

India 2013-03

Antigenic Variation

Impressions on FluTrackers' thread:

[India's National Institute of Virology finds "small mutation" in circulating H1N1 virus](#)

Clarification on the recently published quotes from the **National Institute of Virology of India** is required due to **editorial error** in the news article. The facts in this **GeneWurx RnR Analytic** synopsis are derived from two recent deposits made to **GISAID** by the **Centers for Disease Control** of the United States. No age, gender or clinical outcome data were provided. **Administration Note:** The **NIV** polymorphism numbering used in the news article must be adjusted in order to compare directly with the **GeneWurx** detections. Please add 3 to the numbering from the **Indian NIV** statements to align their work with the **GeneWurx** polymorphism details that follow, e.g. **NIV HA 97N** + 3 Amino Acid Positions = **GeneWurx HA 100N**.

The sequences on file at **GISAID** indicate that all 15 **pH1N1 Hemagglutinin** segments sampled from India in the month between 2012_12_25 and 2012_11_26 fall onto the most widespread **pH1N1** clade, **Clade2:188T**, according to circulation sampling. **CladeCrossing** from **Clade3:186P** is demonstrated as a mixture on a sequence that was sampled 2012_11_26. That [sequence](#), **India2018_E3_2012_11_26**, also demonstrates candidate antigenic revision at **HA 87D**, **166I**, **194I** & **226R** with **mixed traces** at 3 amino acid locations, potentially indicating co-infection. **Rare changes** are [seeded](#) throughout India.

In a related note, the **pH1N1 Hemagglutinin** reservoir has continued a **variation ascent** at aa87 with candidate zoonotic acquisitions of **HA 87D** [**H6N1**, **avH1N1_{farm}**], **87G** [**H6N1**], **87I** [**H5N1_{LAu}**, **zH3N2_{LAd}**], **87N** [**H5N1**, **H6N1**, **H10**, **avH1N1_{farm}**] and **syn87S** (**AGc**) [**H5N1**]. The **HA 87N** and **syn87S** are found on the **High-CFR pH1N1 Clade1.Upsilon** branch while the **HA 87I** appears on **pH1N1** sequences that carry the **TamiFlu Resistance** marker **NA 247N**. India [follows](#) the **pH1N1** trend of **HA 87D**, **87G** & **87I** co-circulation. **India2005_E3_2012_11_24** is [genetically imprinted](#) for **Vaccine Escape** potential. Additionally, the **pH1N1 HA trend** at aa166 includes India.

Hemagglutinin variation is **over-represented** at the recognised **Receptor Binding Site** positions of 225 (2 instances) and 226 (3 instances). **HA 194I** & **237I** polymorphisms found up- and down-stream elevate risk of antigen escape. **Mixed traces**, where more than one value is derived from nucleotide data found at a single location, also are **over-represented** in this group of **HA** segments from India. The quantity of trace mixtures is suggestive of **open promiscuity** and high receptivity of the present circulation **to internal and external** serotype partnering for genetic acquisition.

The polymorphism at question within the news article was not actually stated due either to typographical errors or editorial shortcoming. We estimate that the **NIV of India** researchers are referring to **HA 286E**, a marker potentially gained from **Avian H6N1**. **HA 286E** is becoming a mainstay on one **modern hydrae** of **Clade2:188T** displaying **strong fitness bases** in the Southern and Northern Hemispheres.

More reasonable points of study include **India2205_E3_2012_12_24**, an embryonated egg-passaged isolate demonstrating **HA 225G**. This sequence properly focuses [risk beyond](#) the media discussion due to quantity and placement of **HA** polymorphisms (22), including **hydrae-defining 237I**, **286E** & **502K** on the same sequence as the zoonotic **152M** and **255I**. Furthermore, [within](#) the 19 **HA** changes on **India2055_E3_2012_12_03** (also with **HA 225G**), we find a potential **HA 54N** demonstration of inter-group import from **zH3N2**. **Antigenic diversity** is firmly rooted on the **sub-continent**.

The matters of **antigenic diversity** & **zoonotic transfer** represent the crux of India's public health risk.

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pH1N1

India 2013 Deposits

HA Polymorphisms

pH1N1 Influenza Hemagglutinin & Neuraminidase Segments elucidated at 2013-02-21-18_34_07_54294 by GeneWurx see.PolyDetector v0, Copyright 2007-2013.
 Sequences discussed in this analysis are variously stored publicly at GenBank and privately at GISAID. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GenBank and from GISAID's EpiFlu™ Database on which this research is based. A GISAID-generated list is detailed in a PDF titled "GeneWurx_GISAID_CDC_Citations_India_2013_03_21.pdf" for completeness in citation.

HA Polymorphisms

2013_02_21_CDC

GISAID

.... India2019_E3_2012_11_26 (
 GISAID HA [EPI422607](#)
 22 Polymorphisms (9 Amino and 13 Silent)
 syn#4Y (TAc),
 syn39K (AAa),
 syn77S (AGt),
 100N,
 syn179L (CTg),
 188T,
 194I,
 237I,
 syn272D (GAc),
 286E,
 syn308K (AAg),
 syn333F (TTc),
 syn338G (GGc),
 syn370S (AGt),
 syn372Q (CAa),
 377K,
 syn396V (GTg),
 syn428L (CTa),
 syn448L (TTg),
 454N,
 475N,
 502K)

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.... India2018_E3_2012_11_26 (
..... GISAID HA [EPI422604](#)
..... **CladeCrossing** Clade3:186P onto Clade2:188T
..... 25 Polymorphisms (12 Amino and 13 Silent)
..... #6M,
..... syn34N (AAt),
..... **87D** [Avian H6N1],
..... [avH1N1_{farm}],
..... syn122K (AAa),
..... 146G,
..... **166I**,
..... **186P** mix wt,
..... 188T,
..... syn194L (cTa) mix,
..... **194I** mix,
..... 200T,
..... **226R** mix wt,
..... syn258F (TTt),
..... syn275V (GTt),
..... syn337A (GCt),
..... syn338G (GGc),
..... 377K,
..... syn401N (AAt),
..... 454N,
..... syn465N (AAt),
..... syn487Y (TAc) **mix wt**,
..... syn488D (GAt),
..... **523A**,
..... syn524A (GCt),
..... syn538F (TTt))

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.... India2005_E3_2012_11_24 (
 GISAID HA [EPI422601](#)
 23 Polymorphisms (10 Amino and 13 Silent)
 ~ **Bangladesh5011_C2_55F_2012_09_26_VxX**
 GISAID HA [EPI418006](#)
 #6M,
 syn#5L (CTg),
 syn34N (AAAt),
 syn66G (GGg) [H5N1],
 **87G** [Avian H6N1],
 syn102E (GAa),
 syn122K (AAa),
 **142D** [**pH1N1 Rare** ([31](#))],
 [Co-location **pH1N1_u** Polymorphisms (15)],
 [Co-location **pH1N1 VxX** [indicators](#) 158E mix, 159D mix],
 [Co-location **pH1N1** [166Q](#)],
 [Co-location **pH1N1** [189D](#), [189T_xL](#), [190G](#)],
 [Co-location **pH1N1 RBS** 225G (2), 226R, 233H],
 [Co-location early **pH1N1** [237I](#)],
 [Co-location **pH1N1** Isolated [from Blood \(Serum\)](#)],
 [Studied with **pH1N1** Severe and Fatal [cases](#)],
 [**Wisconsin28_55M_2011_12_01**
 swine-like human H1N1 **variant** case
 with **pH1N1 PA** & **M** gene segments],
 [H9N2],
 [H13 LookAside_u],
 [zH3N2 LookAside_{d2}],
 [zH6N1 LookAside_{d2}],
 146G,
 188T,
 **194I**,
 200T,
 syn223V (GTa),
 syn240G (GGg),
 syn258F (TTt),
 syn338G (GGc),
 377K,
 **430I** [**pH1N1 Rare** ([18](#))],

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..... [Origin Era **pH1N1** (12)],
 [Re-Emergent **pH1N1** Norway, India and Canada within **33 day** time span],
 [**CladeCrossing pH1N1** on **Norway46_M2_55F_2012_12_18** [with](#) 166R],
 [Co-location **pH1N1_u** Polymorphisms (20)],
 [Co-location **pH1N1 VxX** [indicator](#) 156N],
 [Co-location **pH1N1** [186P](#), [189T](#), [218T](#)],
 [Co-location **pH1N1 RBS** [225G](#), [226R mix](#)],
 [**pH1N1** Severe [on](#) **BrazilRioDeJaneiro2459_25M_2009_07_02** **s**],
 [avH1N1_{farm}],
 [Avian H6N1],
 [Avian H7],
 454N,
 syn465N (AAt),
 syn515Q (CAa),
 syn524A (GCt),
 syn538F (TTt))

2013_02_08_CDC
GISAID

.... India2227_2012_12_25 (
 GISAID HA [EPI418234](#)
 17 Polymorphisms (8 Amino and 9 Silent)
 syn#4Y (TAc),
 syn77S (AGt),
 **87I** [H5N1 LookAside_u],
 [zH3N2 LookAside_d],
 100N,
 syn179L (CTg),
 188T,
 **237I**,
 **286E**,
 syn308K (AAG),
 syn333F (TTc),
 syn338G (GGc),
 syn372Q (CAa),
 377K,
 syn396V (GTg),

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..... syn448L (TTg),
..... 454N,
..... 502K)

.... India2205_2012_12_24 (
..... GISAID HA [EPI418232](#)
..... 20 Polymorphisms (8 Amino and 12 Silent)
..... syn#4Y (TAc),
..... syn39K (AAa),
..... syn77S (AGt),
..... 100N,
..... syn111V (GTa),
..... 152M [H5N1 LookAside_u],
..... [H7 LookAside_u],
..... [H9N2 LookAside_u],
..... syn179L (CTg),
..... 188T,
..... 237I,
..... 286E,
..... syn308K (AAG),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn448L (TTg),
..... 454N,
..... 502K,
..... syn538F (TTt))

.... India2205_E3_2012_12_24 (
..... GISAID HA [EPI417177](#)
..... 22 Polymorphisms (10 Amino and 12 Silent)
..... syn#4Y (TAc),
..... syn39K (AAa),
..... syn77S (AGt),
..... 100N,
..... syn111V (GTa),

..... 152M [H5N1 LookAside_u],
 [H7 LookAside_u],
 [H9N2 LookAside_u],
 syn179L (CTg),
 188T,
 225G,
 237I [avH1N1_{farm}],
 [H10],
 [H5N1 LookAside_u],
 [H6N1 LookAside_u],
 [H7 LookAside_u],
 [H9N2 LookAside_u],
 255I [avH1N1_{farm} LookAside_{u3}],
 [H5N1 LookAside_{u3}],
 [H6N1 LookAside_{u3}],
 [H7 LookAside_{u3}],
 [H9N2 LookAside_{u3}],
 [H10 LookAside_{u3}],
 286E [Avian H6N1],
 [H9N2 LookAside_u],
 syn308K (AAg),
 syn333F (TTc),
 syn338G (GGc),
 syn372Q (CAa),
 377K,
 syn396V (GTg),
 syn448L (TTg),
 454N,
 502K,
 syn538F (TTt))

.... India2192_E3_2012_12_22 (
 GISAID HA [EPI417194](#)
 20 Polymorphisms (10 Amino and 10 Silent)
 syn#4Y (TAc),
 54N [zH3N2],
 syn77S (AGt),
 100N,

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..... syn179L (CTg),
..... 188T,
..... 194I,
..... 237I,
..... 286E,
..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],
..... syn308K (AAG),
..... syn321L (TTa),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn448L (TTg),
..... 454N,
..... 502K)

.... India2181_E4_2012_12_21 (
..... GISAID HA [EPI418165](#)
..... 20 Polymorphisms (10 Amino and 10 Silent)
..... syn#4Y (TAc),
..... 54N [zH3N2],
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 226R,
..... 237I,
..... 286E,
..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],
..... syn308K (AAG),
..... syn321L (TTa),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn448L (TTg),

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Antigenic Variation

..... 454N,
..... 502K)

.... India2181_2012_12_21 (
..... GISAID HA [EPI418231](#)
..... 19 Polymorphisms (9 Amino and 10 Silent)
..... syn#4Y (TAc),
..... 54N [zH3N2],
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 237I,
..... 286E,
..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],
..... syn308K (AAg),
..... syn321L (TTa),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn448L (TTg),
..... 454N,
..... 502K)

.... India2171_E4_2012_12_19 (
..... GISAID HA [EPI418162](#)
..... 19 Polymorphisms (10 Amino and 9 Silent)
..... syn#4Y (TAc),
..... 54N [zH3N2],
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 194I,
..... 237I,
..... 286E,

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Antigenic Variation

..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],

..... syn308K (AAg),

..... syn333F (TTc),

..... syn338G (GGc),

..... syn372Q (CAa),

..... 377K,

..... syn396V (GTg),

..... syn448L (TTg),

..... 454N,

..... 502K)

.... India2150_C2_2012_12_17 (

..... GISAID HA [EPI418008](#)

..... 22 Polymorphisms (11 Amino and 11 Silent)

..... syn#4Y (TAc),

..... 54N [zH3N2],

..... syn77S (AGt),

..... 100N,

..... syn179L (CTg),

..... 188T,

..... 237I,

..... 267S [pH1N1 Novel [until](#) Austria73_St1_48M_2013_02_04],

..... 286E,

..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],

..... syn308K (AAg),

..... syn333F (TTc),

..... syn338G (GGc),

..... syn341E (GAg) mix wt [Widespread Avian],

..... syn356H (CAc),

..... syn372Q (CAa),

..... 377K,

..... syn396V (GTg),

..... 442N mix wt [Avian H7],

..... syn448L (TTg),

..... 454N,

..... 502K)

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Antigenic Variation

.... India2150_2012_12_17 (
..... GISAID HA [EPI417960](#)
..... 19 Polymorphisms (9 Amino and 10 Silent)
..... syn#4Y (TAc),
..... 54N [zH3N2],
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 237I,
..... 286E,
..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],
..... syn308K (AAg),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn356H (CAc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn448L (TTg),
..... 454N,
..... 502K)

.... India2080_2012_12_06 (
..... GISAID HA [EPI418228](#)
..... 21 Polymorphisms (8 Amino and 13 Silent)
..... syn#4Y (TAc),
..... syn39K (AAa),
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 237I,
..... syn239P (CCa),
..... 286E,
..... syn304G (GGg),
..... syn308K (AAg),
..... syn333F (TTc),

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..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn408E (GAa),
..... syn448L (TTg),
..... 454N,
..... 475N [Avian H6N1],
..... [avH1N1farm],
..... [H13],
..... [zH3N2],
..... 502K)

.... India2080_E4_2012_12_06 (
..... GISAID HA [EPI418168](#)
..... 22 Polymorphisms (9 Amino and 13 Silent)
..... syn#4Y (TAc),
..... syn39K (AAa),
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 194I mix wt,
..... 226R mix wt,
..... 237I,
..... syn239P (CCa),
..... 286E,
..... syn304G (GGg),
..... syn308K (AAG),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn408E (GAa),
..... syn448L (TTg),
..... 454N,
..... 502K)

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Antigenic Variation

.... India2055_E3_2012_12_03 (
..... GISAID HA [EPI418005](#)
..... 19 Polymorphisms (10 Amino and 9 Silent)
..... syn#4Y (TAc),
..... 54N [zH3N2],
..... syn77S (AGt),
..... 100N,
..... syn179L (CTg),
..... 188T,
..... 225G,
..... 237I,
..... 286E,
..... 298V [zH3N2, avH1N1_{farm}, H6N1, H7, H9N2],
..... syn308K (AAg),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... syn448L (TTg),
..... 454N,
..... 502K)

pH1N1 Influenza Hemagglutinin Segments elucidated at 2013-02-21-18_34_07_542940 by GeneWurx see.PolyDetector v0, Copyright 2007-2013.

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Antigenic Variation

HA 142D Polymorphism

.... Tanzania2085_E3_30F_2012_12_10 (
..... GISAID HA [EPI422630](#)
..... GISAID Isolate [EPI_ISL_135825](#)
..... 26 Polymorphisms (12 Amino and 14 Silent)
..... #6M,
..... syn#5L (CTg),
..... syn22V (GTg),
..... syn34N (AAt),
..... 87G,
..... syn102E (GAa),
..... syn122K (AAa),
..... 142D,
..... 146G,
..... 172R,
..... 175K,
..... 188T,
..... 189D,
..... 200T,
..... syn223V (GTa),
..... 226R,
..... syn240G (GGg),
..... syn258F (TTt),
..... syn301I (ATa),
..... syn338G (GGc),
..... 377K,
..... 454N,
..... syn465N (AAt),
..... syn515Q (CAa),
..... syn524A (GCt),
..... syn538F (TTt))

.... India2005_E3_2012_11_24 (
..... GISAID HA [EPI422601](#)
..... GISAID Isolate [EPI_ISL_135815](#)
..... 23 Polymorphisms (10 Amino and 13 Silent)
..... #6M,

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Antigenic Variation

..... syn#5L (CTg),
..... syn34N (AAt),
..... syn66G (GGg),
..... 87G,
..... syn102E (GAa),
..... syn122K (AAa),
..... 142D,
..... 146G,
..... 188T,
..... 194I,
..... 200T,
..... syn223V (GTa),
..... syn240G (GGg),
..... syn258F (TTt),
..... syn338G (GGc),
..... 377K,
..... 430I,
..... 454N,
..... syn465N (AAt),
..... syn515Q (CAa),
..... syn524A (GCt),
..... syn538F (TTt))

.... BelgiumG860_xF_M1_2012_11_08 (
..... GISAID HA [EPI417116](#)
..... GISAID Isolate [EPI_ISL_134396](#)
..... 24 Polymorphisms (8 Amino and 16 Silent)
..... #6M,
..... syn#5L (CTg),
..... syn34N (AAt),
..... syn44L (CTg),
..... 87G,
..... syn102E (GAa),
..... syn122K (AAa),
..... 142D,
..... 146G,
..... 188T,
..... 200T,

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..... syn223V (GTa),
..... syn228G (GGa),
..... syn240G (GGg),
..... syn252V (GTa),
..... syn258F (TTt),
..... syn338G (GGc),
..... 377K,
..... syn420D (GAt),
..... 454N,
..... syn465N (AAt),
..... syn515Q (CAa),
..... syn524A (GCt),
..... syn538F (TTt))

.... Virginia13_M1C1_46F_2012_08_21 (
..... GISAID HA [EPI404817](#)
..... GISAID Isolate [EPI_ISL_131789](#)
..... 26 Polymorphisms (11 Amino and 15 Silent)
..... #6M,
..... syn#5L (CTg),
..... syn34N (AAt),
..... 87G,
..... syn102E (GAa),
..... syn122K (AAa),
..... 132D,
..... 142D,
..... 146G,
..... 166Q,
..... 188T,
..... 200T,
..... syn223V (GTa),
..... syn238E (GAa),
..... syn240G (GGg),
..... syn258F (TTt),
..... syn338G (GGc),
..... 377K,
..... 381T mix wt [Avian H7],
..... syn403L (tTG),

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..... 454N,
..... syn465N (AAAt),
..... syn515Q (CAa),
..... syn524A (GCt),
..... syn530V (GTg),
..... syn538F (TTt))

.... AustraliaBrisbane139_M4_59M_2011_04_07 (
..... GISAID HA [EPI332676](#)
..... GISAID Isolate [EPI_ISL_95091](#)
..... 15 Polymorphisms (7 Amino and 8 Silent)
..... syn34N (AAAt),
..... syn122K (AAa),
..... 142D,
..... 146G,
..... 158E mix wt,
..... 188T,
..... 200T,
..... syn316R (AGg),
..... syn338G (GGc),
..... 377K,
..... syn417G (GGg),
..... syn439D (GAt),
..... 454N,
..... syn465N (AAAt),
..... syn538F (TTt),
..... HA Truncated after aa548)

.... JapanSaitama289_M2+1_2011_04_02 (
..... GISAID HA [EPI329107](#)
..... GISAID Isolate [EPI_ISL_94426](#)
..... 13 Polymorphisms (8 Amino and 5 Silent)
..... #6M,
..... syn34N (AAAt),
..... 76T,
..... syn122K (AAa),
..... 123A,
..... 142D,

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..... 146G,
..... 159D mix wt,
..... syn178V (GTa),
..... 188T,
..... 200T,
..... syn292S (AGt),
..... syn338G (GGc),
..... HA Truncated after aa348)

.... AustraliaVictoria512_M1_46M_2011_02_04 (
..... GISAID HA [EPI331324](#)
..... GISAID Isolate [EPI_ISL_94794](#)
..... 11 Polymorphisms (5 Amino and 6 Silent)
..... syn107Q (CAg),
..... 142D,
..... 188T,
..... 200T,
..... syn338G (GGc),
..... syn343G (GGa),
..... 377K,
..... syn398K (AAG),
..... 454N,
..... syn465N (AAt),
..... syn538F (TTt))

.... SingaporeKK376_C2_14F_2010_06_07 (
..... GISAID HA [EPI385493](#)
..... GISAID Isolate [EPI_ISL_124750](#)
..... 8 Polymorphisms (4 Amino and 4 Silent)
..... syn18T (ACc),
..... syn107Q (CAg),
..... 115K,
..... 142D,
..... syn160S (TCc),
..... 233H,
..... 377K,
..... syn537S (AGc))

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.... SingaporeGP2864_3F_2010_06_03 (
..... GISAID HA [EPI385439](#)
..... GISAID Isolate [EPI ISL 124731](#)
..... 5 Polymorphisms (3 Amino and 2 Silent)
..... Isolation Source [**sera**],
..... syn107Q (CAg),
..... 142D,
..... **233H**,
..... 377K,
..... syn537S (AGc))

.... SingaporeSS34_C1_75F_2010_06_03 (
..... GISAID HA [EPI385418](#)
..... GISAID Isolate [EPI ISL 124723](#)
..... 9 Polymorphisms (4 Amino and 5 Silent)
..... syn107Q (CAg),
..... 142D,
..... syn160S (TCc),
..... **225G**,
..... **233H**,
..... syn272D (GAc),
..... syn339F (TTt),
..... 377K,
..... syn537S (AGc))

.... SingaporeGP2301_17F_2010_05_17 (
..... GISAID HA [EPI385347](#)
..... GISAID Isolate [EPI ISL 124700](#)
..... 8 Polymorphisms (3 Amino and 5 Silent)
..... syn62G (GGa),
..... syn64I (ATt),
..... syn107Q (CAg),
..... 142D,
..... syn160S (TCc),
..... **233H**,
..... 377K,
..... syn537S (AGc))

India 2013-03

Antigenic Variation

.... SingaporeGP1684_11M_2010_04_28 (
..... GISAID HA [EPI385211](#)
..... GISAID Isolate [EPI ISL 124656](#)
..... 8 Polymorphisms (5 Amino and 3 Silent)
..... 0A,
..... syn107Q (CAg),
..... 142D,
..... syn160S (TCc),
..... 208K,
..... 233H,
..... 377K,
..... syn537S (AGc))

.... SingaporeTT150_C2_2010_04_26 (
..... GISAID HA [EPI385172](#)
..... GISAID Isolate [EPI ISL 124641](#)
..... 8 Polymorphisms (4 Amino and 4 Silent)
..... syn107Q (CAg),
..... 142D,
..... syn160S (TCc),
..... 225G,
..... 233H,
..... 377K,
..... syn482V (GTt),
..... syn537S (AGc))

.... SingaporeGP1212_C1_19F_2010_04_12 (
..... GISAID HA [EPI385256](#)
..... GISAID Isolate [EPI ISL 124669](#)
..... 7 Polymorphisms (3 Amino and 4 Silent)
..... syn107Q (CAg),
..... 142D,
..... syn155V (GTc),
..... syn160S (TCc),
..... 233H,
..... 377K,
..... syn537S (AGc))

India 2013-03

Antigenic Variation

.... SingaporeKK111_C1_11M_2010_03_31 (
..... GISAID HA [EPI385125](#)
..... GISAID Isolate [EPI ISL 124627](#)
..... 6 Polymorphisms (3 Amino and 3 Silent)
..... syn107Q (CAg),
..... 142D,
..... syn160S (TCc),
..... 233H,
..... 377K,
..... syn537S (AGc))

.... SingaporeKK98_C1_4F_2010_03_08 (
..... GISAID HA [EPI385142](#)
..... GISAID Isolate [EPI ISL 124632](#)
..... 5 Polymorphisms (3 Amino and 2 Silent)
..... syn107Q (CAg),
..... 142D,
..... 233H,
..... 377K,
..... syn537S (AGc))

.... SingaporeKK90_C1_5M_2010_03_02 (
..... GISAID HA [EPI385157](#)
..... GISAID Isolate [EPI ISL 124637](#)
..... 5 Polymorphisms (3 Amino and 2 Silent)
..... syn107Q (CAg),
..... 142D,
..... 233H,
..... 377K,
..... syn537S (AGc))

.... JapanNagasakiHA1010_M_13F_2010_01_18 (
..... GISAID HA [EPI249892](#)
..... GISAID Isolate [EPI ISL 71896](#)
..... 6 Polymorphisms (3 Amino and 3 Silent)
..... syn94Y (TAt),
..... 142D,
..... syn193S (AGc),

India 2013-03

Antigenic Variation

..... 298V,

..... 307S,

..... syn471Y (TAt))

.... ChinaGuangxiLonganSWL1921_C1_15M_2010_01_14 (

..... GISAID HA [EPI258140](#)

..... GISAID Isolate [EPI_ISL_75063](#)

..... 4 Polymorphisms (2 Amino and 2 Silent)

..... 142D,

..... syn175E (GAg),

..... 502K,

..... syn541C (TGt))

.... JapanNagasakiHA105_M_13F_2010_01_12 (

..... GISAID HA [EPI249899](#)

..... GISAID Isolate [EPI_ISL_71903](#)

..... 7 Polymorphisms (4 Amino and 3 Silent)

..... syn94Y (TAt),

..... 142D,

..... 190G,

..... syn193S (AGc),

..... 298V,

..... 307S,

..... syn471Y (TAt))

.... JapanNagasakiHA104_M_4F_2010_01_04 (

..... GISAID HA [EPI249898](#)

..... GISAID Isolate [EPI_ISL_71902](#)

..... 8 Polymorphisms (5 Amino and 3 Silent)

..... syn94Y (TAt),

..... 142D,

..... syn193S (AGc),

..... 298V,

..... 307S,

..... 340L,

..... 346E,

..... syn471Y (TAt))

India 2013-03

Antigenic Variation

.... TexasHoustonJMS392_xM_2009_12_25 (
..... GISAID HA [EPI252938](#)
..... GISAID Isolate [EPI ISL 73523](#)
..... 2 Polymorphisms (2 Amino and 0 Silent)
..... 142D,
..... 377K)

.... WashingtonDCAF2182_PMK1_29M_2009_12_02 (
..... GISAID HA [EPI276604](#)
..... GISAID Isolate [EPI ISL 78483](#)
..... 6 Polymorphisms (4 Amino and 2 Silent)
..... 100N,
..... syn137A (GCt),
..... 142D,
..... 237L,
..... syn270I (ATc),
..... 377K,
..... HA Truncated after aa386)

.... UKEnglandGerrardsCross94560148_2009_11_04 (
..... GISAID HA [EPI336314](#)
..... GISAID Isolate [EPI ISL 96338](#)
..... 3 Polymorphisms (1 Amino and 2 Silent)
..... syn8I (ATc),
..... 142D,
..... syn428L (tTG))

.... UKEnglandGerrardsCross94560148_2009_11 (
..... GISAID HA [EPI276511](#)
..... GISAID Isolate [EPI ISL 78390](#)
..... 3 Polymorphisms (1 Amino and 2 Silent)
..... syn8I (ATc),
..... 142D,
..... syn428L (tTG))

India 2013-03

Antigenic Variation

.... Wisconsin51_C1C1_5F_2009_09_27 (
..... GISAID HA [EPI217263](#)
..... GISAID Isolate [EPI ISL 62361](#)
..... 5 Polymorphisms (4 Amino and 1 Silent)
..... 142D,
..... 189T,
..... 324I,
..... syn413K (AAg),
..... 499K)

.... ChinaShenzhen33_xM_2009_09_08 (
..... GISAID HA [EPI348003](#)
..... GISAID Isolate [EPI ISL 100954](#)
..... 5 Polymorphisms (3 Amino and 2 Silent)
..... Studied with **pH1N1 Severe** and **Fatal** cases,
..... 40N,
..... 56D,
..... 142D,
..... syn251L (tTA),
..... syn507K (AAa))

.... ChinaShenzhen28_xF_2009_08_31 (
..... GISAID HA [EPI348125](#)
..... GISAID Isolate [EPI ISL 101194](#)
..... 5 Polymorphisms (3 Amino and 2 Silent)
..... Studied with **pH1N1 Severe** and **Fatal** cases,
..... 40N,
..... 56D,
..... 142D,
..... syn251L (tTA),
..... syn507K (AAa))

.... BrazilSaoPaulo70311_7F_2009_08_28 (
..... GISAID HA [EPI335488](#)
..... GISAID Isolate [EPI ISL 95963](#)
..... 5 Polymorphisms (4 Amino and 1 Silent)
..... #12E,
..... 142D,

India 2013-03

Antigenic Variation

..... 206S,
..... 296H,
..... syn480E (GAg))

.... SlovakiaModra1156_2009_07_27 (
..... GISAID HA [EPI210532](#)
..... GISAID Isolate [EPI ISL 60278](#)
..... 1 Polymorphisms (1 Amino and 0 Silent)
..... 142D,
..... HA Truncated after aa389)

.... JapanTottoriST450_M_2009 (
..... GISAID HA [EPI394485](#)
..... GISAID Isolate [EPI ISL 128769](#)
..... 5 Polymorphisms (3 Amino and 2 Silent)
..... 142D,
..... 377V,
..... syn413K (AAG),
..... syn426A (GCa),
..... 440F)

pH1N1 Influenza Hemagglutinin Segments elucidated at 2013-03-20-02_53_42_107960 by GeneWurx see.PolyDetector v0, Copyright 2007-2013.

India 2013-03

Antigenic Variation

HA 267S Polymorphism

.... Austria73_St1_48M_2013_02_04 (
..... GISAID HA [EPI438428](#)
..... GISAID Isolate [EPI_ISL_138292](#)
..... 12 Polymorphisms (5 Amino and 7 Silent)
..... HA Truncated before aa#4,
..... syn77S (AGt),
..... 100N,
..... syn140P (CCc),
..... syn158G (GGg),
..... syn179L (CTg),
..... 188T,
..... 237I,
..... 267S [pH1N1 Rare: [India2150 C2 2012 12 17](#)],
..... 286E,
..... syn308K (AAG),
..... syn333F (TTc),
..... syn338G (GGc),
..... HA Truncated after aa372)

pH1N1 Influenza Hemagglutinin Segments elucidated at 2013-03-20-22_53_57_322420 by GeneWurx see.PolyDetector v0, Copyright 2007-2013.

HA 430I Polymorphism

.... Norway46_M2_55F_2012_12_18 (
..... GISAID HA [EPI416427](#)
..... GISAID Isolate [EPI_ISL_134129](#)
..... **CladeCrossing** Clade1:189T onto Clade2:188T
..... 21 Polymorphisms (12 Amino and 9 Silent)
..... syn#4Y (TAc),
..... syn77S (AGt),
..... 100N,
..... 166R,
..... 176I,
..... syn179L (CTg),
..... 188T,
..... 189T,
..... 218T,
..... 237I,
..... 286E,
..... syn308K (AAg),
..... syn333F (TTc),
..... syn338G (GGc),
..... syn372Q (CAa),
..... 377K,
..... syn396V (GTg),
..... 430I,
..... syn448L (TTg),
..... 454N,
..... 502K)

.... India2005_E3_2012_11_24 (
..... GISAID HA [EPI422601](#)
..... GISAID Isolate [EPI_ISL_135815](#)
..... 23 Polymorphisms (10 Amino and 13 Silent)
..... #6M,
..... syn#5L (CTg),
..... syn34N (AAt),
..... syn66G (GGg),
..... 87G,

..... syn102E (GAa),
..... syn122K (AAa),
..... 142D,
..... 146G,
..... 188T,
..... 194I,
..... 200T,
..... syn223V (GTa),
..... syn240G (GGg),
..... syn258F (TTt),
..... syn338G (GGc),
..... 377K,
..... 430I,
..... 454N,
..... syn465N (AAt),
..... syn515Q (CAa),
..... syn524A (GCt),
..... syn538F (TTt))

.... CanadaAlbertaRV2960_X2C1_23F_2012_11_15 (
..... GISAID HA [EPI407374](#)
..... GISAID Isolate [EPI_ISL_132701](#)
..... 19 Polymorphisms (10 Amino and 9 Silent)
..... 5I mix wt,
..... syn30T (ACt),
..... syn61A (GCg),
..... 100N,
..... 105K mix wt,
..... syn118E (GAa),
..... 141R,
..... syn179L (CTg),
..... 188T,
..... 252L,
..... 264V,
..... syn326S (TCc),
..... syn334G (GGa),
..... syn338G (GGc),
..... syn346G (GGa),

India 2013-03

Antigenic Variation

..... 377K,
..... 430I,
..... syn448L (TTg),
..... 454N)

.... Kenya182_M1_17F_2011_11_15 (
..... GISAID HA [EPI357499](#)
..... GISAID Isolate [EPI ISL 106792](#)
..... 14 Polymorphisms (7 Amino and 7 Silent)
..... syn6L (cTA),
..... syn22V (GTt),
..... 188T,
..... syn237V (GTg),
..... 252L,
..... syn304G (GGg),
..... 324I,
..... syn338G (GGc),
..... 377K,
..... 421V,
..... syn428L (CTa),
..... 430I,
..... 454N,
..... syn477T (ACa))

.... PolandWarsawINS621_30F_2011_02_04 (
..... GISAID HA [EPI408970](#)
..... GISAID Isolate [EPI ISL 133129](#)
..... Clade3:186P
..... 11 Polymorphisms (6 Amino and 5 Silent)
..... syn39K (AAa),
..... 137T,
..... 186P,
..... syn212K (AAa),
..... syn290N (AAt),
..... 377G,
..... syn408E (GAa),
..... 430I,
..... syn474C (TGt),

India 2013-03

Antigenic Variation

..... 512M,

..... 530I)

.... NewMexico01_MXC1_26F_2010_01_05 (
..... GISAID HA [EPI247384](#)
..... GISAID Isolate [EPI ISL 71407](#)
..... 7 Polymorphisms (3 Amino and 4 Silent)
..... #1V,
..... syn40H (CAc),
..... 377G,
..... syn413K (AAG),
..... 430I,
..... syn445V (GTt),
..... syn490P (CCc))

.... NetherlandsNoordHolland1039_M3_15F_2009_08_25 (
..... GISAID HA [EPI269380](#)
..... GISAID Isolate [EPI ISL 76456](#)
..... 2 Polymorphisms (2 Amino and 0 Silent)
..... 3T,
..... 430I)

.... BrazilRioDeJaneiro2459_25M_2009_07_02_s (
..... GISAID HA [EPI221367](#)
..... GISAID Isolate [EPI ISL 63323](#)
..... 5 Polymorphisms (4 Amino and 1 Silent)
..... #12E,
..... 206S,
..... syn294P (CCc),
..... 296H,
..... 430I)

.... CanadaABRV2621_xF_P1_2009_06_26 (
..... GISAID HA [EPI302713](#)
..... GISAID Isolate [EPI ISL 86228](#)
..... 6 Polymorphisms (5 Amino and 1 Silent)
..... #12E,
..... 206S,

India 2013-03

Antigenic Variation

..... 296H,
..... 405T [H9N2],
..... 430I,
..... syn492Y (TAt),
..... HA Truncated after aa543)

.... Pennsylvania13_C2_51F_2009_06_19 (
..... GISAID HA [EPI227792](#)
..... GISAID Isolate [EPI ISL 65019](#)
..... 1 Polymorphisms (1 Amino and 0 Silent)
..... 430I)

.... Mexico4108_C1E2_4M_2009_04_03 (
..... GISAID HA [EPI180605](#)
..... GISAID Isolate [EPI ISL 30500](#)
..... 5 Polymorphisms (2 Amino and 3 Silent)
..... 206S,
..... syn377E (GAa),
..... 430I,
..... syn456L (cTA),
..... syn534G (GGa))

.... Mexico4108_E2_4M_2009_04_02 (
..... GISAID HA [EPI179083](#)
..... GISAID Isolate [EPI ISL 30084](#)
..... 6 Polymorphisms (3 Amino and 3 Silent)
..... 206S,
..... 226R mix wt,
..... syn377E (GAa),
..... 430I,
..... syn456L (cTA),
..... syn534G (GGa))

.... Mexico4108_C1C1_4M_2009_04_02 (
..... GISAID HA [EPI177341](#)
..... GISAID Isolate [EPI ISL 29731](#)
..... 5 Polymorphisms (2 Amino and 3 Silent)
..... 206S,

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Antigenic Variation

..... syn377E (GAa),
..... 430I,
..... syn456L (cTA),
..... syn534G (GGa))

.... Mexico4108_E1_4M_2009_04_02 (
..... GISAID HA [EPI177335](#)
..... GISAID Isolate [EPI ISL 29730](#)
..... 5 Polymorphisms (2 Amino and 3 Silent)
..... 206S,
..... syn377E (GAa),
..... 430I,
..... syn456L (cTA),
..... syn534G (GGa))

.... Mexico4108_C1_4M_2009_04_02 (
..... GISAID HA [EPI177288](#)
..... GISAID Isolate [EPI ISL 29712](#)
..... 5 Polymorphisms (2 Amino and 3 Silent)
..... 206S,
..... syn377E (GAa),
..... 430I,
..... syn456L (cTA),
..... syn534G (GGa))

.... Mexico4108_C1IR_4M_2009_04_02 (
..... GISAID HA [EPI177338](#)
..... GISAID Isolate [EPI ISL 29614](#)
..... 5 Polymorphisms (2 Amino and 3 Silent)
..... 206S,
..... syn377E (GAa),
..... 430I,
..... syn456L (cTA),
..... syn534G (GGa))

.... Mexico3955_E2_9F_2009_04_02 (
..... GISAID HA [EPI179080](#)
..... GISAID Isolate [EPI ISL 30083](#)

India 2013-03

Antigenic Variation

..... 7 Polymorphisms (4 Amino and 3 Silent)

..... 73P mix wt,

..... 206S,

..... 225G,

..... syn377E (GAa),

..... 430I,

..... syn456L (cTA),

..... syn534G (GGa))

.... JapanTottoriST537_M_2009_01 (

..... GISAID HA [EPI394535](#)

..... GISAID Isolate [EPI_ISL_128819](#)

..... 16 Polymorphisms (8 Amino and 8 Silent)

..... syn34N (AAt),

..... syn42G (GGa),

..... 156N,

..... 188T,

..... 200T,

..... syn296Q (CAa),

..... 297D,

..... syn338G (GGc),

..... 377K,

..... 430I,

..... syn447N (AAt),

..... syn451K (AAa),

..... 454N,

..... syn465N (AAt),

..... 502K,

..... syn538F (TTt))

pH1N1 Influenza Hemagglutinin Segments elucidated at 2013-03-21-03_56_20_060490 by GeneWurx see.PolyDetector v0, Copyright 2007-2013.