~~WHAT IS CLAIMED:~~

~~1. A reassortant influenza virus comprising:~~

~~internal gene segments PB1, PB2, PA, M, NP and NS from a first influenza virus A subtype and hemagglutinin (HA) and neuraminidase (NA) genes from the influenza virus subtype from which the internal gene segments are derived, the internal gene segments derived from a first strain of an influenza A subtype and the HA and NA genes derived from a second strain in the influenza A subtype.~~

~~2. A purified reassortant influenza virus of claim 1 comprising internal gene segmetns PB1, PB2, PA, M, NP and NS of an H5N1 strain of influenza A and hemagglutinin (HA) and neuraminidase (NA) genes from an H5N1 influenza A virus, the HA and NA genes derived from the same viral strain.~~

~~3. The reassortant virus of claim 2 wherein the HA and NA genes are from a first H5N1 clade and the internal genes are from a second H5N1 clade.~~

~~4. The reassortant virus of claim 2 wherein the HA and NA genes and the internal genes are from the same H5N1 clade.~~

~~5. The reassortant virus of claim 1 or claim 2, the HA gene modified to produce an attenuated virus.~~

~~6. The virus of claim 5, said HA gene modified at a polybasic cleavage site.~~

~~7. The virus of claim 1 or claim 2 characterized by the ability to propagate in mammalian cell culture.~~

~~8. The virus of claim 7, wherein the mammalian cells are selected from the group consisting of MRC-5, MRC-9, Lederle 130, Chang liver and WI-38; U937,Vero, CV-1, IMR-90 and IMR-91, MDCK, MDBK, HEK, H9, CEM and CD4 expressing HUT78, PerC6, BHK-21 cells, BSC and LLC-MK2.~~

~~9. The virus of claim 7, wherein the mammalian cell culture is a Vero cell culture.~~

~~10. The virus of claim 1, said internal genes derived from an H5N1 strain selected from the group consisting of A/Vietnam/1203/2004, A/Hong Kong/213/03, A/Indonesia/5/05, A/turkey/Turkey/1/05, A/Anhui/1/05, A/Cambodia/R0405050/2007(H5N1), A/chicken/Nakorn-Patom/Thailand/CU-K2/04, A/chicken/Vietnam/C58/04,~~

~~A/quail/Vietnam/36/04, MDk/JX/1653/05, MDk/1657/JX/05, BH goose/QH/65/05, Gs/GD/l/96-like, Dk/Vietnam/568/05, Gs/GX/345/05, MDk/JX/1701/05, MDk/JX/2136/05, MDk/JX/2295/05, MDk/JX/2300/05, Dk/GX/351/04, Dk/GX/380/04, Dk/ST/4610/03, Ck/MYS/5858/04, Ck/Salatiga/BBVet-I/05, and Dk/VNM/S654/05, A/chicken/Vietnam/CSδ/OS, A/Muscovy Duck/Vietnam/453/2004, A/duck/Singapore/3/97, A/HK/156/97, and A/Hong Kong/156/1996.~~

~~11. The virus of claim 1 , said HA and NA genes derived from an H5N1 strain selected from the group consisting of A/Vietnam/1203/2004, A/Hong Kong/213/03, A/Indonesia/5/05, A/Hong Kong/156/97 (H5N1), A/Indonesia/5/05 (H5N1), A/turkey/Turkey/01/2005(H5Nl), A/Anhui/l/05(H5Nl), A/Cambodia/R0405050/2007(H5N1), A/chicken/Nakorn-Patom/Thailand/CU-K2/04, A/chicken/Vietnam/C58/04, A/quail/Vietnam/36/04, MDk/JX/1653/05, MDk/1657/JX/05, BH goose/QH/65/05, Gs/GD/l/96-like, Dk/Vietnam/568/05, Gs/GX/345/05, MDk/JX/1701/05, MDk/JX/2136/05, MDk/JX/2295/05, MDk/JX/2300/05, Dk/GX/351/04, Dk/GX/380/04, Dk/ST/4610/03, Ck/MYS/5858/04, Ck/Salatiga/BBVet-I/05, and Dk/VNM/S654/05, A/chicken/Vietnam/C58/05, A/Muscovy Duck/Vietnam/453/2004, A/duck/Singapore/3/97, A/HK/156/97, and A/Hong Kong/156/1996.~~

~~12. The virus of claim 1 wherein the internal genes and the HA and NA genes are derived from the same virus strain.~~

~~13. The virus of claim 1 wherein the internal genes and the HA and NA genes are derived from different virus strains.~~

~~14. The virus of any one of claims 1 to 13, said internal genes from the H5N1 strain A/Vietnam/ 1203/2004.~~

~~15. The virus of any one of claims 1 to 14, wherein the HA and NA genes are from the H5N1 strain A/Vietnam/ 1203/2004.~~

~~16. The virus of any one of claims 1 to 14, wherein the HA and NA genes are from the H5N1 strain A/Indonesia/5/05.~~

~~17. The virus of any one of claims 1 to 16 wherein the modification at the polybasic cleavage site is mutation from RERRRKKR (SEQ ID NO: 13)→ TETR (SEQ ID NO: 14).~~

WHAT IS CLAIMED:

~~18.~~1. An antigenic reassortant influenza virus composition comprising,

(i) internal gene segments PB1, PB2, PA, M, NP and NS from a first H5N1 influenza virus A ~~subtype~~ strain and (ii) hemagglutinin (HA) and neuraminidase (NA) genes from ~~the~~ a second H5N1 influenza virus ~~subtype from which the internal gene segments are derived, the internal gene segments derived from a first strain of an influenza A subtype and the HA and NA genes derived from a second strain in the influenza A subtype~~A strain, the HA and NA genes being from the same viral strain.

~~19. The antigenic reassortant virus composition of claim 18, the antigenic composition comprising internal gene segments PB1, PB2, PA, M, NP and NS derived from an H5N1 strain of influenza A and hemagglutinin (HA) and neuraminidase (NA) genes derived from an H5N1 influenza A virus, the HA and NA genes derived from the same viral strain.~~

~~20.~~2. The antigenic ~~reassortant influenza virus~~ composition of claim ~~18 or claim 19~~1, said HA gene modified to produce an attenuated virus.

~~21.~~3. The antigenic ~~reassortant influenza virus~~ composition of claim ~~20~~2, said HA gene modified at a polybasic cleavage site.

~~22.~~4. The antigenic ~~reassortant influenza virus~~ composition virus of claim ~~18 or claim 19~~1, said influenza virus characterized by the ability to propagate in mammalian cell culture, optionally wherein the mammalian cells are selected from the group consisting of MRC-5, MRC-9, Lederle 130, Chang liver and WI-38; U937, Vero, CV-1, IMR-90 and IMR-91, MDCK, MDBK, HEK, H9, CEM and CD4-expressing HUT78, PerC6, BHK-21 cells, BSC and LLC-MK2, preferably wherein the mammalian cell culture is a Vero cell culture.

~~23.~~5. The antigenic composition of claim ~~19~~1, said HA and NA genes derived from an H5N1 strain selected from the group consisting of A/Vietnam/1203/2004, A/Hong Kong/213/03, A/Indonesia/5/05, A/Hong Kong/156/97, A/turkey/Turkey/01/2005, A/Anhui/1/05, A/Cambodia/R0405050/2007, A/chicken/Nakorn-Patom/Thailand/CU-K2/04, A/chicken/Vietnam/C58/04, A/quail/Vietnam/36/04, MDk/JX/1653/05, MDk/1657/JX/05, BH goose/QH/65/05, Gs/GD/l/96-like, Dk/Vietnam/568/05, Gs/GX/345/05, MDk/JX/1701/05, MDk/JX/2136/05, MDk/JX/2295/05, MDk/JX/2300/05, Dk/GX/351/04, Dk/GX/380/04, Dk/ST/4610/03, Ck/MYS/5858/04, Ck/Salatiga/BBVet-I/05, and Dk/VNM/S654/05, ~~A/chicken/Vietnam/C58/05,~~and A/Muscovy Duck/Vietnam/453/2004~~, A/duck/Singapore/3/97, A/HK/156/97, and A/Hong Kong/156/1996~~.

~~24.~~6. The antigenic composition of claim ~~19~~1, said internal genes derived from an H5N1 strain selected from the group consisting of A/Vietnam/1203/2004, A/Hong Kong/213/03, A/Indonesia/5/05, A/Hong Kong/156/97, A/turkey/Turkey/01/2005, A/Anhui/1/05, A/Cambodia/R0405050/2007, A/chicken/Nakorn-Patom/Thailand/CU-K2/04, A/chicken/Vietnam/C58/04, A/quail/Vietnam/36/04, MDk/JX/1653/05, MDk/1657/JX/05,

BH goose/QH/65/05, Gs/GD/1/96-like, Dk/Vietnam/568/05, Gs/GX/345/05, MDk/JX/1701/05, MDk/JX/2136/05, MDk/JX/2295/05, MDk/JX/2300/05, Dk/GX/351/04, Dk/GX/380/04, Dk/ST/4610/03, Ck/MYS/5858/04, Ck/Salatiga/BBVet-I/05, and Dk/VNM/S654/05, ~~A/chicken/Vietnam/CS8/OS,~~and A/Muscovy Duck/Vietnam/453/2004~~, A/duck/Singapore/3/97, A/HK/156/97, and A/Hong Kong/156/1996~~.

~~25.~~7. The antigenic composition of claim ~~18~~1, wherein the internal gene segments and the HA and NA genes are derived from the same virus strain.

~~26.~~8. The antigenic composition of claim ~~18~~1, wherein the internal gene segments and the HA and NA genes are derived from different virus strains.

~~27.~~9. The antigenic composition of any one of claims ~~18~~ 1 to ~~26~~8, wherein the internal gene segments are from A/Vietnam/ 1203/2004.

~~28.~~10. The antigenic composition of any one of claims ~~18~~ 1 to ~~27~~8, wherein the HA and NA genes are from the H5N1 strain A/Vietnam/ 1203/2004 or from the H5N1 strain A/Indonesia/5/05.

~~29. The antigenic composition of any one of claims 18 to 27, wherein the HA and NA genes are from the H5N1 strain A/Indonesia/5/05.~~

~~30.~~11. The antigenic composition of ~~any one of claims 21 to 29~~claim 3, wherein the modification at the polybasic cleavage site is mutation from **R**ERRRK**K**R (SEQ ID NO: 13) → **TET**R (SEQ ID NO: 14).

~~31.~~12. The antigenic composition of any one of claims ~~18~~ 1 to ~~29~~ 8 further comprising a pharmaceutically acceptable carrier.

~~32. A vaccine comprising a reassortant influenza virus, the virus comprising:~~

~~a polynucleotide encoding for surface protein HA and a polynucleotide encoding for surface protein NA, each of HA and NA derived from an first strain of an influenza virus A subtype; a polynucleotide encoding for PB1; a polynucleotide encoding for PA, a polynucleotide encoding for PB2, a polynucleotide encoding for M, a polynucleotide encoding for NP, a polynucleotide encoding for NS,, the polynucleotides for PB1, PA, PB2, M, NP and NS derived from a second strain of an influenza A virus subtype,~~

~~wherein the polynucleotides are operatively linked to allow packaging of the reassorted polynucleotides into a virion.~~

~~33.~~13. A vaccine comprising a reassortant influenza A virus ~~of claim 32~~, the virus comprising: ~~a polynucleotide encoding for surface protein HA and a polynucleotide encoding for surface protein NA, each of HA and NA derived from an H5N1 influenza virus,~~(i) a polynucleotide encoding for PB1; a polynucleotide encoding for PA, a polynucleotide encoding for PB2, a polynucleotide encoding for M, a polynucleotide encoding for NP, a polynucleotide encoding for NS, the polynucleotides for PB1, PA, PB2, M, NP and NS derived from ~~an~~ a first H5N1 influenza virus, and (ii) a polynucleotide encoding for surface protein HA and a polynucleotide encoding for surface protein NA, each of HA and NA derived from a second H5N1 influenza virus, the polynucleotides being operatively linked to allow packaging of the reassorted polynucleotides into a virion.

~~34.~~14. The ~~antigenic reassortant influenza virus composition~~vaccine of claim ~~32 or claim 33~~13, said HA gene modified to produce an attenuated virus.

~~35.~~15. The ~~antigenic reassortant influenza virus composition~~vaccine of claim ~~34~~14, said HA gene modified at a polybasic cleavage site.

~~36.~~16. The vaccine of claim ~~33~~13, said internal genes derived from an H5N1 strain selected from the group consisting of A/Vietnam/1203/2004, A/Hong Kong/213/03, A/Indonesia/5/05, A/Hong Kong/156/97, A/turkey/Turkey/01/2005, A/Anhui/1/05, A/Cambodia/R0405050/2007A/chicken/Nakorn-Patom/Thailand/CU-K2/04, A/chicken/Vietnam/C58/04, A/quail/Vietnam/36/04, MDk/JX/1653/05, MDk/1657/JX/05, BH goose/QH/65/05, Gs/GD/1/96-like, Dk/Vietnam/568/05, Gs/GX/345/05, MDk/JX/1701/05, MDk/JX/2136/05, MDk/JX/2295/05, MDk/JX/2300/05, Dk/GX/351/04, Dk/GX/380/04, Dk/ST/4610/03, Ck/MYS/5858/04, Ck/Salatiga/BBVet-I/05, and Dk/VNM/S654/05, ~~A/chicken/Vietnam/C58/05,~~and A/Muscovy Duck/Vietnam/453/2004~~, A/duck/Singapore/3/97, A/HK/156/97, and A/Hong Kong/156/1996~~.

~~37.~~17. The vaccine of claim ~~33~~13, said HA and NA genes derived from an H5N1 strain selected from the group consisting of A/Vietnam/1203/2004, A/Hong Kong/213/03, A/Indonesia/5/05, A/Hong Kong/156/97, A/turkey/Turkey/01/2005, A/Anhui/1/05, A/Cambodia/R0405050/2007A/chicken/Nakorn-Patom/Thailand/CU-K2/04, A/chicken/Vietnam/C58/04, A/quail/Vietnam/36/04, MDk/JX/1653/05, MDk/1657/JX/05, BH goose/QH/65/05, Gs/GD/1/96-like, Dk/Vietnam/568/05, Gs/GX/345/05, MDk/JX/1701/05, MDk/JX/2136/05, MDk/JX/2295/05, MDk/JX/2300/05, Dk/GX/351/04, Dk/GX/380/04, Dk/ST/4610/03, Ck/MYS/5858/04, Ck/Salatiga/BBVet-I/05, and Dk/VNM/S654/05, ~~A/chicken/Vietnam/C58/05,~~and A/Muscovy Duck/Vietnam/453/2004~~, A/duck/Singapore/3/97, A/HK/156/97, and A/Hong Kong/156/1996~~.

~~38.~~18. The vaccine of ~~any one of claims 32 or 33~~claim 13, wherein the internal gene segments and the HA and NA genes are derived from the same virus strain.

~~39.~~19. The vaccine of ~~any one of claims 32 or 33~~claim 13, wherein the internal gene segments and the HA and NA genes are derived from different virus strains.

~~40.~~20. The vaccine of ~~any one of claims 32 to 39~~claim 13, wherein the HA and NA genes are from the H5N1 strain A/Vietnam/1203/2004 or from H5N1 strain A/Indonesia/5/05.

~~41. The vaccine of any one of claims 32 to 39, wherein the HA and NA genes are from the H5N1 strain A/Indonesia/5/05.~~

~~42.~~21. The vaccine of ~~any one of claims 32 to 41~~claim 13, wherein the HA is modified at the polybasic cleavage site by mutation from **R**E*RRRK***K**R (SEQ ID NO: 13)→ **T**E**T**R (SEQ ID NO: 14).

~~43.~~22. The vaccine of ~~any one of claims 32 to 42~~claim 13 further comprising an adjuvant.

~~44.~~23. The vaccine of ~~any one of claims 32 to 43~~claim 13, wherein the vaccine is an inactivated vaccine.

~~45.~~24. The vaccine of ~~any one of claims 32 to 44~~claim 13 comprising an HA content of from 1 μg to 100 μg HA.

~~46.~~25. ~~Use of an~~The antigenic composition of any one of claims ~~18~~ 1 to ~~31~~ 8 or ~~a~~ the vaccine of any one of claims ~~32~~ 13 to ~~45~~ 24 ~~in the manufacture of a medicament~~ for use in eliciting an immune response to at least one pandemic influenza virus strain in a subject in an amount effective to protect the subject against infection of at least one H5N1 influenza virus strain.

~~47.~~26. ~~Use of a virus of any one of claims 1 to 17, an~~The antigenic composition of any one of claims ~~18~~ 1 to ~~31~~ 8 or ~~a~~ the vaccine of any one of claims ~~32~~ 13 to ~~45~~ 24 ~~in the manufacture of a medicament~~ for use in preventing infection of a subject by an influenza virus.

~~48. Use of a virus of any one of claims 1 to 17, an antigenic composition of any one of claims 18 to 31 or a vaccine of any one of claims 32 to 45 in the manufacture of a medicament for preventing infection of a subject by an H5N1 influenza virus.~~

27. Use of the antigenic composition of any one of claims 1 to 8 or the vaccine of any one of claims 13 to 24 in the manufacture of a medicament for eliciting an immune response to at least one pandemic influenza virus strain in a subject, wherein the medicament is in an amount effective to protect the subject against infection of at least one H5N1 influenza virus strain.

28. Use of the antigenic composition of any one of claims 1 to 8 or the vaccine of any one of claims 13 to 24 in the manufacture of a medicament for preventing infection of a subject by an influenza virus.

~~49.~~29. The ~~use~~ antigenic composition or vaccine of claim ~~48~~26 or use of claim 28, wherein the vaccine comprises an HA content of from 1 μg to 100 μg HA.

~~50.~~30. The antigenic composition or vaccine or use of claim ~~49~~29, wherein the vaccine comprises an HA content of from 1 μg to 30 μg HA.

~~51.~~31. The antigenic composition or vaccine or use of claim ~~49~~29, wherein the vaccine comprises 1 μg to 15 μg HA.

~~52.~~32. The antigenic composition or vaccine~~use~~ of claim ~~48~~26 or use of claim 28, wherein the vaccine comprises an HA content of 10 ng to 1 μg HA units.

~~53.~~33. A method of making a vaccine comprising a reassortant influenza virus comprising, internal gene segments PB1, PB2, PA, M, NP and NS of ~~an~~ a first H5N1 strain of influenza A and the hemagglutinin (HA) and neuraminidase (NA) genes from ~~an~~ a second H5N1 influenza A virus, the HA and NA genes derived from the same viral strain and the HA gene modified at a polybasic cleavage site to produce an attenuated HA gene, the method comprising transfecting the virus in ex vivo mammalian cells under conditions suitable for growth of the reassortant virus.

~~54.~~34. The method of claim ~~53~~33, wherein the mammalian cells are selected from the group consisting of MRC-5, MRC-9, Lederle 130, Chang liver and WI-38; U937,Vero, CV-1, IMR-90 and IMR-91, MDCK, MDBK, HEK, H9, CEM and CD4-expressing HUT78, PerC6, BHK-21 cells, BSC and LLC-MK2.

~~55.~~35. The method of claim ~~53~~33, wherein the mammalian cells are Vero cells.