



2013-03-04

Several US states are currently reporting *all-time high counts* for Influenza Hospitalisations & Fatalities, topping the record-setting 2009 Pandemic H1N1 season. Please review our **GeneWurx** charts and summary on the next page concerning Indiana Influenza Fatalities where *at least 43% of the deaths* were in subjects with *confirmed* vaccinations by *certified* health care providers. More who died were confirmed as vaccinated than as unvaccinated.

Additionally, the world's leading public health institutions have *failed again* this season to select Vaccine Influenza strains that properly match the diseases in current circulation.

The two primary components (Influenza A/pH1N1 & A/sH3N2) of the trivalent Influenza vaccine are genetically *mismatched this year* (2013). Influenza B (the third component) has a maximum potential match of 50% because two Influenza B strains are actively circulating.

We have evaluated the genetics of *actual circulating human* pH1N1 & sH3N2 disease strains that have recently been deposited in private databases by the US CDC, the World Health Organisation (WHO) and public health organizations from leading nations. Using our breakthrough technology, the **GeneWurx RnR** investigations examine the disease at the *most detailed genetic* level for polymorphisms within each of the infecting Influenza A serotypes (pH1N1 & seasonal H3N2) and then compare those changes / variations to animal and human reservoirs in an effort to establish potential donor origin. By establishing potential origins, pathology and morbidity (*danger levels*) may be ascertained.

The most current sequences demonstrate *wide disparity from the vaccine* due to a high count of changes and a variation pattern at antigenic locations typically leading to higher morbidity & mortality (illness & fatality). A synoptic **GeneWurx** polymorphism report from a *recent full batch* of each circulating serotype trails the Indiana Fatality Summary.

When we examined the historical facts on vaccine strain selection, **GeneWurx** found that world public health authorities revised Influenza vaccine selections when as few as 5 to 7 delta values (HA or NA segments) are documented in circulating strains.

Our report documents current genetic change *beyond* levels that have previously led to *new vaccine selections*. On a galling note, *Vaccine Escape* is also regularly described in the body of Influenza research when certain *single* changes land at locations that are antigenetically sensitive. Furthermore & more importantly, the detailed **GeneWurx RnR** analytics (available to viral disease researchers) demonstrate another crucial aspect of viral antigenicity . . . these particular polymorphisms in circulation have, in fact, landed at locations with amino acid values that *individually* are known to *confer Vaccine Resistance*.

GeneWurx.com
NS1.

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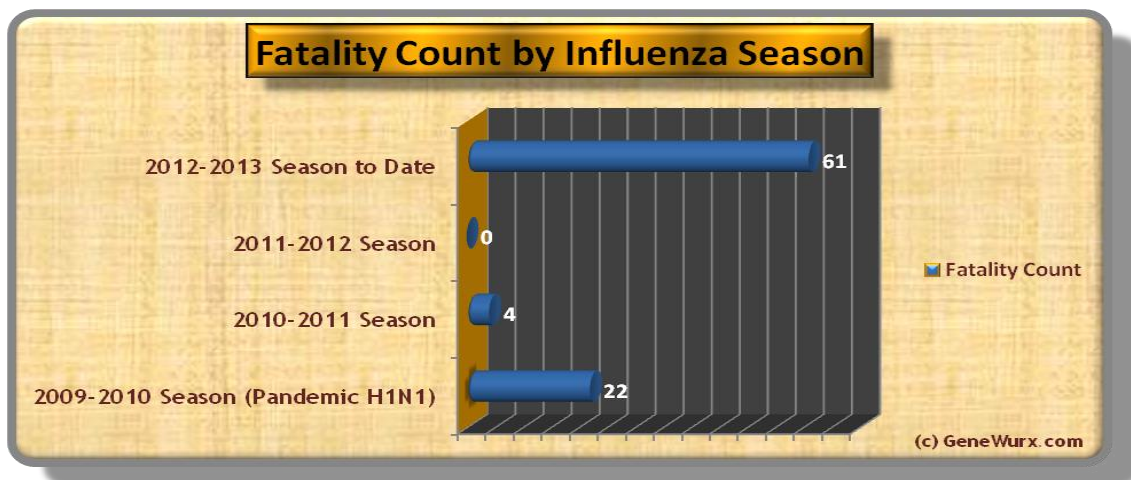
Indiana

Fatality Total after 2013 Week 08

State Record Influenza Fatality Count of 61 Citizens . . . so far this season.

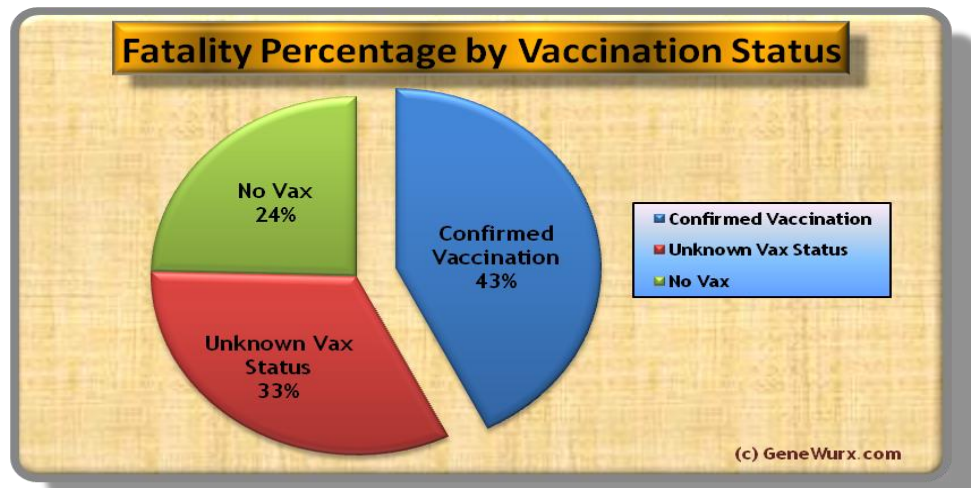
Fatality Count History for Indiana

- 2011-2012 Season **00**
- 2010-2011 Season **04**
- 2009-2010 Season **22** Previous State Record during Pandemic H1N1



2012-2013 Fatality Count by Vaccine Status

- Confirmed Vaccination **26**
- Unknown Vaccine Status **20**
- No Vaccination **15**



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pH1N1

2013_01_22_CDC

HA & NA Polymorphisms

pH1N1 Influenza Hemagglutinin & Neuraminidase Segments elucidated at 2013-01-22-18_29_55_797930 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. GISAID Citations are attached as PDF.

HA 308 Polymorphisms Averaging ~20.5 per Segment
NA 193 Polymorphisms Averaging ~12.9 per Segment
HA & NA 501 Polymorphisms Averaging ~33.4 per Sequence

.... India2192_2012_12_22 (
..... GISAID HA [EPI413162](#)
..... GISAID NA [EPI413161](#)
..... 19 Polymorphisms (9 Amino and 10 Silent)
..... 12 Polymorphisms (5 Amino and 7 Silent))

.... Minnesota26_C1_31F_2012_12_13 (
..... GISAID HA [EPI409917](#)
..... GISAID NA [EPI409916](#)
..... 21 Polymorphisms (8 Amino and 13 Silent)
..... 12 Polymorphisms (6 Amino and 6 Silent))

.... Florida57_M1C1_25M_2012_12_12 (
..... GISAID HA [EPI409898](#)
..... GISAID NA [EPI409897](#)
..... 19 Polymorphisms (8 Amino and 11 Silent)
..... 12 Polymorphisms (6 Amino and 6 Silent))

.... RhodeIsland10_C2_44M_2012_12_05 (
..... GISAID HA [EPI409889](#)
..... GISAID NA [EPI409888](#)
..... 22 Polymorphisms (10 Amino and 12 Silent)
..... 12 Polymorphisms (6 Amino and 6 Silent))

.... NewYork45_C2_51F_2012_12_02 (
..... GISAID HA [EPI414444](#)
..... GISAID NA [EPI409900](#)
..... 28 Polymorphisms (11 Amino and 17 Silent)
..... 16 Polymorphisms (8 Amino and 8 Silent))

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pH1N1

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.... Indiana167_M1C1_52F_2012_11_25 (
 GISAID HA [EPI409909](#)
 GISAID NA [EPI409908](#)
 22 Polymorphisms (9 Amino and 13 Silent)
 16 Polymorphisms (8 Amino and 8 Silent))

.... NewHampshire20_C1_60M_2012_11_24 (
 GISAID HA [EPI409915](#)
 GISAID NA [EPI409914](#)
 18 Polymorphisms (8 Amino and 10 Silent)
 12 Polymorphisms (5 Amino and 7 Silent))

.... ChinaGansu_Ganzhou33_E2E1_2012_11_19 (
 GISAID HA [EPI409924](#)
 GISAID NA [EPI409923](#)
 19 Polymorphisms (8 Amino and 11 Silent)
 13 Polymorphisms (6 Amino and 7 Silent))

.... ChinaGansu_Ganzhou35_C1C1_2012_11_19 (
 GISAID HA [EPI409922](#)
 GISAID NA [EPI409921](#)
 20 Polymorphisms (9 Amino and 11 Silent)
 12 Polymorphisms (6 Amino and 6 Silent))

.... India5416_X1C1_30M_2012_11_10_TmX247 (
 GISAID HA [EPI409892](#)
 GISAID NA [EPI409891](#)
 18 Polymorphisms (8 Amino and 10 Silent)
 15 Polymorphisms (5 Amino and 10 Silent))

.... Peru2023_C1_7F_2012_10_26 (
 GISAID HA [EPI409903](#)
 GISAID NA [EPI409902](#)
 20 Polymorphisms (8 Amino and 12 Silent)
 14 Polymorphisms (4 Amino and 10 Silent))

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pH1N1

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.... Brazil3479_C1C1_14M_2012_10_16 (
..... GISAID HA [EPI409895](#)
..... GISAID NA [EPI409894](#)
..... 19 Polymorphisms (8 Amino and 11 Silent)
..... 9 Polymorphisms (4 Amino and 5 Silent))

.... Peru0505_C1_27M_2012_10_12 (
..... GISAID HA [EPI409906](#)
..... GISAID NA [EPI409905](#)
..... 21 Polymorphisms (8 Amino and 13 Silent)
..... 12 Polymorphisms (5 Amino and 7 Silent))

.... India1214_X1C1_39F_2012_10_05 (
..... GISAID HA [EPI414445](#)
..... GISAID NA [EPI409919](#)
..... 18 Polymorphisms (7 Amino and 11 Silent)
..... 13 Polymorphisms (3 Amino and 10 Silent))

.... Peru0429_C1_24M_2012_09_04 (
..... GISAID HA [EPI409912](#)
..... GISAID NA [EPI409911](#)
..... 24 Polymorphisms (10 Amino and 14 Silent)
..... 13 Polymorphisms (5 Amino and 8 Silent))

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sH3N2 2013_01_16_CDC HA & NA Polymorphisms

sH3N2 Influenza Hemagglutinin & Neuraminidase Segments elucidated at 2013-01-22-01_19_34_490910 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. GISAID Citations are attached as PDF.

HA 282 Polymorphisms Averaging ~25.6 per Segment
NA 210 Polymorphisms Averaging ~19.1 per Segment
HA & NA 492 Polymorphisms Averaging ~44.7 per Sequence

.... Virginia15_C2_85F_2012_12_05 (
..... GISAID HA [EPI408604](#)
..... GISAID NA [EPI408603](#)
..... 38 Polymorphisms (16 Amino and 22 Silent)
..... 29 Polymorphisms (7 Amino and 22 Silent))

.... RhodeIsland09_C2_19M_2012_11_28 (
..... GISAID HA [EPI408606](#)
..... GISAID NA [EPI408605](#)
..... 17 Polymorphisms (9 Amino and 8 Silent)
..... 9 Polymorphisms (2 Amino and 7 Silent))

.... NewJersey08_C2_93M_2012_11_28 (
..... GISAID HA [EPI408601](#)
..... GISAID NA [EPI408600](#)
..... 16 Polymorphisms (10 Amino and 6 Silent)
..... 16 Polymorphisms (5 Amino and 11 Silent))

.... Nebraska11_C2_33F_2012_11_26 (
..... GISAID HA [EPI408613](#)
..... GISAID NA [EPI408612](#)
..... 19 Polymorphisms (8 Amino and 11 Silent)
..... 14 Polymorphisms (5 Amino and 9 Silent))

.... Missouri13_C2_79M_2012_11_26 (
..... GISAID HA [EPI408611](#)
..... GISAID NA [EPI408610](#)
..... 21 Polymorphisms (8 Amino and 13 Silent)
..... 11 Polymorphisms (4 Amino and 7 Silent))



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sH3N2

2013_01_16_CDC

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.... Maryland43_C2_2M_2012_11_13 (
..... GISAID HA [EPI408608](#)
..... GISAID NA [EPI408607](#)
..... 37 Polymorphisms (15 Amino and 22 Silent)
..... 27 Polymorphisms (8 Amino and 19 Silent))

.... Virginia14_X1C2_7M_2012_11_13 (
..... GISAID HA [EPI408598](#)
..... GISAID NA [EPI408597](#)
..... 36 Polymorphisms (15 Amino and 21 Silent)
..... 26 Polymorphisms (7 Amino and 19 Silent))

.... SouthDakota10_C1_73M_2012_10_12 (
..... GISAID HA [EPI408616](#)
..... GISAID NA [EPI408615](#)
..... 20 Polymorphisms (9 Amino and 11 Silent)
..... 11 Polymorphisms (3 Amino and 8 Silent))

.... Alaska25_C2_5F_2012_10_11 (
..... GISAID HA [EPI408596](#)
..... GISAID NA [EPI408595](#)
..... 34 Polymorphisms (15 Amino and 19 Silent)
..... 25 Polymorphisms (6 Amino and 19 Silent))

.... ChinaXinjiang_Tianshan1411_C3C1_2012_04_01_VxX (
..... GISAID HA [EPI408591](#)
..... GISAID NA [EPI408590](#)
..... 34 Polymorphisms (15 Amino and 19 Silent)
..... 32 Polymorphisms (15 Amino and 17 Silent))

.... Vietnam51_CXC2_2012_02_26_VxX (
..... GISAID HA [EPI408588](#)
..... GISAID NA [EPI408587](#)
..... 10 Polymorphisms (6 Amino and 4 Silent)
..... 10 Polymorphisms (5 Amino and 5 Silent))