara ligation kit ver. II (Takara). After 5 hours, the ligated genes were transformed into JM109 (PB2, M, and NS genes) or DH5alpha (PA, PB1, and NP). Six colonies for each gene were cultured in TB for 8 hours. The plasmids were extracted from the bacteria culture, and four clones per gene were sequenced.

The PA, NP, M, and NS genes in pT7Blue were excised by Bsm BI enzyme (New England Biolabs). The PB1 gene was excised by Bsa I (New England Biolabs). The excised genes were ligated overnight with pPolIR vector which contains the human RNA polymerase I promoter and the mouse RNA polymerase I terminator which had been digested with Bsm BI. The front fragment of the PB2 gene in pT7Blue was excised by Bsr GI (New England Biolabs) and Bam HI (Roche), and the rear fragment was excised by Bsr GI (New England Biolabs) and Spe I (Roche). The excised fragments were mixed and digested by Bsa I. After 6 hours, the digested genes were purified using a PCR purification kit (Qiagen) and ligated overnight between the Bsm BI sites of the pPolIR vector.

The ligated PB1, PA, NP, M, and NS-pPolIR genes were used to transform JM109 (M and NS genes) or DH5alpha (PB1, PA and NP genes) overnight. The colonies of transformed bacteria were cultured in LB overnight. The ligated PB2-pPolIR was used to transform JM109 overnight.

The plasmids were extracted from the bacterial cultures and gene inserts were confirmed by enzyme digestion. The colonies of bacteria transformed by PB2-PolIR were cultured in LB for 8 hours. The plasmids were then extracted and the gene insertion was confirmed by enzyme digestion. All pPol constructs were sequenced to ensure that they did not contain unwanted mutations.

The pPolIR constructs for PR8HG were transfected into 293T human embryonic kidney cells with A/WSN/33 (WSN)-HA and NA, A/Hong Kong/483/97(HK)-HAavir and NA, or A/Kawasaki/01(Kawasaki)-HA and NA PolI constructs and four protein-expression constructs for the polymerase proteins and NP of A/WSN/33. The supernatants from transfected 293T cells were serially diluted (undiluted to 10^{-7}) and infected into the allantoic cavities of 9-day-old embryonated chicken eggs. The allantoic fluids of the infected eggs were harvested and their virus titers tested by HA assay (Table 1).

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TABLE 1

5	Virus pos- sessing PR8 genes together with the	HA titer (HAU/ml) of allantoic fluid from eggs inoculated with 293T supernatants diluted at:								
		following HA and NA genes	undi- luted	10 ⁻¹	10 ⁻²	10 ⁻³	10 ⁻⁴	10 ⁻⁵	10 ⁻⁶	10 ⁻⁷
10	WSN-HA NA		<1	<1	200	<1	<1	<1	<1	<1
	HK-HAavir		100	<1	<1	<1	<1	<1	<1	<1
	NA									
	Kawasaki- HA NA		<1	<1	<1	<1	<1	<1	<1	<1

HA-positive samples (virus with WSN-HA NA at 10^{-2} and virus with HK-HAavir NA at undiluted) were diluted serially from 10^{-2} to 10^{-8} and 100 ul of each dilution was infected into embryonated chicken eggs. The allantoic fluids of the infected eggs were harvested and their virus titers tested by HA assay (Table 2). The 50% egg infectious dose (EID₅₀) of A/Puerto Rico/8/34 (H1N1) prepared from plasmids was $10^{10.33}$ /ml, and the HA titer was 1:3200.

A recombinant virus having the HA and NA genes from A/Hong Kong/213/2003 (H5N1) and the remainder of the type A influenza virus genes from PR8HG was prepared. The titer of the recombinant virus was $10^{10.67}$ EID₅₀/ml, and the HA titer was 1:1600.

TABLE 2

Virus pos- sessing PR8 genes together with the following HA	HA titer (HAU/ml) in each dilution						
	10 ⁻²	10 ⁻³	10 ⁻⁴	10 ⁻⁵	10 ⁻⁶	10 ⁻⁷	10 ⁻⁸
WSN-HA NA	160	40	40	320	40	640	<1
HK-HAavir NA	400	800	400	400	400	800	<1

Sequences of PR8 Genes:

PA (SEQ ID NO: 1)
AGCGAAAGCA GGTACTGATC CAAAATGGAA GATTTTGTGC
GACAATGCTT CAATCCGATG ATTGTCGAGC TTGCGGAAAA
AACAAATGAAA GAGTATGGGG AGGACCTGAA AATCGAAACA
AACAAATTTG CAGCAATATG CACTCACTTG GAAGTATGCT
TCATGTATTC AGATTTTCAC TTCATCAATG AGCAAGCGCA
GTCAATAATC GTAGAACTTG GTGATCCAAA TGCACTTTTG
AAGCACAGAT TTGAAATAAT CGAGGGAAGA GATCGCACAA
TGGCCTGGAC AGTAGTAAAC AGTATTTGCA ACACTACAGG
GGCTGAGAAA CCAAAGTTTC TACCAGATTT GTATGATTAC
AAGGAGAATA GATTCATCGA AATTGGAGTA ACAAGGAGAG
AAGTTCACAT ATACTATCTG GAAAAGGCCA ATAAATTA
ATCTGAGAAA ACACACATCC ACATTTTCTC GTTCACTGGG
GAAGAAATGG CCACAAAGGC AGACTACACT CTCGATGAAG
AAAGCAGGGC TAGGATCAAA ACCAGACTAT TCACCATAAG

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ACAAGAAATG GCCAGCAGAG GCCTCTGGGA TTCCTTTCGT
 CAGTCCGAGA GAGGAGAAGA GACAATTGAA GAAAGGTTTG
 AAATCACAGG AACAAATGCGC AAGCTTGCCG ACCAAAGTCT
 CCCGCCGAAC TTCTCCAGCC TTGAAAATTT TAGAGCCTAT
 GTGGATGGAT TCGAACCAGAA CGGCTACATT GAGGGCAAGC
 TGTCTCAAAT GTCCAAAGAA GTAAATGCTA GAATTGAACC
 TTTTTTGAAA ACAACACCAC GACCACTTAG ACTTCCGAAT
 GGGCCTCCCT GTTCTCAGCG GTCCAAATTC CTGCTGATGG
 ATGCCTTAAA ATTAAGCATT GAGGACCCAA GTCATGAAGG
 AGAGGGAATA CCGCTATATG ATGCAATCAA ATGCATGAGA
 ACATTCTTTG GATGGAAGGA ACCCAATGTT GTTAAACCAC
 ACGAAAAGGG AATAAATCCA AATTATCTTC TGTCATGGAA
 GCAAGTACTG GCAGAACTGC AGGACATTGA GAATGAGGAG
 AAAATTCCAA AGACTAAAA TATGAAGAAA ACAAGTCAGC
 TAAAGTGGCG ACTTGGTGAG AACATGGCAC CAGAAAAGGT
 AGACTTTGAC GACTGTAAAG ATGTAGGTGA TTTGAAGCAA
 TATGATAGTG ATGAACCAGA ATTGAGGTGC CTGCAAGTT
 GGATTCAAGAA TGAGTTTAAAC AAGGCATGCG AACTGACAGA
 TTCAAGCTGG ATAGAGCTCG ATGAGATTGG AGAAGATGTG
 GCTCCAATTG AACACATTGC AAGCATGAGA AGGAATTATT
 TCACATCAGA GGTGTCTCAC TGCAGAGCCA CAGAATACAT
 AATGAAGGGA GTGTACATCA ATACTGCCCTT GCTTAATGCA
 TCTTGTGCG CAATGGATGA TTTCCAATTA ATTCCAATGA
 TAAGCAAGTG TAGAACTAAG GAGGGAAGGC GAAAGACCAA
 CTTGTATGGT TTCATCATAA AAGGAAGATC CCACTTAAGG
 AATGACACCG ACGTGGTAAA CTTTGTGAGC ATGGAGTTTT
 CTCTCACTGA CCCAAGACTT GAACCACATA AATGGGAGAA
 GTACTGTGTT CTTGAGATAG GAGATATGCT TATAAGAAGT
 GCCATAGGCC AGGTTTCAAG GCCCATGTTC TTGTATGTGA
 GAACAAATGG AACCTCAAAA ATTAAATGA AATGGGGAAT
 GGAGATGAGG CGTTGCCTCC TCCAGTCACT TCAACAAATT
 GAGAGTATGA TTGAAGCTGA GTCCTCTGTC AAAGAGAAAG
 ACATGACCAA AGAGTTCTTT GAGAACAAAT CAGAAACATG
 GCCCATTTGA GAGTCCCCCA AAGGAGTGGG GGAAGTTCC
 ATTGGAAGG TCTGCAGGAC TTTATTAGCA AAGTCGGTAT
 TCAACAGCTT GTATGCATCT CCACAAC TAGAAGATTTTC
 AGCTGAATCA AGAAAACATGC TTCTTATCGT TCAGGCTCTT
 AGGGACAACC TGGAACCTGG GACCTTTGAT CTGCGGGGCG
 TATATGAAGC AATTGAGGAG TGCCTGATTA ATGATCCCTG
 GGTTTTGCTT AATGCTTCTT GGTTCAACTC CTTCTTACA
 CATGCATTGA GTTAGTTGTG GCAGTGCTAC TATTTGCTAT

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CCATACTGTC CAAAAAAGTA CCTTGTCTTCT ACT
 PB1
 5 AGCGAAAGCA GGCAAAACCAT TTGAATGGAT GTCAATCCGA (SEQ ID NO: 2)
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 CACAACTTTC CCTTATACTG GAGACCCCTC TTACAGCCAT
 10 GGGACAGGAA CAGGATACAC CATGGATACT GTCAACAGGA
 CACATCAGTA CTCAGAAAAG GGAAGATGGA CAACAAACAC
 CGAAACTGGA GCACCGCAAC TCAACCCGAT TGATGGGCCA
 15 CTGCCAGAAG ACAATGAACC AAGTGTTTAT GCCCAACAG
 ATTGTGTATT GGAGGCGATG GCTTTCCTTG AGGAATCCCA
 TCCTGGTATT TTTGAAAAC CGTGTATTGA AACGATGGAG
 20 GTTGTTGAGC AAACACGAGT AGACAAGCTG ACACAAGGCC
 GACAGACCTA TGACTGGACT CTAAATAGAA ACCAACCTGC
 TGCAACAGCA TTGGCCAACA CAATAGAAGT GTTCAGATCA
 25 AATGGCCTCA CGGCCAATGA GTCTGGAAGG CTCATAGACT
 TCCTTAAGGA TGTAATGGAG TCAATGAACA AAGAAGAAAT
 GGGGATCACA ACTCATTTTC AGAGAAAGAG ACGGGTGAGA
 30 GACAATATGA CTAAGAAAAT GATAACACAG AGAACAATGG
 GTAAAAAGAA GCAGAGATTG AACAAAAGGA GTTATCTAAT
 TAGAGCATTG ACCCTGAACA CAATGACCAA AGATGCTGAG
 35 AGAGGGAAGC TAAAACGGAG AGCAATTGCA ACCCCAGGGA
 TGCAATAAG GGGGTTTGTA TACTTTGTG AGACACTGGC
 AAGGAGTATA TGTGAGAAAC TTGAACAATC AGGGTTGCCA
 40 GTTGGAGGCA ATGAGAAGAA AGCAAAGTTG GCAATGTTG
 TAAGGAAGAT GATGACCAAT TCTCAGGACA CCGAAGTTTC
 TTTCACCATC ACTGGAGATA ACACCAAATG GAACGAAAAT
 45 CAGAATCCTC GGATGTTTTT GGCCATGATC ACATATATGA
 CCAGAAATCA GCCCGAATGG TTCAGAAATG TTCTAAGTAT
 TGCTCCAATA ATGTTCTCAA ACAAATGGC GAGACTGGGA
 50 AAAGGGTATA TGTTTGAGAG CAAGAGTATG AAAGTTAGAA
 CTCAAATACC TGCAGAAATG CTAGCAAGCA TCGATTTGAA
 ATATTTCAAT GATTCAACAA GAAAGAAGAT TGAAAAATC
 CGACCGCTCT TAATAGAGGG GACTGCATCA TTGAGCCCTG
 55 GAATGATGAT GGGCATGTTC AATATGTTAA GCACTGTATT
 AGGCGTCTCC ATCCTGAATC TTGGACAAAA GAGATACACC
 AAGACTACTT ACTGGTGGGA TGGTCTTCAA TCCTCTGACG
 60 ATTTTGCTCT GATTGTGAAT GCACCCAATC ATGAAGGGAT
 TCAAGCCGGA GTCGACAGGT TTTATCGAAC CTGTAAGCTA
 CTTGGAATCA ATATGAGCAA GAAAAAGTCT TACATAAACA
 65 GAACAGGTAC ATTTGAATTC ACAAGTTTTT TCTATCGTTA

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TGGGTTTGTT GCCAATTTC A GCATGGAGCT TCCCAGTTTT
 GGGGTGTCTG GGATCAACGA GTCAGCGGAC ATGAGTATTG
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 TGGTCCAGCA ACAGCTCAAA TGGCCCTTCA GTTGTTCATC
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 CACAAATACA AACCCGAAGA TCATTTGAAA TAAAGAACT
 GTGGGAGCAA ACCCGTTCCA AAGCTGGACT GCTGGTCTCC
 GACGGAGGCC CAAATTTATA CAACATTAGA AATCTCCACA
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 TGTGCAACA ACACACTCCT GGATCCCCAA AAGAAATCGA
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 AGTATGGTGG AGGCTATGGT TTCCAGAGCC CGAATTGATG
 CACGGATTGA TTTGCAATCT GGAAGGATAA AGAAGAAGA
 GTTCACTGAG ATCATGAAGA TCTGTCCAC CATTGAAGAG
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 AAAAAATGCC TTGTTTCTAC T

PB2

(SEQ ID NO: 3)

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 GATACTCACA AAAACCACCG TGGACCATAT GGCCATAATC
 AAGAAGTACA CATCAGGAAG ACAGGAGAAG AACCCAGCAC
 TTAGGATGAA ATGGATGATG GCAATGAAAT ATCCAATTAC
 AGCAGACAAG AGGATAACGG AAATGATTCC TGAGAGAAAT
 GAGCAAGGAC AAACCTTTATG GAGTAAATG AATGATGCCG
 GATCAGACCG AGTGATGGTA TCACCTCTGG CTGTGACATG
 GTGGAATAGG AATGGACCAA TAACAAATAC AGTTCATTAT
 CCAAAAATCT ACAAACCTTA TTTTGAAAGA GTCGAAAGGC
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 ATCGGAATCG CAACTAACGA TAACCAAGA GAAGAAAGAA
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25

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NP
(SEQ ID NO: 4)

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 ACGAAAAACA AGAATTGCTT ATGAAAGAAT GTGCAACATT
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 GTTCGAAGAT CTCACTTTTT TAGCACGGTC TGCACCTATA
 TTGAGAGGGT CGGTTGCTCA CAAGTCCTGC CTGCCTGCCT
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 AAGGGAGGGA TACTCTCTAG TCGGAATAGA CCCTTTCAGA
 CTGCTTCAA ACAGCCAAGT GTACAGCCTA ATCAGACCAA
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M
(SEQ ID NO: 5)

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 CTAAAGACAA GACCAATCCT GTACCTCTG ACTAAGGGGA
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 GCAAATATCA TTGGGATCTT GCACTTGACA TTGTGGATT
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 GGAGTAAAA ACTACCTTGT TTCTACT
 NS
(SEQ ID NO: 6)

AGCAAAAGCA GGGTGACAAA AACATAATGG ATCCAAACAC
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 CGTGCTGGAA AGCAGATAGT GGAGCGGATT CTGAAAGAAG
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 TCGCTCGCGT TACCTAACTG ACATGACTCT TGAGGAAATG
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TTCGAGTCTC TGAACTCTA CAGAGATTCG CTTGGAGAAG
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AAACGAGAAA TGGCGGGAAC AATTAGGTCA GAAGTTTGAA
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AGATAACAGA GAATAGTTTT GAGCAAATAA CATTTATGCA
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TGTTTCTACT

HA

(SEQ ID NO: 7)

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GGATGGTATGGTTATCATCATCAGAATGAACAGGGATCAGGCT
ATGCAGCGGATCAAAAAGCACACAAATGCCATTAACGGGAT
TACAACAAGGTGAACACTGTTATCGAGAAAATGAACATTCAA

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TTCACAGCTGTGGGTAAAGAATTCAACAAATTAGAAAAAAGGA
TGGAAAAATTTAAATAAAAAAGTTGATGATGGATTTCTGGACAT
TTGGACATATAATGCAGAATTGTTAGTTCTACTGGAAAATGAA
AGGACTCTGGATTTCCATGACTCAAATGTGAAGAATCTGTATG
AGAAAGTAAAAAGCCAATTAAAGAATAATGCCAAAGAAATCGG
AAATGGATGTTTTGAGTTCTACCACAAGTGTGACAATGAATGC
ATGGAAAGTGTAAGAAATGGGACTTATGATTATCCCAATATT
CAGAAGAGTCAAAGTTGAACAGGGAAAAGGTAGATGGAGTGAA
ATTGGAATCAATGGGGATCTATCAGATTCTGGCGATCTACTCA
ACTGTCGCCAGTTCACTGGTGCTTTTGGTCTCCCTGGGGGCAA
TCAGTTTCTGGATGTGTTCTAATGGATCTTTGCAGTGCAGAAT
ATGCATCTGAGATTAGAATTTAGAGATATGAGGAAAAACACC
CTTGTTTCTACT

NA

(SEQ ID NO: 8)

AGCAAAAGCAGGGGTTTAAATGAATCCAAATCAGAAAATAAT
AACCATTGGATCAATCTGTCTGGTAGTCGGAATAATTAGCCTA
ATATTGCAAAAGGGAATATAATCTCAATATGGATTAGCCATT
CAATTCAAACCTGGAAGTCAAACCATACTGGAATATGCAACCA
AAACATCATTACCTATAAAAAATAGCACCTGGGTAAAGGACACA
ACTTCAGTGATATTAACCGGCAATTCATCTCTTTGTCCCATCC
GTGGGTGGGCTATATACAGCAAAGACAATAGCATAAGAATTGG
TTCCAAAGGAGACGTTTTTGTCTAAGAGAGCCCTTTATTTC
TGTCTCACTTGAATGCAGGACCTTTTTTCTGACCCAAGGTG
CCTTACTGAATGACAAGCATTCAAGTGGGACTGTTAAGGACAG
AAGCCCTTATAGGCGCTTAATGAGCTGCCCTGTGCGTGAAGCT
CCGTCCCGGTACAATTCAAGATTTGAATCGGTTGCTTGGTCAG
CAAGTGCATGTCTGATGGCATGGGCTGGCTAACAAATCGGAAT
TTCAGGTCCAGATAATGGAGCAGTGGCTGTATTAAATAACAAC
GGCATAATAACTGAAACCATAAAAAAGTTGGAGGAAGAAAATAT
TGAGGACACAAGAGTCTGAATGTGCCTGTGTAAATGGTTTCATG
TTTTACTATAATGACTGATGGCCGAGTGTGGCTGGCCTCG
TACAAAATTTTCAAGATCGAAAAGGGGAAGGTTACTAAATCAA
TAGAGTTGAATGCACCTAATTCTCACTATGAGGAATGTTCTTG
TTACCCGTGATACCGGCAAGTGTGTGTGTGTCAGAGACAAT
TGGCATGGTTCGAACCGGCCATGGGTGCTTTTCGATCAAAACC
TGGATTATCAAAATAGGATACATCTGCAGTGGGTTTTTCGGTGA
CAACCCGCGTCCCGAAGATGGAACAGGCAGCTGTGGTCCAGTG
TATGTTGATGGAGCAAACGGAGTAAAGGGATTTTCATATAGGT
ATGGTAATGGTGTTTGGATAGGAAGGACCAAAAGTCAAGTTT
CAGACATGGGTTTGGATGATTTGGGATCCTAATGGATGGACA

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GAGACTGATAGTAAGTTCCTGTGAGGCAAGATGTTGTGGCAA
 TGACTGATTGGTCAGGGTATAGCGGAAGTTTCGTTCAACATCC
 TGAGCTGACAGGGCTAGACTGTATGAGCCGTGCTTCTGGGT
 GAATTAATCAGGGGACGACCTAAAGAAAAACAATCTGGACTA
 GTGCGAGCAGCATTTCTTTTGTGGCGTGAATAGTGATACTGT
 AGATTGGTCTTGGCCAGCGGTGCTGAGTTGCCATTGAGCATT
 GACAAGTAGTCTGTTCAAAAACTCCTTGTCTTCTACT

Example 2

Influenza virus A/Hong Kong/213/2003 (H5N1, HK213) replicates systemically in chickens, causing lethal infection. Furthermore, this virus is lethal to chicken embryos. Thus, although its surface proteins are highly related to the currently circulating pathogenic avian influenza viruses, HK213 cannot be used as a vaccine strain as attempts to grow it in embryonated chicken eggs result in the production of poor-quality allantoic fluid. Additionally, the use of this highly virulent virus in the production of vaccines is unsafe for vaccine workers. To test the feasibility of using A/PR/8/34 as a master vaccine strain, the cleavage site of the hemagglutinin (HA) gene of HK213 (containing multiple basic amino acids) was mutated from a virulent to an avirulent phenotype (from RERRRKKR (SEQ ID NO:29) to -TETR (SEQ ID NO:30)). A virus containing the mutated HA gene produced non-lethal, localized infection in chickens. Additionally, the mutated virus was non-lethal to chicken embryos. Thus, growth of the mutated virus in embryonated eggs yielded high-quality allantoic fluid, and in this attenuated form, the virus is safe for vaccine producers.

A recombinant virus containing the neuraminidase (NA) and mutated HA genes from HK213, and all the remaining genes from high-titer A/PR/8/34 (H1N1, HG-PR8) virus (Example 1), which grows 10 times better than other A/PR/8/34 PR8 strains in eggs (10^{10} EID₅₀/ml; HA titer: 1:8,000), was generated in embryonated chicken eggs. This recombinant virus, which expresses surface proteins related to the currently circulating pathogenic avian influenza virus, grew to high titers in embryonated chicken eggs (FIGS. 1A and 1B). Thus, replacement of the HA and NA genes of HG-PR8 with those of a currently circulating strain of influenza virus resulted in a vaccine strain that can be safely produced, and demonstrates the use of PR8-HG as a master vaccine strain.

Example 3

In Hong Kong in 1997, a highly pathogenic H5N1 avian influenza virus was transmitted directly from birds to humans, causing 18 confirmed infections and 6 deaths (Subbarao et al., 1998; Claas et al., 1998). In 2004-6, the geographic distribution of H5N1 viruses expanded in Asia, spreading to several adjacent European countries and to Africa. Altogether, 96 people infected with the virus have died in Vietnam, Thailand, Cambodia, Indonesia, China, Turkey, and Iraq (Li et al., 2004; WHO). These fatal outbreaks and the continued threat of a pandemic have led to the development of H5N1 virus vaccines for use in humans. However, because pathogenic H5N1 viruses grow poorly in embryonated chicken eggs and pose serious biosafety concerns for vaccine producers, reverse genetics has been used to generate vaccine candidates (Subbarao et al., 2003; Webby et al., 2004; Stephanson et al., 2004; Wood & Robertson, 2004).

Recombinant (6:2 reassortant) viruses that possess modified avirulent-type hemagglutinin (HA) and neuraminidase

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(NA) genes, both derived from a pathogenic H5N1 strain, with all remaining genes from a donor virus that grows well in eggs, are among the candidates to be produced by this method. The World Health Organization (WHO) recommends A/Puerto Rico/8/34 (H1N1; PR8) as a donor virus, because of its safety in humans and vigorous growth in eggs (Wood & Robertson, 2004; Webby & Webster, 2003). Recently, it was shown that such recombinant viruses grow less well in eggs than does the wild-type PR8 strain, even though they possess the same PR8 "internal" genes (i.e., those other than the HA and NA) (Horimoto et al., 2006).

Since vigorous growth in eggs is an essential property of vaccine seed viruses used in the production of inactivated vaccines, as described below, H5N1 vaccine candidates were generated that grow as well as the PR8 donor strain in eggs. First, the molecular basis for the high growth of PR8 in eggs was determined by defining the genes responsible for this property using reassortment analysis between PR8 and a WSN strain that grows poorly in eggs. It was found that HA-NA balance and PB1 function are important growth determinants. With this knowledge, a series of H5N1 viruses was produced with altered HA-NA combinations, with the PR8 background, to assess their growth in eggs against more conventional 6:2 reassortants, including the WHO-recommended NIBRG-14 virus.

Methods

Cells and Viruses

293T human embryonic kidney cells were maintained in Dulbecco's modified Eagle's minimal essential medium (DMEM) with 10% fetal calf serum and antibiotics. Madin-Darby canine kidney (MDCK) cells were grown in MEM with 5% newborn calf serum and antibiotics. African green monkey Vero WCB cells, which had been established after biosafety tests for use in human vaccine production (Sugawara et al., 2002), were maintained in serum-free VP-SFM medium (GIBCO-BRL) with antibiotics. Cells were maintained at 37° C. in 5% CO₂. The A/Vietnam/1194/2004 and A/Vietnam/1203/2004 (H5N; VN1194 and VN1203) strains, isolated from humans, were propagated in 10-day-old embryonated chicken eggs for 2 days at 37° C., after which time the allantoic fluids containing virus were harvested and used for further experiments. All experiments with these viruses were carried out in a Biosafety Level 3 containment laboratory. The WHO-recommended vaccine seed virus, NIBRG-14 (VN1194/PR8 6:2 reassortant virus), was kindly gifted by Drs. John Wood and Jim Robertson at the National Institute for Biological Standards and Control, UK.

Construction of Plasmids and Reverse Genetics

To generate reassortants of influenza A viruses, a plasmid-based reverse genetics (Neumann et al., 1999) was used. Viral RNA from VN1194 or VN1203 was extracted from allantoic fluid by using a commercial kit (ISOGEN LS, Nippon Gene) and was converted to cDNA by using reverse transcriptase (SuperScript III; GIBCO-BRL) and primers containing the consensus sequences of the 3' ends of the RNA segments for the H5 viruses. The full-length cDNAs were then PCR-amplified with ProofStart polymerase (QIAGEN) and H5 subtype-specific primer pairs, and cloned into a plasmid under control of the human polymerase I promoter and the mouse RNA polymerase I terminator (Poll plasmids), generating a Poll-VN1194/HA or a Poll-VN1203/HA construct containing the VN1194 or VN1203 HA gene, respectively. By inverse PCR using back-to-back primer pairs, followed by ligation, the HA cleavage site sequence of the wild-type VN1194 or VN1203 (RERRRKKR; SEQ ID NO:29) virus was altered to create the avirulent-type sequence (RETR; SEQ ID NO:31) as described in Horimoto et al. (2006), the disclosure of which is incorporated by reference herein. A Poll-VN1203NA containing the VN1203 NA gene was constructed by the RT-PCR procedure (described above) with N1-specific primers. A series of pPoll

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NA mutant plasmids were prepared by inverse PCR. Using the PolI-VN1203NA as a template, pPolI-NAfill was constructed, which encodes a mutant NA containing a 20-amino acid (aa) (CNQSIITYENNTWVNQTYVN; SEQ ID NO:32) insertion derived from A/goose/Guangdong/1/96 (H5N1; GsGd96) NA into the NA stalk between 48-Pro and 49-Ile. pPolI-NAfill.N2 and -NAfill.N2N9, in which N2 (12 aa) or N2+N9 (12+12 aa) sequences derived from the stalk region of each NA subtype were inserted into the NA stalk between 42-Asn and 43-Gin, were constructed as described in Castrucci et al. (1993). All of these constructs were sequenced to ensure the absence of unwanted mutations.

A previously produced series of PolI constructs, derived from A/WSN/33 (H5N1; WSN) and PR8 strains was used, for reverse genetics (Horimoto et al., 2006; Neumann et al., 1999). Additionally, PolI constructs containing NA genes derived from A/Hong Kong/213/03 (H5N1; HK213), and A/Kanagawa/173/2001 (H1N1; Kanagawa) were used in this study (Horimoto et al., 2006; Kobasa et al., 2004; Peiris et al., 2004).

Plasmids expressing WSN or PR8 NP, PA, PB1, or PB2 under control of the chicken β -actin promoter were used for all reverse genetics experiments (Horimoto et al., 2006; Neumann et al., 1999). Briefly, PolI plasmids and protein expression plasmids were mixed with a transfection reagent, Trans-IT 293T (Panvera), incubated at room temperature for 15 min, and then added to 293T cells. Transfected cells were incubated in Opti-MEM I (GIBCO-BRL) for 48 hours. For reverse genetics in Vero WCB cells, an electroporator (Amaxa) was used to transfect the plasmid mixtures according to the manufacturer's instructions. Sixteen hours after transfection, freshly prepared Vero WCB cells were added onto the transfected cells and TPCK-trypsin (1 μ g/ml) was added to the culture 6 hours later. Transfected cells were incubated in serum-free VP-SFM for a total of 4 days. Supernatants containing infectious viruses were harvested, biologically cloned by limiting dilution in embryonated eggs, and used in further experiments.

Properties of Viral Replication in Eggs

Virus was inoculated into the allantoic cavity of 10-day-old embryonated chicken eggs, and incubated at 37° C. for 48 hours. Virus in the allantoic fluids was then titrated by HA assay using either 0.5% chicken erythrocytes or 0.8% guinea pig erythrocytes or in eggs to determine the median egg infectious dose (EID₅₀)/ml of virus. For some viruses, plaque titration was conducted with MDCK cells and TPCK-trypsin (1 μ g/ml). The growth kinetics of some viruses was assessed in eggs after inoculating 10⁴ EID₅₀ of virus.

Virus Elution Assay from Chicken Erythrocytes

Fifty μ l of twofold dilutions of virus containing the HA titers of 1:1024 were incubated with 50 μ l of 0.5% chicken erythrocytes in a microtiter plate at 4° C. for 1 hour. The plate was then stored at 37° C., and the reduction of HA titers was recorded periodically. Phosphate-buffered saline with 6.8 mM CaCl₂ was used as a diluent.

Results

Molecular Basis for the High Growth Property of PR8 in Chicken Eggs

Although PR8 is recommended by WHO for use as a donor virus to generate reverse genetics-based H5 influenza vaccine, the molecular basis of its high growth property is not fully understood. The M gene was said to be responsible for the vigorous growth of PR8 in eggs (Subbarao et al., 2003), but this claim is apparently not found in the published original data (Kilbourne et al., 1969). Thus, a reassortment analysis was conducted using a WSN strain that grows poorly in eggs. Table 3 shows the compatibility between the HAs and NAs of PR8 versus the WSN strain in terms of viral growth in embryonated chicken eggs. All reassortant test viruses grew better than the wild-type WSN, but less well

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than the egg-adapted PR8, demonstrating that both surface glycoproteins and internal proteins are responsible for the high growth property of PR8.

TABLE 3

Compatibility between the HAs and NAs of PR8 versus WSN strains, assessed by viral growth in chicken embryonated eggs

Gene constellation of reassortant			HA titer ^{b)}	
HA	NA	6 others ^{a)}	Chicken RBC	Guinea pig RBC
WSN	WSN	WSN	16/8	32/8
PR8	WSN	WSN	64/32	64/32
WSN	PR8	WSN	16/16	32/16
PR8	PR8	WSN	128/128	128/128
WSN	WSN	PR8	64/64	64/64
PR8	WSN	PR8	64/128	64/128
WSN	PR8	PR8	512/512	512/512
PR8	PR8	PR8	2048/2048	2048/2048

^{a)}Genes encoding the internal proteins PB1, PB2, PA, NP, M, and NS.

^{b)}Growth of each reassortant virus in chicken eggs, assessed in HA assays with 0.5% chicken RBC and 0.8% guinea pig RBC. HA titers from two independent experiments are shown.

Since the growth of a reassortant virus containing both of the PR8 glycoproteins and all six internal proteins derived from WSN was drastically reduced in eggs, as compared with that of PR8 (Tables 3 and 4), a series of reassortant viruses was produced to define the internal proteins responsible for this property. A single-gene reassortant virus containing the WSN PB1 and all remaining genes from PR8 grew poorly, at a level similar to that of a reassortant containing all of the WSN genes encoding internal proteins, whereas a reassortant containing the PR8 PB1 and WSN genes encoding all remaining internal proteins replicated to a high titer (Table 4). Thus, the PR8 PB1 likely possesses the optimal polymerase activity for viral genome replication in eggs, in contrast to a previous report implicating the M segment in this role (Subbarao et al., 2003).

TABLE 4

Compatibility among genes encoding internal proteins of PR8 and WSN viruses, assessed by viral growth in chicken embryonated eggs

Gene constellation of reassortant ^{a)}								
HA	NA	PB2	PB1	PA	NP	M	NS	HA titer ^{b)}
PR8	PR8	PR8	PR8	PR8	PR8	PR8	PR8	2048/2048/1024
PR8	PR8	PR8	PR8	PR8	PR8	PR8	WSN	1024/1024/1024
PR8	PR8	PR8	PR8	PR8	PR8	WSN	PR8	2048/1024/1024
PR8	PR8	PR8	PR8	PR8	PR8	WSN	WSN	1024/1024/512
PR8	PR8	PR8	PR8	WSN	PR8	PR8	PR8	1024/1024/512
PR8	PR8	PR8	PR8	WSN	PR8	PR8	PR8	1024/512/256
PR8	PR8	PR8	WSN	PR8	PR8	PR8	PR8	128/64/64
PR8	PR8	WSN	PR8	PR8	PR8	PR8	PR8	1024/1024/1024
PR8	PR8	WSN	WSN	WSN	WSN	PR8	PR8	64/64/32
PR8	PR8	WSN	WSN	WSN	WSN	WSN	WSN	128/64/64
PR8	PR8	WSN	PR8	WSN	WSN	WSN	WSN	1024/512/512

^{a)}Both the HA and NA genes were derived from PR8 in all reassortant viruses, while some of the genes encoding internal proteins were from the WSN strain.

^{b)}Growth rate of each reassortant virus in chicken eggs was assessed with HA assays in 0.5% chicken RBC. HA titers, obtained in three independent experiments, are shown.

Generation of H5N1 Vaccine Seed Candidates with Enhanced Growth Ability in Chicken Eggs

In an earlier study, the growth of WSN in eggs was shown to be enhanced by lengthening the NA stalk to increase NA function: the longer the stalk, the better the replication of the virus (Castrucci et al., 1993). This finding prompted the production of a series of H5N1 viruses comprising mutated or heterologous N1s with the PR8 background and compare their growth in eggs. The A/Vietnam/1203/2004 (H5N1; VN1203) NA contains a 20-amino acid (20-aa) deletion in its stalk region (hence, 24 aa in the stalk). Therefore, a mutant NA, VN1203fill, was constructed containing a 44-aa stalk like the H5N1 precursor virus A/goose/Guangdong/1/96 (H5N1) (Xu et al., 1999), as well as other NA mutants, VN1202fill.N2 and VN1203fill.N2N9 that contained longer stalks, 58- and 72-aa, respectively (FIG. 2). The heterologous N1 from A/Hong Kong/213/03 (H5N1; HK213) containing 44-aa in the stalk was also examined. The NAs from H1N1 strains such as PR8, A/Kanagawa/173/2001 (H1N1; Kanagawa), and WSN, all of which possess 24-aa in the stalk, were also tested. Using these NA constructs, a total of eight reassortant viruses was generated, seven 6:2 and one 7:1 with the modified avirulent-type VN1203 HA and PR8 background (Table 5). Another series of reassortant viruses was constructed with the modified avirulent-type A/Vietnam/1194/2004 (H5N1; VN1194) HA. By comparison with constructs containing the parental VN1203 NA, only the 7:1 reassortant virus and a 6:2 reassortant containing a combination of the modified VN1194 HA and VN1203fill NA, showed enhanced growth in eggs.

Further testing of selected reassortant viruses by a plaque assay of the stock viruses demonstrated a greater than 3-fold higher titer ($p=0.003$, Student t-test) for the reassortant virus containing PR8 NA compared with the virus containing parental VN1203 NA, although it did not grow as well as egg-adapted PR8 (FIG. 3). Assessment of the growth kinetics of reassortant viruses with the PR8, VN1203fill or VN1203 NA in eggs revealed a superior growth rate for the virus with PR8 NA (7:1 reassortant) (FIG. 4).

To determine the molecular basis of the high growth property observed in the 7:1 reassortant virus, the NA function of reassortant viruses was tested by an assay evaluating virus elution from chicken erythrocytes (FIG. 5). Reassortant viruses containing PR8 or VN1203fill NA were eluted from erythrocytes more rapidly than those with the parental VN1203 NA, indicating greater NA activity for PR8 or VN1203fill.NA. These results support the idea that high NA function enhances viral growth in eggs (Castrucci et al., 1993).

Growth Comparison of H5N1 Vaccine Seed Candidates Produced in this Study with the WHO-Recommended Vaccine Seed Virus, NIBRG-14, in Eggs

To validate the potential of candidate seed viruses in the production of H5N1 vaccines, their infectivity titers were compared with that of the WHO-provided NIBRG-14 virus under the same experimental conditions. The 7:1 reassortant viruses containing either VN1194 or VN1203-derived HAs and all the other genes from our PR8 strain showed significantly higher titers ($p<0.05$, Student t-test) than the NIBRG-14 virus in eggs, as assessed by EID₅₀ (Table 6) and plaque

TABLE 5

Viral titers of H5N1/PR8 reassortant viruses in chicken embryonated eggs ^{a)}						
HA titer/Infectivity titer (log ₂ /log ₁₀ EID ₅₀ /ml)						
NA derived from ^{d)}						
HA ^{b)}	Experiment ^{c)}	VN1203	VN1203fill	VN1203fill.N2	VN1203fill.N2N9	HK213
VN1203	1	9.2 ± 0.4/8.9 ± 0.3 ^{d)}	9.6 ± 0.5/8.8 ± 0.6	9.2 ± 0.5/8.9 ± 0.4	9.0 ± 0.0/8.8 ± 0.5	9.6 ± 0.5/8.8 ± 0.1
	2	9.0 ± 1.0/9.4 ± 0.2	9.0 ± 0.0/9.7 ± 0.2	8.3 ± 0.6/8.6 ± 0.2	8.0 ± 0.0/ND	8.7 ± 0.6/8.5 ± 0.3
VN1194	1	8.7 ± 0.6/8.7 ± 0.2	9.3 ± 0.6/ 9.3 ± 0.2	9.3 ± 0.6/9.2 ± 0.2	9.0 ± 0.0/8.6 ± 0.2	ND/ND
NA derived from ^{d)}						Wild-type
HA ^{b)}	Experiment ^{c)}	PR8	Kanagawa	WSN	PR8 ^{e)}	
VN1203	1	9.6 ± 0.5/ 9.5 ± 0.4	9.8 ± 0.4/9.4 ± 0.2	<1.0/ND	10.7 ± 0.6/10.3 ± 0.4	
	2	9.7 ± 0.6/ 10.1 ± 0.2	ND/ND	ND/ND	11.0 ± 0.0/ 10.3 ± 0.4	
VN1194	1	9.3 ± 0.6/ 9.5 ± 0.3	9.0 ± 0.0/8.8 ± 0.9	<1.0/5.2 ± 0.2	10.7 ± 0.6/10.1 ± 0.2	

^{a)} Eggs (10-day-old) were inoculated with virus (10⁴ EID₅₀), and incubated for 48 hours at 37° C.; viral titers in allantoic fluids were determined.

^{b)} Two H5 HA genes (VN1203 and VN1194) were used to generate reassortant viruses with a PR8 background. The HA cleavage sites of both VN1203 and VN1194 were modified to that of the avirulent-type H5 HA.

^{c)} Two independent experiments, each using 3 to 5 eggs, were performed for VN1203 constructs, while a single experiment was done for VN1194.

^{d)} A total of eight NA genes were used to generate reassortant viruses; three insertion mutant NAs (VN1203fill, VN1203fill.N2, and VN1203fill.N2N9) were prepared to assess the influence of NA stalk length on virus growth in eggs by comparison to parental VN1203 NA; the other NAs were derived from an H5N1 human isolate (HK213) or H1N1 viruses (PR8, Kanagawa, and WSN). Thus, all reassortant viruses except one containing PR8 NA (7:1 reassortant) are 6:2 reassortant viruses with a PR8 background.

^{e)} Growth of wild-type PR8 was also assessed as a control for each experiment.

^{f)} Growth of each reassortant virus in eggs was assessed by either HA or infectivity assay, and reported as mean ± s.d. of HA titer (log₂)/mean ± s.d. of infectivity titer (log₁₀EID₅₀/ml). Significantly enhanced HA and infectivity titers ($p < 0.05$, t-test), by comparison to those of standard viruses containing VN1203 HA and VN1203 NA or VN1194 HA and VN1203 NA, are shown in boldface type.

ND, not determined.

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titration (FIG. 6). Interestingly, even the 6:2 reassortant virus containing both its HA and NA from the VN1194 virus grew significantly better (about 7-fold, $p=0.047$) than NIBRG-14 (also a VN1194/PR8 6:2 reassortant virus) by plaque titration (FIG. 5). This difference in the growth of two 6:2 reassortant viruses possessing identical VN1194 HAs and NAs indicates that the PR8 strain used in this study would be superior to the one used to generate NIBRG-14 for supporting high viral growth during vaccine production in eggs.

TABLE 6

Growth comparison of H5N1/PR8 reassortant viruses generated in this study with the WHO-recommended vaccine seed virus (NIBRG-14) ^{a)}					
Infectivity titer ($\log_{10}\text{EID}_{50}/\text{ml}$)					
Hours Postinfection	Reassortants made in this study ^{b)}				NIBRG-14
	VN1194/VN1194	VN1194/PR8	VN1203/VN1203	VN1203/PR8	VN1194/VN1194
48	8.7 \pm 0.4	9.4 \pm 0.2	9.1 \pm 0.2	9.5 \pm 0.3	8.2 \pm 0.3
60	8.3 \pm 0.5	8.9 \pm 0.5	8.6 \pm 0.4	9.2 \pm 0.3	7.4 \pm 0.2

^{a)}Growth of reassortant viruses was assessed by inoculating eggs ($n = 3$) with each virus, harvesting allantoic fluid at the indicated times, and determining the EID_{50} . The data are shown as mean \pm s.d. of infectivity titers ($\log_{10}\text{EID}_{50}/\text{ml}$). Significantly enhanced infectivity titers ($p < 0.05$, t-test), by comparison with those of NIBRG-14, are shown in boldface type.

^{b)}Categorized by the derivation of the HA/NA. The HA cleavage site of both VN1203 and VN1194 were modified to that of the avirulent-type H5 HA.

Discussion

Recombinant viruses possessing modified avirulent-type HA and NA genes, both derived from an H5N1 human isolate, and all remaining genes from the PR8 strain (6:2 reassortant) have been produced and used as seed viruses for inactivated influenza vaccines now being tested in human clinical trials (Wood & Robertson, 2004). Seed strains used in this way must grow well in embryonated eggs. Although egg-adapted PR8 meets this requirement, some 6:2 reassortant viruses, despite containing six internal genes from PR8, do not grow well in eggs (Tables 3 and 5). Here it is demonstrated that the growth of egg-adapted PR8 in chicken eggs is affected by the functional balance of the HA and NA surface glycoproteins.

It is likely that low yields of some 6:2 reassortant viruses with a PR8 background and surface glycoproteins from highly pathogenic avian viruses may result not only from an HA-NA functional imbalance for growth in eggs but also from genetic (and/or functional) incompatibility between the avian surface glycoprotein genes and the internal genes from PR8. Here it is shown that among the internal genes of PR8, PB1 is very important for its high growth in eggs. This information suggests another strategy for reverse genetics-based H5N1 vaccine production: that is, the PB8 PB1 gene alone may be sufficient to generate vigorously growing reassortants for vaccine seed viruses. Thus, by using genes that encode non-PB1 internal proteins from strains other than PR8, one might avoid genetic incompatibility between avian and PR8 viruses. Studies to dissect the molecular basis for the high growth property of PR8 PB1 in eggs would be of considerable interest. One could, for example, analyze the structural and functional differences between the PB1s or PB1-F2s of PR8 and WSN (which differ by 18 and 10 amino acids, respectively; Chen et al., 2004).

The 7:1 reassortant viruses produced in this study replicated significantly better (more than 20-fold by plaque titration) than the WHO-recommended 6:2 reassortant virus

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NIBRG-14. Even the 6:2 reassortant that was identical to the NIBRG-14 except for the PR8 strain of origin replicated 7-fold better than the recommended virus. These findings suggest that the PR8 strain used in this study may be a superior donor virus for the production of reverse genetics-based pandemic vaccines.

One could argue that the 7:1 reassortant viruses would induce a loss of protective immune response due to antigenic differences in the NA proteins (even though both PR8 and the highly pathogenic viruses contain N1 NAs) (Murphy et al., 1972; Kilbourne et al., 1968; Chen et al., 2000). However, since the HA is the major protective antigen in inactivated vaccines, the higher growth property conferred by the PR8 NA would likely offset the limited antigenic mismatch in this minor protective antigen. In the event of a pandemic caused by a highly pathogenic avian influenza virus, chicken eggs will be in short supply. It is proposed that under such conditions, 7:1 reassortant-based vaccine seed viruses possessing an enhanced growth property in eggs would offer an attractive option for the generation of reverse genetics-based H5 vaccine viruses.

Example 4

To identify the genes responsible for the high growth rate of an H5N1 vaccine seed virus in chicken embryonated eggs, the growth of reassortant H5N1 viruses possessing PR8(UW) or PR8(Cambridge) internal genes in chicken embryonated eggs was assessed (FIG. 7). The HA and NA genes of all of the reassortant viruses were derived from A/Vietnam/1194/2002. All other genes were derived from either PR8(UW) or PR8(Cambridge), which also provided the non-HA and -NA genes of the NIBRG-14 vaccine strain. Higher titers were obtained when the majority of internal genes were from PR8(UW).

The effect of the M and NS genes on the growth of viruses in chicken embryonated eggs is shown in FIG. 8. For PR8(UW)/1194-CamM and PR8(UW)/1194-CamNS, the M and NS gene segments, respectively, were derived from PR8(Cambridge), while the other internal segments came from PR8(UW). The HA and NA segments were derived from A/Vietnam/1194/2004. Highest titers were with the M gene segment of PR8(UW) and the NS gene of PR8 (Cambridge).

The results in FIGS. 7-8 show that the polymerase subunit (PA, PB1, and PB2) and NP genes of PR8(UW) enhanced the growth of an H5N1 vaccine seed virus in chicken embryonated eggs. Also, the NS gene of PR8(Cambridge) enhanced the growth of an H5N1 vaccine seed virus in chicken embryonated eggs.

To identify the gene and amino acid(s) responsible for the high growth rate of the H5N1 vaccine seed virus in MDCK cells, the growth of PR8(UW)/1194 and NIBRG-14 virus in MDCK cells was assessed. The data in FIG. 9 show that the growth of PR8(UW)/1194 was significantly better than that of NIBRG-14 in MDCK cells. Moreover, the PB2 segment of PR8(UW) enhanced the growth of the vaccine seed virus in MDCK cells (FIG. 10). The tyrosine residue at position 360 in PB2 of PR8(UW) is likely responsible for the high growth rate of the vaccine seed virus in MDCK cells (FIG. 11).

To identify a combination of genes responsible for the high growth of an H5N1 vaccine seed virus in MDCK cells, the growth rates in MDCK cells of reassortants with different HA, NA, and NS genes was determined. NS from PR8(Cambridge) and NA with a long stalk (e.g., from

A/Hong Kong/213/2003 or VN1203Fill) enhanced virus growth in MDCK cells (FIG. 12).

To determine which amino acids in NS are responsible for the high growth rate of the H5N1 vaccine seed virus in MDCK cells, the growth in MDCK cells of the H5N1 vaccine seed virus containing a heterologous NS segment was measured. An amino acid substitution from K [PR8 (UW)NS] to E [PR8(Cambridge)] at position 55 of NS1 enhanced the growth of the H5N1 vaccine seed viruses in MDCK cells (FIG. 13).

FIG. 14 summarizes the genotype of an H5N1 seed virus with high growth capacity in chicken embryonated eggs or MDCK cells.

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All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

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ctctatcatc ccgtcaggcc ccctcaaagc cgagatcgca cagagacttg aagatgtctt    120
tgcagggaag aacaccgata ttgaggttct catggaatgg ctaaagacaa gaccaatcct    180
gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg    240
aggactgcag cgtagacgct ttgtccaaaa tgcccttaat gggaacgggg atccaaataa    300
catggacaaa gcagttaaac tgtataggaa gctcaagagg gagataacat tccatggggc    360
caaagaaatc tactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata    420
caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga    480
acagattgct gactccagc atcggtctca taggcaaatg gtgacaacaa ccaatccact    540
aatcagacat gagaacagaa tggttttagc cagcactaca gctaaggcta tggagcaaat    600
ggctggatcg agtgacaag cagcagaggc catggagggt gctagtcagg ctagacaaat    660
ggtgcaagcg atgagaacca ttgggactca tcctagctcc agtgctggtc tgaaaaatga    720
tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa    780
gtgatcctct cactattgcc gcaaataatc ttgggatctt gcacttgaca ttgtggattc    840
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cttctacgga aggagtgcc aagtctatga gggaagaata tcgaaaggaa cagcagagtg    960
ctgtggatgc tgacgatggt cattttgtca gcatagagct ggagtaaaaa actaccttgt   1020
ttctact                                           1027

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<210> SEQ ID NO 6

<211> LENGTH: 890

<212> TYPE: DNA

<213> ORGANISM: Influenza A

<400> SEQUENCE: 6

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tccttgatcg gcttcgccga gatcagaaat ccctaagagg aaggggcagt actctcggtc    180
tggacatcaa gacagccaca cgtgctggaa agcagatagt ggagcggatt ctgaaagaag    240
aatccgatga ggcacttaaa atgaccatgg cctctgtacc tgcgtcgcgt tacctaactg    300
acatgactct tgaggaaatg tcaagggact ggtccatgct cataccaag cagaaagtgg    360
caggccctct ttgtatcaga atggaccagg cgatcatgga taagaacatc atactgaaag    420
cgaaattcag tgtgatTTTT gaccggctgg agactctaatt attgctaagg gctttcaccg    480
aagagggagc aattgttggc gaaatttcac cattgccttc tcttcagga cactactgtg    540
aggatgtcaa aaatgcagtt ggagtcctca tcggaggact tgaatggaat gataacacag    600
ttcgagtctc tgaaactcta cagagattcg cttggagaag cagtaatgag aatgggagac    660
ctccactcac tccaaaacag aaacgagaaa tggcgggaac aattaggtca gaagtttgaa    720
gaaataagat ggttgattga agaagtgaga cacaaactga agataacaga gaatagtttt    780
gagcaaataa catttatgca agccttacat ctattgcttg aagtggagca agagataaga    840
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<210> SEQ ID NO 7

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<211> LENGTH: 1775

<212> TYPE: DNA

<213> ORGANISM: Influenza A

<400> SEQUENCE: 7

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agcaaaagca ggggaaaata aaaacaacca aaatgaaggc aaacctactg gtcctgttat      60
gtgcacttgc agctgcagat gcagacacaa tatgtatagg ctacctgcg aacaattcaa      120
ccgacactgt tgacacagta ctcgagaaga atgtgacagt gacacactct gttaacctgc      180
tcgaagacag ccacaacgga aaactatgta gattaaaagg aatagcccca ctacaattgg      240
ggaaatgtaa catcgccgga tggctcttgg gaaaccaga atgcgaccca ctgcttccag      300
tgagatcatg gtcctacatt gtagaaacac caaactctga gaatggaata tgttatccag      360
gagatttcat cgactatgag gagctgaggg agcaattgag ctgagtgtca tcattcgaaa      420
gattcgaaat atttcccaaa gaaagctcat ggcccaacca caacacaaac ggagtaacgg      480
cagcatgctc ccatgagggg aaaagcagtt ttacagaaa ttgctatgg ctgacggaga      540
aggagggtc atacccaaag ctgaaaaatt cttatgtgaa caaaaaggg aaagaagtcc      600
ttgtactgtg gggatttcat ccccgcta acagtaagga acaacagaat ctctatcaga      660
atgaaaaatg ttatgtctct gtatgactt caaattataa caggagattt acccggaaa      720
tagcagaaag acccaaagta agagatcaag ctgggaggat gaactattac tggaccttgc      780
taaaacccgg agacacaata atatttgagg caaatggaaa tctaatagca ccaatgtatg      840
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atatacacc agtcacaata ggagagtgc caaatacgt caggagtgc aaattgagga      1020
tggttacagg actaaggaa attccgtcca tcaatccag aggtctattt ggagccattg      1080
ccggttttat tgaaggggga tggactggaa tgatagatgg atggtatggt tatcatcatc      1140
agaatgaaca gggatcaggc tatgcagcgg atcaaaaaag cacacaaaat gccattaacg      1200
ggattacaaa caagtgtaac actgttatcg agaaaatgaa cattcaattc acagctgtgg      1260
gtaaagaatt caacaaatta gaaaaaagga tggaaaattt aaataaaaaa gttgatgatg      1320
gatttctgga catttggaac tataatgcag aattgttagt tctactggaa aatgaaagga      1380
ctctggattt ccatgactca aatgtgaaga atctgtatga gaaagtaaaa agccaattaa      1440
agaataatgc caaagaaatc ggaaatggat gttttgagtt ctaccacaag tgtgacaatg      1500
aatgcatgga aagtgtgaag aatgggactt atgattatcc caaatattca gaagagtcaa      1560
agttgaacag ggaaaaggta gatggagtga aattggaatc aatggggatc tatcagattc      1620
tggcgatcta ctcaactgtc gccagttcac tgggtctttt ggtctccctg ggggcaatca      1680
gtttctggat gtgttcta atggatcttgc agtgcagaat atgcacttga gattagaatt      1740
tcagagatat gaggaaaaac acccttgttt ctact                                     1775

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<210> SEQ ID NO 8

<211> LENGTH: 1413

<212> TYPE: DNA

<213> ORGANISM: Influenza A

<400> SEQUENCE: 8

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gtctggtagt cggactaatt agcctaatat tgcaaatagg gaatataatc tcaatatgga      120
ttagccattc aattcaaact ggaagtcaaa accatactgg aatatgcaac caaacatca      180

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ttacctataa aaatagcacc tgggtaaagg acacaacttc agtgatatta accggcaatt	240
catctctttg tcccatecgt ggggtgggcta tatacagcaa agacaatagc ataagaattg	300
gttccaaagg agacgttttt gtcataagag agccctttat ttcattgttct cacttggaat	360
gcaggacctt tttttgacc caaggtgcct tactgaatga caagcattca agtgggactg	420
ttaaggacag aagcccttat agggccttaa tgagctgccc tgcgggtgaa gctccgtccc	480
cgtacaattc aagatttgaa tcgggttgctt ggtcagcaag tgcattgcat gatggcatgg	540
gctggctaac aatcggaatt tcagggtccag ataatggagc agtggctgta ttaaaataca	600
acggcataat aactgaaacc ataaaaagt ggaggaagaa aatattgagg acacaagagt	660
ctgaatgtgc ctgtgtaaat ggttcattgtt ttactataat gactgatggc ccgagtgatg	720
ggctggcctc gtacaaaatt ttcaagatcg aaaaggggaa ggttactaaa tcaatagagt	780
tgaatgcacc taattctcac tatgaggaat gttcctgtta ccctgatacc ggcaaagtga	840
tgtgtgtgtg cagagacaat tggcatggtt cgaaccggcc atgggtgtct ttcgatcaaa	900
acctggatta tcaaatagga tacatctgca gtggggtttt cggtgacaac ccgcgtcccg	960
aagatggaac aggcagctgt ggtccagtgt atgttgatgg agcaaacgga gtaaagggat	1020
ttcatatag gtatggaat ggtgtttgga taggaaggac caaaagtcac agttccagac	1080
atgggtttga gatgatattg gatcctaag gatggacaga gactgatagt aagttctctg	1140
tgaggcaaga tgttgtggca atgactgatt ggtcagggtg tagcggaagt ttcgttcaac	1200
atcctgagct gacagggcta gactgtatga ggccgtgctt ctgggttgaa ttaatcaggg	1260
gacgacctaa agaaaaaaca atctggacta gtgcgagcag catttctttt tgtggcgtga	1320
atagtatac ttagatttgg tcttggccag acggtgctga gttgccattc agcattgaca	1380
agtagtctgt tcaaaaaact ccttgtttct act	1413

<210> SEQ ID NO 9
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 9

cacacacggt ctccgggagc gaaagcaggc a	31
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<210> SEQ ID NO 10
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 10

ccaggacact gaaatttctt tcac	24
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<210> SEQ ID NO 11
 <211> LENGTH: 35
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 11

cacacaggtc tcctattagt agaaacaagg cattt	35
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<210> SEQ ID NO 12
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 12

cacacaggtc tccgggagcg aaagcaggtc 30

<210> SEQ ID NO 13
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 13

cacacacgtc tccatcatac aatcctcttg 30

<210> SEQ ID NO 14
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 14

ctcctctgat ggtggcatac 20

<210> SEQ ID NO 15
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 15

cacacaggtc tcctattagt agaaacaagg tcgttt 36

<210> SEQ ID NO 16
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 16

cacacacgtc tccgggagcg aaagcaggta c 31

<210> SEQ ID NO 17
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 17

cacacacgtc tcctattagt agaaacaagg tactt 35

<210> SEQ ID NO 18
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

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<400> SEQUENCE: 18

cacacacgtc tccgggagca aaagcagggg

30

<210> SEQ ID NO 19

<211> LENGTH: 37

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 19

cacacacgtc tcctattagt agaaacaagg gtgtttt

37

<210> SEQ ID NO 20

<211> LENGTH: 31

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 20

cacacacgtc tccgggagca aaagcaggg t a

31

<210> SEQ ID NO 21

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 21

cacacacgtc tcctattagt agaaacaagg gtattttt

38

<210> SEQ ID NO 22

<211> LENGTH: 31

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 22

cacacaggtc tccgggagca aaagcaggag t

31

<210> SEQ ID NO 23

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 23

cacacaggtc tggtattagt agaaacaagg agtttttt

38

<210> SEQ ID NO 24

<211> LENGTH: 31

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 24

cacacacgtc tccgggagca aaagcaggta g

31

<210> SEQ ID NO 25

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<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 25

cacacacgtc tcctattagt agaaacaagg tagttttt 38

<210> SEQ ID NO 26
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 26

cacacacgtc tccgggagca aaagcagggt g 31

<210> SEQ ID NO 27
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 27

cacacacgtc tcctattagt agaaacaagg gtgtttt 37

<210> SEQ ID NO 28
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 28

gggtttgtat ttgtgtgtca cc 22

<210> SEQ ID NO 29
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Influenza A

<400> SEQUENCE: 29

Arg Glu Arg Arg Arg Lys Lys Arg
1 5

<210> SEQ ID NO 30
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic peptide

<400> SEQUENCE: 30

Thr Glu Thr Arg
1

<210> SEQ ID NO 31
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic peptide

<400> SEQUENCE: 31

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Arg Glu Thr Arg
1

<210> SEQ ID NO 32
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic peptide

<400> SEQUENCE: 32

Cys Asn Gln Ser Ile Ile Thr Tyr Glu Asn Asn Thr Trp Val Asn Gln
1 5 10 15

Thr Tyr Val Asn
20

<210> SEQ ID NO 33
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza A

<400> SEQUENCE: 33

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aagaagtaca catcaggaag acaggagaag aaccagcac ttaggatgaa atggatgatg    180
gcaatgaaat atccaattac agcagacaag aggataacgg aaatgattcc tgagagaaat    240
gagcaaggac aaactttatg gagtaaaatg aatgatgccg gatcagaccg agtgatggta    300
tcacctctgg ctgtgacatg gtggaatagg aatggaccaa tgacaaatac agttcattat    360
ccaaaaatct acaaaaactta ttttgaaaga gtcgaaaggc taaagcatgg aacctttggc    420
cctgtccatt ttagaaacca agtcaaaata cgtcggagag ttgacataaa tcctgggtcat    480
gcagatctca gtgccaaagg ggcacaggat gtaatcatgg aagttgtttt ccctaacgaa    540
gtgggagcca ggataactac atcggaatcg caactaacga taaccaaaaga gaagaaagaa    600
gaactccagg attgcaaaat ttctcctttg atggttgcat acatgttgga gagagaactg    660
gtccgcaaaa cgagattcct ccagtggtc ggtggaacaa gcagtgtgta cattgaagtg    720
ttgcatttga ctcaaggaa atgctgggaa cagatgtata ctccaggagg ggaagtgaag    780
aatgatgatg ttgatcaaag cttgattatt gctgctagga acatagttag aagagctgca    840
gtatcagcag acccactagc atctttattg gagatgtgcc acagcacaca gattggtgga    900
attaggatgg tagacatcct taagcagaac ccaacagaag agcaagccgt ggatatatgc    960
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gccatactca gaaaagcaac caggagattg attcagctga tagtgagtgg gagagacgaa   1200
cagtcgattg ccgaagcaat aattgtggcc atggtatttt cacaagagga ttgtatgata   1260
aaagcagtta gaggtgatct gaatttcgtc aatagggcga atcagcgact gaatcctatg   1320
catcaacttt taagacattt tcagaaggat gcgaaagtgc tttttcaaaa ttggggagtt   1380
gaacctatcg acaatgtgat gggaatgatt gggatattgc ccgacatgac tccaagcate   1440
gagatgtcaa tgagaggagt gagaatcagc aaaatgggtg tagatgagta ctccagcacg   1500
gagagggtag tggtagcat tgaccggttc ttgagagtca gggaccaacg aggaaatgta   1560

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ctactgtctc ccgaggaggt cagtgaaca caggaacag agaaactgac aataacttac 1620
tcacgtgcaa tgatgtggga gattaatggt cctgaatcag tgttggtcaa tacctatcaa 1680
tggatcatca gaaactggga aactgttaaa attcagtggg cccagaaccc tacaatgcta 1740
tacaataaaa tggaatttga accatttcag tctttagtac ctaaggccat tagaggccaa 1800
tacagtgggt ttgtaagaac tctgttccaa caaatgaggg atgtgcttgg gacatttgat 1860
accgcacaga taataaaact tcttccttc gcagccgctc caccaaagca aagtagaatg 1920
cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatact tgtaaggggc 1980
aattctctcg tattcaacta caacaaggcc acgaagagac tcacagtctc cggaaggat 2040
gctggcactt taaccgaaga cccagatgaa ggcacagctg gagtggagtc cgctgttctg 2100
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gaactgagca accttgcgaa aggagagaag gctaattgtc taattgggca aggagacgtg 2220
gtgttggtaa tgaaacgaaa acgggactct agcatactta ctgacagcca gacagcgacc 2280
aaaaagaattc ggatggccat caattagtgt cgaatagttt aaaaacgacc ttgtttctac 2340
t 2341

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<210> SEQ ID NO 34
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza A

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<400> SEQUENCE: 34

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ccagcacaaa atgctataag cacaacttcc ccttataccg gagaccctcc ttacagccat 120
gggacaggaa caggatcac catggatact gtcaacagga cacatcagta ctgagaaaag 180
ggaagatgga caacaacac cgaaactgga gcaccgcaac tcaaccgat tgatgggcca 240
ctgccagaag acaatgaacc aagtgggtat gcccaaacag attgtgtatt ggaagcaatg 300
gctttccttg aggaatccca tcctgggtatt tttgaaaact cgtgtattga aacgatggag 360
gttgttcagc aaacacgagt agacaagctg acacaaggcc gacagaccta tgactggact 420
ttaaatagaa accagcctgc tgcaacagca ttggccaaca caatagaagt gttagatca 480
aatggcctca cggccaatga gtcaggaagg ctcataagct tccttaagga tgtaatggag 540
tcaatgaaaa aagaagaat ggggatcaca actcatttcc agagaaagag acgggtgaga 600
gacaatatga ctaagaaaat gataacacag agaacaatag gtaaaaggaa acagagattg 660
aacaaaaggg gttatctaata tagagcattg accctgaaca caatgaccaa agatgctgag 720
agaggggaagc taaaacggag agcaattgca accccaggga tgcaaataag ggggtttgta 780
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gttgagggca atgagaagaa agcaaagtgt gcaaatgttg taaggaagat gatgaccaat 900
tctcaggaca ccgaacttcc tttcaccatc actggagata acaccaaatg gaacgaaaat 960
cagaatcctc ggatgttttt ggccatgatc acatatatga ccagaaatca gcccgaaatg 1020
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aaagggtata tgtttgagag caagagtatg aaacttagaa ctcaaatacc tgcagaaatg 1140
ctagcaagca ttgatttgaa atatttcaat gattcaacaa gaaagaagat tgaaaaaatc 1200
cgaccgctct taatagaggg gactgcacaa ttgagccctg gaatgatgat gggcatgttc 1260

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aatatgttaa gcaactgtatt aggcgtctcc atcctgaatc ttggacaaaa gagatacacc	1320
aagactactt actgggtggga tgggtcttcaa tctctgacg attttgcctt gattgtgaat	1380
gcacccaatc atgaagggat tcaagccgga gtcgacaggt tttatcgaac ctgtaagcta	1440
cttggaatca atatgagcaa gaaaaagtct tacataaaca gaacaggtac attgaattc	1500
acaagttttt tctatcgta tgggtttgtt gccaatcca gcatggagct tcccagtttt	1560
ggggtgtctg ggatcaacga gtcagcggac atgagtattg gagttactgt catcaaaaac	1620
aatatgataa acaatgatct tgggtccagca acagctcaaa tggcccttca gttgttcac	1680
aaagattaca ggtacacgta ccgatgccat agaggtgaca cacaatatca aaccgaaga	1740
tcatttgaat taaagaaact gtgggagcaa acccggtcca aagctggact gctggtctcc	1800
gacggaggcc caaatattata caacattaga aatctccaca ttctgaagt ctgcctaaaa	1860
tgggaattga tggatgagga ttaccagggg cgtttatgca acccactgaa cccatttgtc	1920
agccataaag aaattgaatc aatgaacaat gcagtgatga tgccagcaca tgggtccagcc	1980
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<211> LENGTH: 2233

<212> TYPE: DNA

<213> ORGANISM: Influenza A

<400> SEQUENCE: 35

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<210> SEQ ID NO 36

<211> LENGTH: 1565

<212> TYPE: DNA

<213> ORGANISM: Influenza A

<400> SEQUENCE: 36

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<210> SEQ ID NO 37
<211> LENGTH: 1027
<212> TYPE: DNA
<213> ORGANISM: Influenza A

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<400> SEQUENCE: 37

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gtgatcctct cgctattgcc gcaaatatca ttgggatctt gcacttgata ttgtggattc 840
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<210> SEQ ID NO 38
<211> LENGTH: 890
<212> TYPE: DNA
<213> ORGANISM: Influenza A

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<400> SEQUENCE: 38

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What is claimed is:

1. A composition comprising a plurality of influenza virus vectors, comprising

a) i) a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the cDNAs for PB1, PB2, PA, NP, NA, and M have sequences that encode a polypeptide having at least 99% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-5 and a polypeptide having at least 90% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:8, a cDNA for NS that has a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38 and encodes a polypeptide having at least 97% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:6, and wherein the cDNA for HA has sequences from a different influenza virus strain than a strain having gene segments with sequences corresponding to the cDNAs for PB1, PB2, PA, NP, M, NS, and NA having SEQ ID Nos. 1-6 and 8; or

ii) a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the cDNAs for PB1, PB2, PA, NP, and M have sequences that encode a polypeptide having at least 99% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-5, a cDNA for NS that has a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38 and encodes a polypeptide having at least 97% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:6, wherein the cDNA for NA is from the one or more influenza viruses that replicate to high titers in embryonated eggs or has sequences for a heterologous NA, and wherein the cDNA for HA has sequences for a heterologous HA;

or iii) a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination

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sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the cDNAs for PB1, PB2, PA, NP, and M have sequences that encode a polypeptide having at least 99% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-5, wherein the PB2 has a tyrosine at position 360, a cDNA for NS that has a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38 and encodes a polypeptide having at least 97% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:6, wherein the cDNA for NA has sequences for a heterologous NA, and wherein the cDNA for HA has sequences for a heterologous HA; and

b) a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NS2,

wherein the plurality of vectors of a)i) or a)ii) and b), when introduced to cells, result in production of influenza virus which is capable of enhanced replication in embryonated eggs relative to a corresponding influenza virus that does not have a NA with sequences that encode polypeptide having at least 90% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:8, does not have a NA from an influenza virus that replicates to high titers in embryonated eggs or does not have sequences for a heterologous NA, or does not have a NS with a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38; or

wherein the plurality of vectors of a)iii) and b), when introduced to cells, result in production of influenza virus which is capable of enhanced replication in MDCK cells relative to a corresponding influenza virus that does not have a NA with sequences for a heterologous NA, has a PB2 with a serine at position 360, or does not have a NS with a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38.

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2. The composition of claim 1, wherein the cDNAs for PB1, PB2, PA, NP, and M encode a polypeptide encoded by SEQ ID NOs:1-5.

3. The composition of claim 1, wherein the cDNA for NS encodes a polypeptide encoded by SEQ ID NO:38.

4. The composition of claim 1, wherein the promoter is a RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T3 promoter or a T7 promoter.

5. The composition of claim 1, wherein a plurality of the vectors of a) comprise a RNA polymerase I promoter or a RNA polymerase II promoter.

6. The composition of claim 5, wherein the RNA polymerase I promoter is a human RNA polymerase I promoter.

7. The composition of claim 1, wherein each vector of a) is on a separate plasmid.

8. The composition of claim 1, wherein the NA or HA is a chimeric NA or HA.

9. The composition of claim 1, wherein the cDNA for HA does not encode a polypeptide corresponding to the polypeptide encoded by SEQ ID NO:7.

10. A method to prepare influenza virus, comprising: contacting a cell with one of:

i) a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the cDNAs for PB1, PB2, PA, NP, NA, and M have sequences that encode a polypeptide having at least 99% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-5 and a polypeptide having at least 90% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:8, a cDNA for NS that has a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38 and encodes a polypeptide having at least 97% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:6, and wherein the cDNA for HA has sequences from a different influenza virus strain than a strain having gene segments with sequences corresponding to the cDNAs for PB1, PB2, PA, NP, M, NS, and NA having SEQ ID Nos. 1-6 and 8;

and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector com-

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- prising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NS2;
- ii) a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the cDNAs for PB1, PB2, PA, NP, and M have sequences that encode a polypeptide having at least 99% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-5, a cDNA for NS that has a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38 and encodes a polypeptide having at least 97% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:6, wherein the cDNA for NA is from the one or more influenza viruses that replicate to high titers in embryonated eggs or has sequences for a heterologous NA, and wherein the cDNA for HA has sequences for a heterologous HA; and
- a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NS2; or
- iii) a vector comprising a promoter operably linked to an influenza virus PA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 cDNA linked to a transcription termination sequence, a vector comprising a promoter operably

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linked to an influenza virus HA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA cDNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the cDNAs for PB1, PB2, PA, NP, and M have sequences that encode a polypeptide having at least 99% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-5, wherein the PB2 has a tyrosine at position 360, a cDNA for NS that has a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38 and encodes a polypeptide having at least 97% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:6, wherein the cDNA for NA has sequences for a heterologous NA, and wherein the cDNA for HA has sequences for a heterologous HA; and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector comprising a promoter operably linked to a DNA segment encoding influenza virus NS2;

in an amount effective to yield infectious influenza virus, wherein the vectors of i) or ii), when introduced to cells, result in production of influenza virus which is capable of enhanced replication in embryonated eggs relative to a corresponding influenza virus that does not have a NA with sequences that encode polypeptide having at least 90% contiguous amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NO:8, does not have a NA from an influenza virus that replicates to high titers in embryonated eggs or does not have sequences for a heterologous NA, or does not have a NS with a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38; or

wherein the vectors of iii), when introduced to cells, result in production of influenza virus which is capable of enhanced replication in MDCK cells relative to a corresponding influenza virus that does not have a NA with sequences for a heterologous NA, has a PB2 with a serine at position 360, or does not have a NS with a Glu residue at position 55 corresponding to position 55 in a NS1 polypeptide encoded by SEQ ID NO:38.

11. The method of claim 10 further comprising isolating the virus.

12. An isolated recombinant influenza virus comprising i) a viral segment for PB1, PB2, PA, NP, M, and NA that is

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from an influenza virus that replicates to high titers in embryonated eggs, a viral segment for NS with a Glu residue at position 55 which corresponds to position 55 in a NS1 polypeptide encoded by SEQ ID NO:6, and a viral segment for a heterologous HA; ii) a viral segment for PB1, PB2, PA, NP, and M that is from an influenza virus that replicates to high titers in embryonated eggs, a viral segment for NS with a Glu residue at position 55 which corresponds to position 55 in a NS1 polypeptide encoded by SEQ ID NO:6, a viral segment for NA that is from a virus that replicates to high titers in embryonated eggs, and a viral segment for a heterologous HA; or iii) a viral segment for PB2 that encodes a PB2 having at least 99% amino acid sequence identity to a PB2 encoded by SEQ ID NO:3 or SEQ ID NO:33 which PB2 has a serine or tyrosine at position 360 which corresponds to position 360 in a PB2 polypeptide encoded by SEQ ID NO:3 but which viral segment does not encode a PB2 encoded by SEQ ID NO:3 or SEQ ID NO:33.

13. The isolated recombinant virus of claim **12**, wherein the influenza virus that replicates to high titers is PR8HG.

14. The isolated recombinant influenza virus of claim **12** ii, wherein the viral segment for PB1, PB2, PA, NP, and M is from PR8HG.

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15. The isolated recombinant influenza virus of claim **12** ii, wherein the viral segment for NA is from PR8.

16. The isolated recombinant influenza virus of claim **12** ii, wherein the viral segment for NA is heterologous to the viral segments for PB1, PB2, PA, NP, and M.

17. The isolated recombinant influenza virus of claim **12** ii, wherein the viral segment for HA is for H5.

18. The isolated recombinant virus of claim **12** iii, which has one or more but less than 20 substitutions relative to SEQ ID NO:3.

19. The isolated recombinant virus of claim **18**, wherein the one or more substitutions include conservative substitutions.

20. The composition of claim **1** a)i), wherein the PB2 has a serine at position 360.

21. The composition of claim **1** a)ii), wherein the cDNAs for PB1, PB2, PA, or NP encode a polypeptide encoded by one of SEQ ID NOs:33-36.

22. The composition of claim **1** a)ii), wherein the PB2 has a serine at position 360.

23. The composition of claim **1** a)iii), wherein the cDNAs for PB1, PB2, PA, and NP do not encode a polypeptide encoded by one of SEQ ID NOs:33-36.

* * * * *