# Febrile Respiratory Illness (FRI) Surveillance Update

Operational Infectious Diseases, Naval Health Research Center, San Diego, CA

**2016 Week 48 (through 3 December 2016)**


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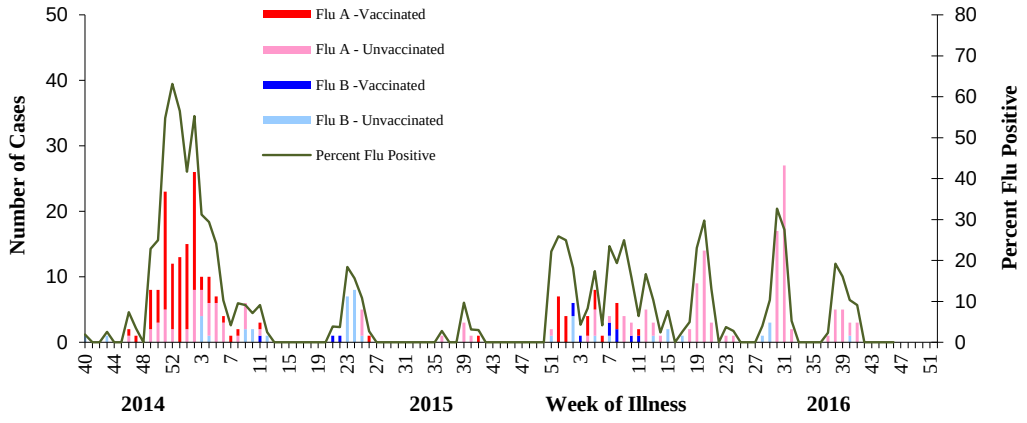
## *Influenza*

NHRC Laboratory-Confirmed Influenza Cases, US Military Basic Trainees

| | Current Week* | | | | Since Oct.1, 2016 | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Site | A/ Untyp. | A/H3 | A/H1 | B | A/ Untyp. | A/H3 | A/H1 | B | No. Tested |
| Ft. Benning | | | | | | | | | 35 |
| Ft. Jackson | | | | | | 5 | | | 19 |
| Ft. Leonard Wood | | | | | | | | | 7 |
| NRTC Great Lakes | | | | | | | | 1 | 16 |
| Lackland AFB | | | | | | | | | 4 |
| MCRD Parris Island | | | | | | | | | 5 |
| MCRD San Diego | | | | | | | | | 42 |
| CGTC Cape May | | | | | | | | | 30 |
| Total | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 1 | 158 |

- NHRC also conducts shipboard FRI surveillance that includes large-deck ships of the US Fleet Forces (Atlantic), 3rd (Pacific), and 7th (Far East) Fleets.
- NHRC conducts FRI surveillance among (non-active duty) DoD beneficiaries in Illinois and San Diego (details on page 7).
- NHRC-CDC-BIDS collaborative border FRI/SARI surveillance program is ongoing at 7 US-Mexico border sites in San Diego (2) and Imperial (5) counties in California. Details on page 8.
- For more information about NHRC FRI surveillance programs, please contact NHRC.

**Vaccination Status of Confirmed Influenza Cases Among US Military Basic Trainees, 2014-16**




### *Other Items of Interest*

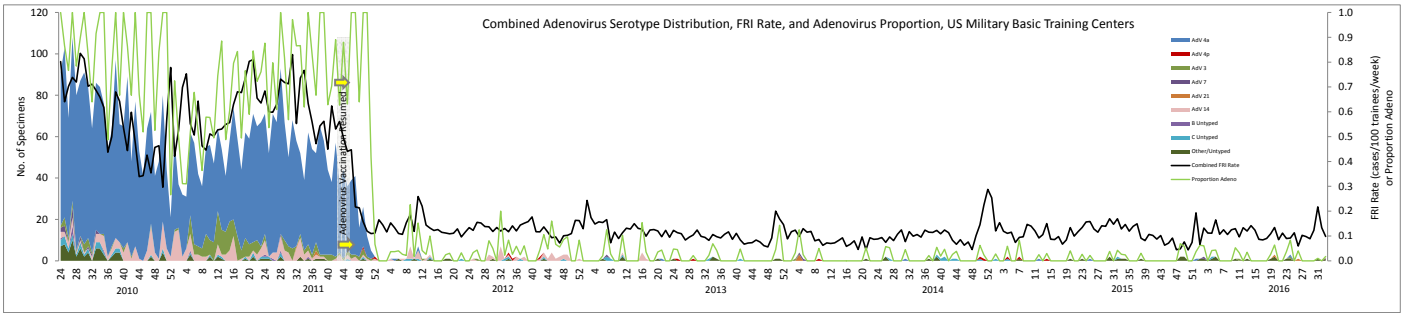
- NHRC is conducting laboratory-based surveillance for meningococcal disease. The program's purpose is to track and characterize meningococcal cases among DoD medical beneficiaries. For more information and the most recent data, click here.

## *Items of Note*

- *Elevated FRI rates at Fort Benning and MCRD Parris Island*
- *NHRC is able to test for novel influenza strains, MERS coronavirus, enterovirus EV-68, Ebola virus, and Zika virus*

## *Adenovirus*

- Vaccination against types 4 and 7 adenovirus was instituted at all basic training centers by mid-November 2011.
- FRI rates and the proportion of FRI cases positive for adenovirus have decreased markedly since vaccine was reintroduced.
- Sporadic adenovirus cases at basic training centers 2012-16. FRI rates remain low in general.




## *FRI Rates*

- FRI surveillance is ongoing at 8 U.S. military basic training centers, representing all service branches. As each week's FRI count is reported, FRI Rate Status is classified into one of 3 categories:
  - At or below expected value (expected value shown as dashed line)
  - Moderately elevated
  - Substantially elevated

Week ending 3 December 2016:

- **At or below expected value:**

Fort Jackson
Fort Leonard Wood
Naval Recruit Training Command, Great Lakes
Marine Corps Recruit Depot, San Diego
Lackland Air Force Base (data through 29 Oct.)
Coast Guard Training Center, Cape May

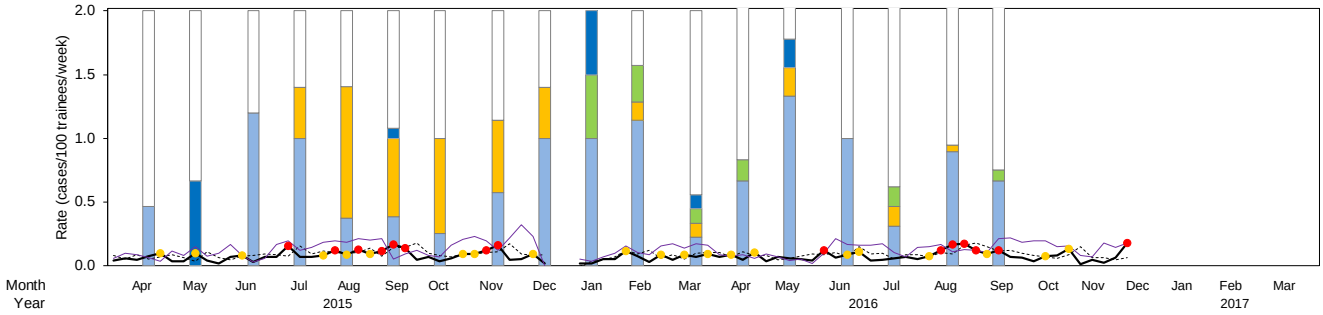
- **Moderately elevated:**

None

- **Substantially elevated:**

Fort Benning
Marine Corps Recruit Depot, Parris Island

Ft. Benning FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)

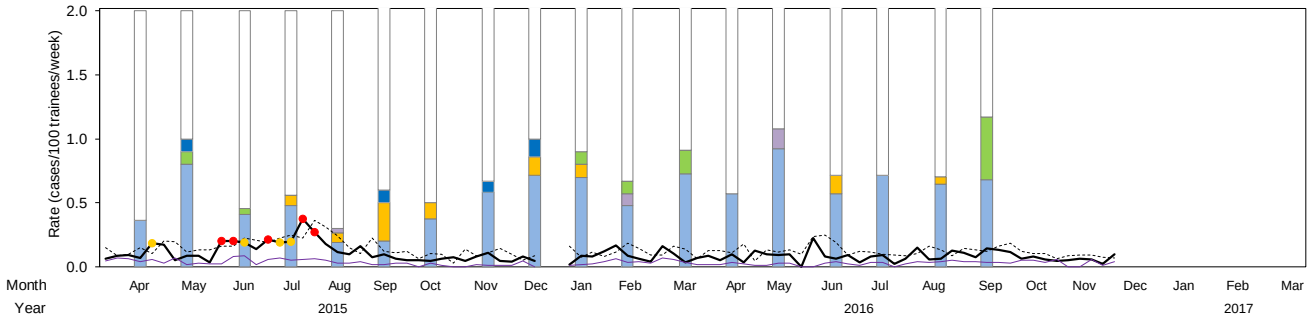



| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **13** | **6** | **10** | **20** | **27** | **26** | **24** | **35** | **10** | **4** | **14** | **18** | **12** | **9** | **26** | **13** | **38** | **24** |
| Adenovirus | | 33% | | | | 4% | | | | 25% | | 6% | | 11% | | | | |
| Influenza | | | | | | | | | | 25% | 14% | 6% | 8% | | | 8% | | 4% |
| RSV | | | | | | | | | | | | | | | | | | |
| *C. pneumo* | | | | | | | | | | | | | | | | | | |
| *M. pneumo* | | | | 20% | 52% | 31% | 38% | 29% | 20% | | 7% | 6% | | 11% | | 8% | 3% | |
| Rhinovirus | 23% | | 60% | 50% | 19% | 19% | 13% | 29% | 50% | 50% | 57% | 11% | 33% | 67% | 50% | 15% | 45% | 33% |

| Influenza Subtype | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | | | | | | | | 0% | 100% | 100% | 100% | | | 100% | | 0% |
| A/H3 | | | | | | | | | | 0% | 0% | 0% | 0% | | | 0% | | 100% |
| A/pH1 | | | | | | | | | | 100% | 0% | 0% | 0% | | | 0% | | 0% |
| Untyped | | | | | | | | | | 0% | 0% | 0% | 0% | | | 0% | | 0% |

Back to FRI Report

Ft. Jackson FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)




| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **33** | **20** | **44** | **50** | **53** | **20** | **16** | **24** | **14** | **20** | **21** | **11** | **21** | **13** | **14** | **14** | **34** | **41** |
| Adenovirus | | 5% | | | | 5% | | 4% | 7% | | | | | | | | | |
| Influenza | | 5% | 2% | | | | | | | 5% | 5% | 9% | | | | | | 24% |
| RSV | | | | | | | | | | | | | | | | | | |
| *C. pneumo* | | | | | 2% | | | | | | 5% | | | 8% | | | | |
| *M. pneumo* | | | | 4% | 4% | 15% | 6% | | 7% | 5% | | | | | 7% | | 3% | |
| Rhinovirus | 18% | 40% | 20% | 24% | 9% | 10% | 19% | 29% | 36% | 35% | 24% | 36% | 29% | 46% | 29% | 36% | 32% | 34% |

| Influenza Subtype | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | 100% | 100% | | | | | | | 0% | 0% | 0% | | | | | | 0% |
| A/H3 | | 0% | 0% | | | | | | | 0% | 0% | 0% | | | | | | 100% |
| A/pH1 | | 0% | 0% | | | | | | | 100% | 100% | 100% | | | | | | 0% |
| Untyped | | 0% | 0% | | | | | | | 0% | 0% | 0% | | | | | | 0% |

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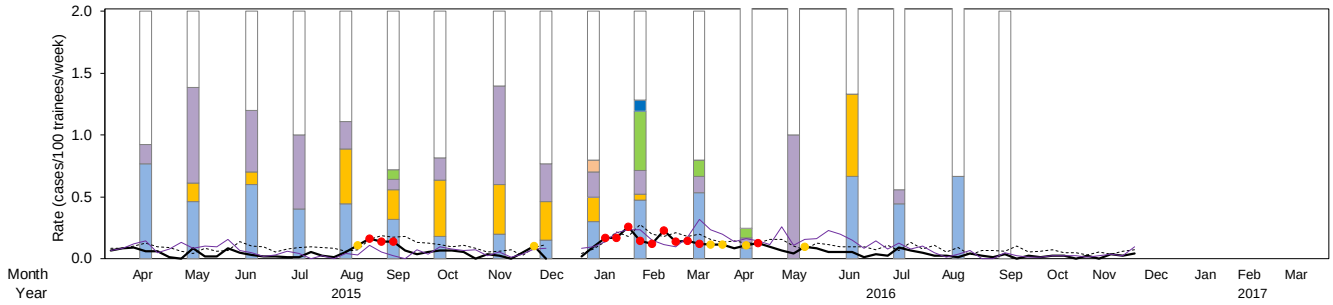
– Observed FRI rate (expected rate = dashed line) • Moderately elevated • Substantially elevated —— Pneumonia rate (incl. afebrile)

Ft. Leonard Wood FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)




| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **26** | **13** | **20** | **10** | **9** | **25** | **22** | **10** | **13** | **20** | **42** | **15** | **24** | **6** | **3** | **18** | **3** | **1** |
| Adenovirus | | | | | | | | | | | 5% | | | | | | | |
| Influenza | | | | | | 4% | | | | | 24% | 7% | 4% | | | | | |
| RSV | | | | | | | | | | 5% | | | | | | | | |
| *C. pneumo* | 8% | 38% | 25% | 30% | 11% | 4% | 9% | 40% | 15% | 10% | 10% | 7% | 4% | 50% | | 6% | | |
| *M. pneumo* | | 8% | 5% | | 22% | 12% | 23% | 20% | 15% | 10% | 2% | | | | 33% | | | |
| Rhinovirus | 38% | 23% | 30% | 20% | 22% | 16% | 9% | 10% | 8% | 15% | 24% | 27% | 4% | | 33% | 22% | 33% | |

| Influenza Subtype | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | | | | 0% | | | | | 20% | 100% | 100% | | | | | |
| A/H3 | | | | | | 100% | | | | | 10% | 0% | 0% | | | | | |
| A/pH1 | | | | | | 0% | | | | | 70% | 0% | 0% | | | | | |
| Untyped | | | | | | 0% | | | | | 0% | 0% | 0% | | | | | |

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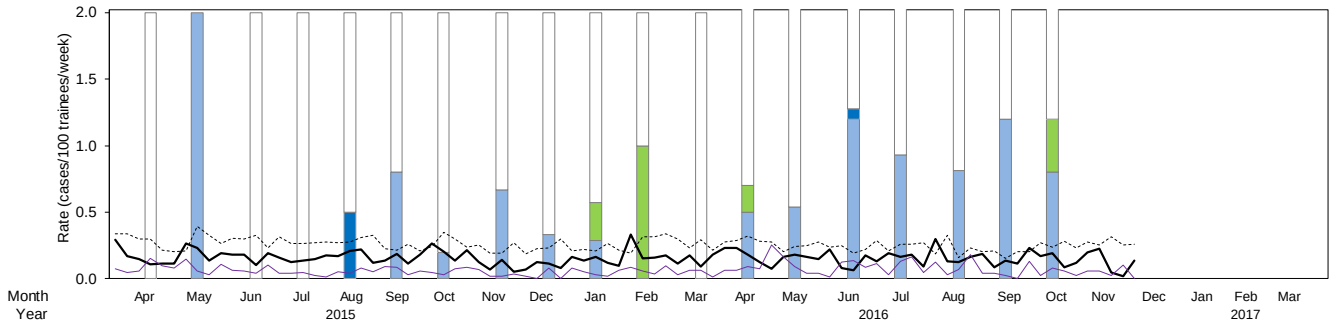
Great Lakes FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)




| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **1** | **1** | **1** | **3** | **4** | **5** | **10** | **3** | **6** | **7** | **2** | **3** | **20** | **26** | **25** | **30** | **32** | **15** | **5** |
| Adenovirus | | | | | 25% | | | | | | | | | | 4% | | | | |
| Influenza | | | | | | | | | | 14% | 50% | | 10% | | | | | | 20% |
| RSV | | | | | | | | | | | | | | | | | | | |
| *C. pneumo* | | | | | | | | | | | | | | | | | | | |
| *M. pneumo* | | | | | | | | | | | | | | | | | | | |
| Rhinovirus | | 100% | | | | 40% | 10% | 33% | 17% | 14% | | | 25% | 27% | 60% | 47% | 41% | 60% | 40% |

| Influenza Subtype | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | | | | | | | | 0% | 0% | | 50% | | | | | | 100% |
| A/H3 | | | | | | | | | | 0% | 0% | | 0% | | | | | | 0% |
| A/pH1 | | | | | | | | | | 100% | 100% | | 50% | | | | | | 0% |
| Untyped | | | | | | | | | | 0% | 0% | | 0% | | | | | | 0% |

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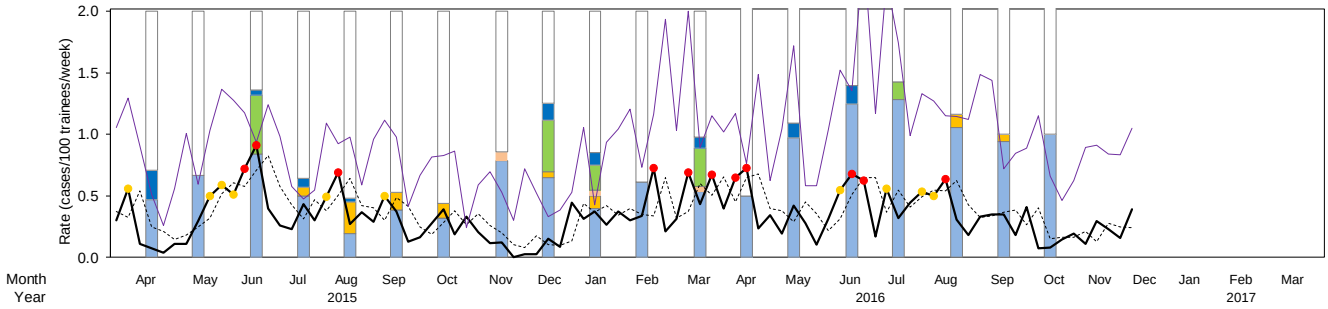
– Observed FRI rate (expected rate = dashed line) • Moderately elevated • Substantially elevated — Pneumonia rate (incl. afebrile)

MCRD SD FRI Rates and Diagnostic Test Results

Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)




| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **34** | **42** | **88** | **56** | **62** | **57** | **50** | **28** | **43** | **40** | **13** | **45** | **48** | **33** | **53** | **42** | **55** | **36** | **4** |
| Adenovirus | 12% | | 2% | 4% | 2% | | | | 7% | 5% | | 4% | | 6% | 8% | | | | |
| Influenza | | | 24% | | | | | | 21% | 10% | | 16% | | | | 7% | | | |
| RSV | | | | | | | | 4% | | 3% | | 2% | | | | | | | |
| *C. pneumo* | | | | | | | | | | | | | | | | | | | |
| *M. pneumo* | | | | 4% | 13% | 7% | 6% | | 2% | 5% | | | | | | | 5% | 3% | |
| Rhinovirus | 24% | 33% | 42% | 25% | 10% | 19% | 16% | 39% | 33% | 20% | 31% | 27% | 25% | 48% | 62% | 64% | 53% | 47% | 50% |

| Influenza Subtype | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | 76% | | | | | | 11% | 0% | | 0% | | | | 100% | | | |
| A/H3 | | | 24% | | | | | | 89% | 100% | | 86% | | | | 0% | | | |
| A/pH1 | | | 0% | | | | | | 0% | 0% | | 14% | | | | 0% | | | |
| Untyped | | | 0% | | | | | | 0% | 0% | | 0% | | | | 0% | | | |

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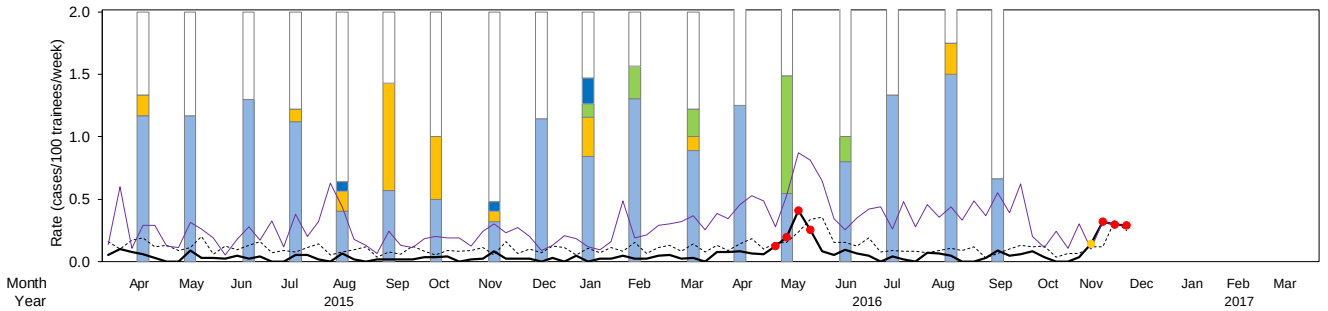
MCRD PI FRI Rates and Diagnostic Test Results

Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)



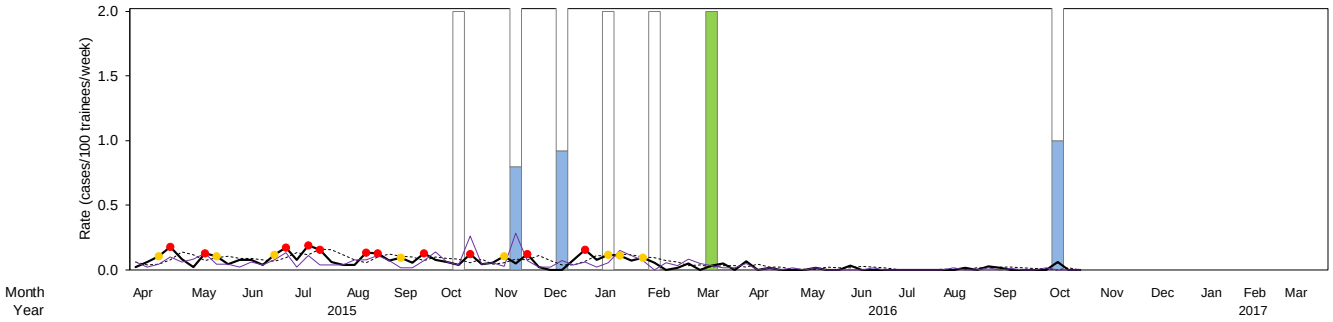

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **12** | **12** | **20** | **41** | **25** | **14** | **4** | **25** | **7** | **19** | **23** | **18** | **8** | **59** | **20** | **6** | **8** | **3** | |
| Adenovirus | | | | | 4% | | | 4% | | 11% | | | | | | | | | |
| Influenza | | | | | | | | | | 5% | 13% | 11% | | 47% | 10% | | | | |
| RSV | | | | | | | | | | | | | | | | | | | |
| *C. pneumo* | | | | | | | | | | | | | | | | | | | |
| *M. pneumo* | 8% | | | 5% | 8% | 43% | 25% | 4% | | 16% | | 6% | | | | | 13% | | |
| Rhinovirus | 58% | 58% | 65% | 56% | 20% | 29% | 25% | 16% | 57% | 42% | 65% | 44% | 63% | 27% | 40% | 67% | 75% | 33% | |

| Influenza Subtype | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | | | | | | | | 0% | 0% | 0% | | 0% | 0% | | | | |
| A/H3 | | | | | | | | | | 0% | 0% | 0% | | 100% | 100% | | | | |
| A/pH1 | | | | | | | | | | 100% | 100% | 100% | | 0% | 0% | | | | |
| Untyped | | | | | | | | | | 0% | 0% | 0% | | 0% | 0% | | | | |

Back to FRI Report

– Observed FRI rate (expected rate = dashed line) • Moderately elevated • Substantially elevated — Pneumonia rate (incl. afebrile)

Lackland AFB FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)




| | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **0** | **0** | **0** | **0** | **0** | **0** | **1** | **5** | **13** | **3** | **2** | **2** | | | | | | | **2** | | | | | |
| Adenovirus | | | | | | | | | | | | | | | | | | | | | | | | |
| Influenza | | | | | | | | | | | | 100% | | | | | | | | | | | | |
| RSV | | | | | | | | | | | | | | | | | | | | | | | | |
| *C. pneumo* | | | | | | | | | | | | | | | | | | | | | | | | |
| *M. pneumo* | | | | | | | | | | | | | | | | | | | | | | | | |
| Rhinovirus | | | | | | | | 40% | 46% | | | | | | | | | | 50% | | | | | |

| Influenza Subtype | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | | | | | | | | | | 50% | | | | | | | | | | | | |
| A/H3 | | | | | | | | | | | | 0% | | | | | | | | | | | | |
| A/pH1 | | | | | | | | | | | | 50% | | | | | | | | | | | | |
| Untyped | | | | | | | | | | | | 0% | | | | | | | | | | | | |

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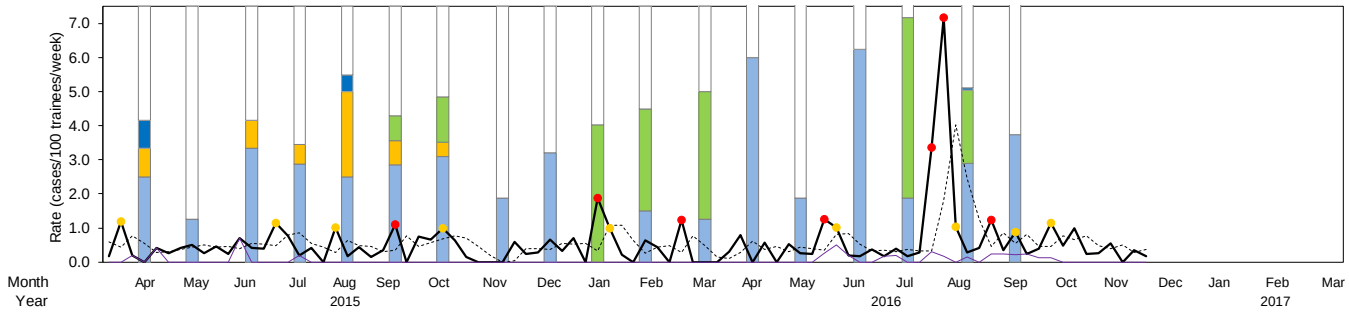
Cape May FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)




| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Samples Received** | **9** | **6** | **9** | **13** | **15** | **21** | **17** | **4** | **7** | **13** | **5** | **6** | **5** | **12** | **6** | **24** | **101** | **10** |
| Adenovirus | 11% | | | | 7% | | | | | | | | | | | | 1% | |
| Influenza | | | | | | 10% | 18% | | | 54% | 40% | 50% | | | | 71% | 29% | |
| RSV | | | | | | | | | | | | | | | | | | |
| *C. pneumo* | | | | | | | | | | | | | | | | | | |
| *M. pneumo* | 11% | | 11% | 8% | 33% | 10% | 6% | | | | | | | | | | | |
| Rhinovirus | 33% | 17% | 44% | 38% | 33% | 38% | 41% | 25% | 43% | | 20% | 17% | 80% | 25% | 83% | 25% | 39% | 50% |

| Influenza Subtype | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| B | | | | | | 0% | 0% | | | 100% | 100% | 0% | | | | 0% | 0% | |
| A/H3 | | | | | | 100% | 100% | | | 0% | 0% | 0% | | | | 100% | 93% | |
| A/pH1 | | | | | | 0% | 0% | | | 0% | 0% | 100% | | | | 0% | 0% | |
| Untyped | | | | | | 0% | 0% | | | 0% | 0% | 0% | | | | 0% | 7% | |

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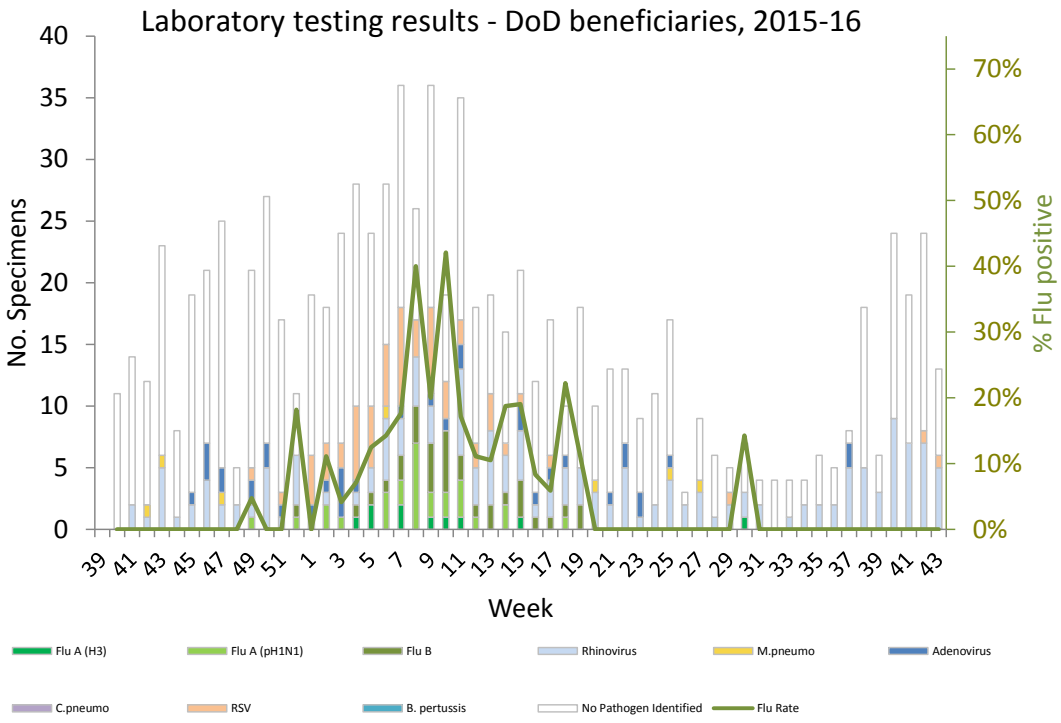
– Observed FRI rate (expected rate = dashed line) • Moderately elevated • Substantially elevated — Pneumonia rate (incl. afebrile)

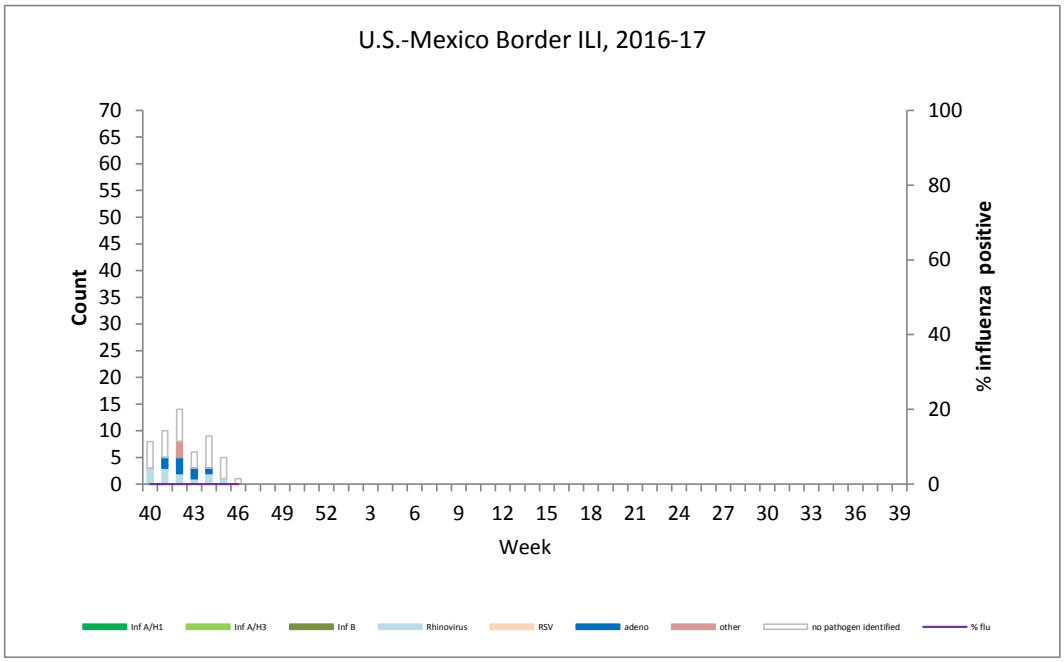
## *DoD Beneficiary Surveillance*

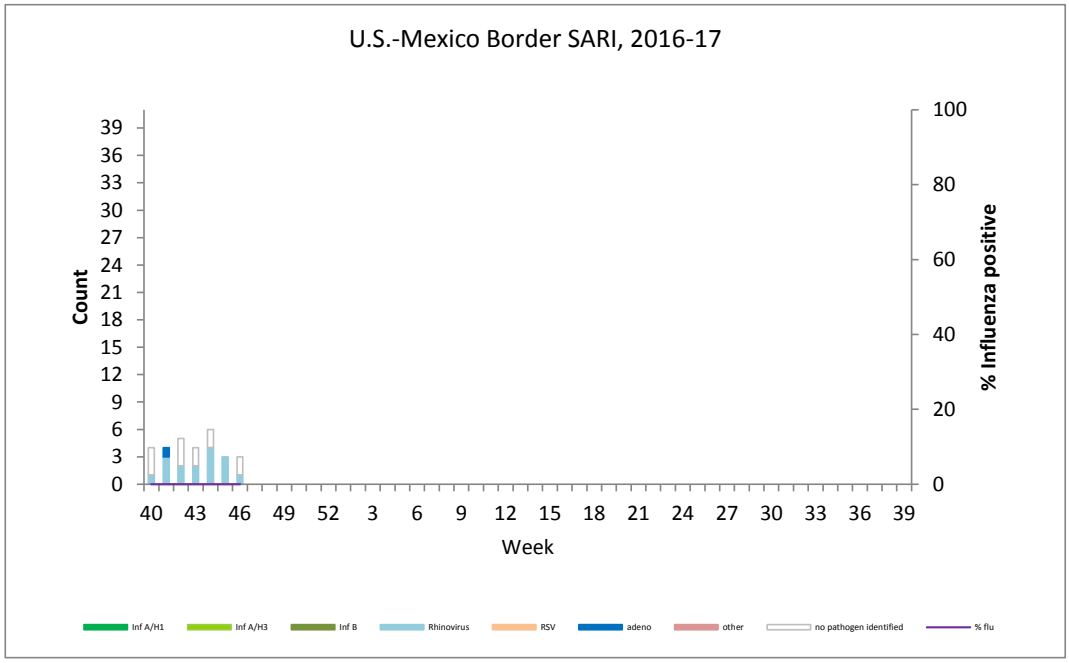
- NHRC conducts FRI surveillance among (non-active duty) DoD beneficiaries at Lovell FHCC (Great Lakes, IL) and in 4 NMC San Diego facilities: the Emergency Department, Pediatric Department, Naval Branch Health Clinic Kearny Mesa, and NH Camp Pendleton.
    - For questions regarding surveillance in this population, please contact the principal investigators at NHRC-FRI_Ben@med.navy.mil.



## *US-Mexico Border Surveillance*

- In collaboration with the CDC Border Infectious Disease Surveillance program and San Diego/Imperial Counties, NHRC performs laboratory testing for FRI cases among civilians near the US-Mexico border. Both outpatient (FRI) and inpatient (Severe Acute Respiratory Illness; SARI) cases are included in the program. Current sites are located in San Diego (2) and Imperial (5) counties in California.



## Phylogenetic Comparison of Influenza A-pandemic 2009 H1N1 (pH1N1) HA and NA Protein Sequences

- **47** analyzed Influenza A pH1N1 HA sequences were derived from MDCK isolates and 4 belonged to clade 6B while 43 belonged to the subclade 6B.1, defined by mutations **S84N, S162T (ADD GLY) and I216T.**
- **46** analyzed Influenza A pH1N1 NA sequences were derived from MDCK isolates.
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown (both HA and NA sequences) are with respect to **A/California/07/2009-like virus.**

## Summary of Influenza A (pH1N1) Protein Homology When Compared to 2015-2016 Vaccine Strain

| Segment | No. Isolates | 2015-2016 Vaccine Strain | Protein Homology |
|---|---|---|---|
| A/pH1N1 HA | 47 | A/California/07/2009 | 97.0-98.0% |
| A/pH1N1 NA | 46 | A/California/07/2009 | 96.1-97.3% |

## Summary of Influenza A (pH1N1) N-Linked Glycosylation Mutations

- Loss or gain of N-linked glycosylation sites affect host innate immune system recognition and the ability to induce adaptive immune response thus altering its viral antigenicity.[1] Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server http://www.cbs.dtu.dk/services/NetNGlyc/

| | Mutation | |
|---|---|---|
| A/pH1N1 Segment | ADD GLY | LOSS GLY |
| **HA** | S162N | |
| **NA** | N44S, S70N | N386K |

1. Sun X. Jayaraman A. Mainprasad P. Raman R. Houser K. Pappas C. ...Tumpey T. (2013).
N-Linked Glycosylation of the Hemagglutin Protein Influences Virulence and Antigenicity of the 1918 Pandemic and Seasonal H1N1 Influenza A Viruses. *Journal of Virology* 8756-8766.
2. Lee H. Tang J. Kong D. Loh T. Chiang D. Lam T. Koay E. (2013). Comparison of Mutation Patterns in Full-Genome A/H3N2 Influenza Sequences Obtained Directly from Clinical Samples and the Same Samples after a Single MDCK Passage. *PLoS One*.

## Phylogenetic Comparison of Influenza A (H3N2) HA and NA Protein Sequences

- **33** analyzed H3N2 HA sequences were derived from MDCK isolates and **17** were derived from clinical specimen.
- **28** analyzed H3N2 NA sequences were derived from MDCK isolates and 9 were derived from clinical specimen.
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown are with respect to 2010 vaccine strain **A/Perth/16/2009-like virus** for HA sequences and **A/Norway/1186/2011** for NA sequences

## Summary of Influenza A (H3N2) Protein Homology When Compared to 2015-2016 Vaccine Strain

| Segment | No. | 2015-2016 Vaccine Strain | Protein Homology |
|---|---|---|---|
| H3N2 HA | 50 | A/Switzerland/9715293/2013 | **96.8-99.6%** |
| H3N2 NA | 37 | A/Switzerland/9715293/2013 | **97.9-98.6%** |

## Summary of Influenza A (H3N2) N-Linked Glycosylation Mutations

- Loss or gain of N-linked glycosylation sites affect host innate immune system recognition and the ability to induce adaptive immune response thus altering its viral antigenicity.[1] Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server http://www.cbs.dtu.dk/services/NetNGlyc/

| | Mutation | |
|---|---|---|
| A/H3N2 Segment | ADD GLY | LOSS GLY |
| **HA** | K160T | S47P N122D T128A N144S N158K N158H T160K T160I |
| **NA** | S245N N329I S331R | S247T N329S N329T |

1. Sun X. Jayaraman A. Mainprasad P. Raman R. Houser K. Pappas C. ...Tumpey T. (2013).
N-Linked Glycosylation of the Hemagglutin Protein Influences Virulence and Antigenicity of the 1918 Pandemic and Seasonal H1N1 Influenza A Viruses. *Journal of Virology* 8756-8766.

## Phylogenetic Comparison of Influenza B (Victoria and Yamagata) HA and NA Protein Sequences

- **52** analyzed Influenza B HA sequences were derived from MDCK isolates. 27 isolates belonged to the V1A clade of the Victoria Lineage and 25 belonged to the Y3 clade of the Yamagata lineage.
- **53** analyzed Influenza B NA sequences were derived from MDCK isolates. 27 isolates belonged to the V1A clade of the Victoria Lineage and 26 belonged to the Y3 clade of the Yamagata lineage.
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown (both HA and NA sequences) are with respect to previous vaccine strains **B/Ohio/01/2005-like virus** for B/Victoria specimens and **B/Florida/04/2006-like virus** for B/Yamagata specimens.

## Summary of Influenza B Protein Homology When Compared to 2015-2016 Vaccine Strain

| Segment | No. Isolates | 2015-2016 Vaccine Strain | Protein Homology |
|---|---|---|---|
| B/Victoria HA | 27 | B/Brisbane/60/2008 | **99.1-99.5%** |
| B/Victoria NA | 27 | B/Brisbane/60/2008 | **98.3-98.54%** |
| B/Yamagata HA | 25 | B/Phuket/3073/2013 | **99.1-99.5%** |
| B/Yamagata NA | 26 | B/Phuket/3073/2013 | **98.7-100.0%** |

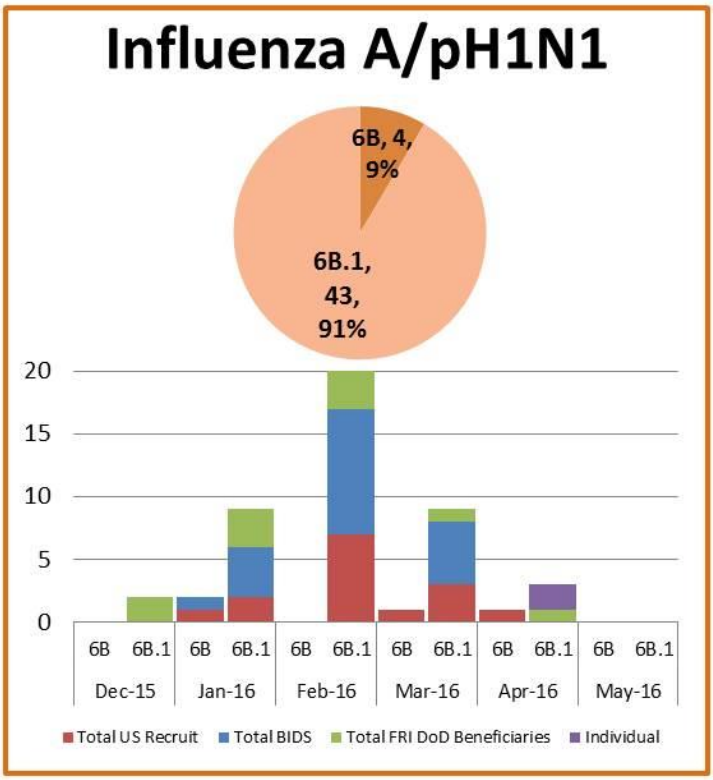
## Summary of Influenza B N-Linked Glycosylation Mutations

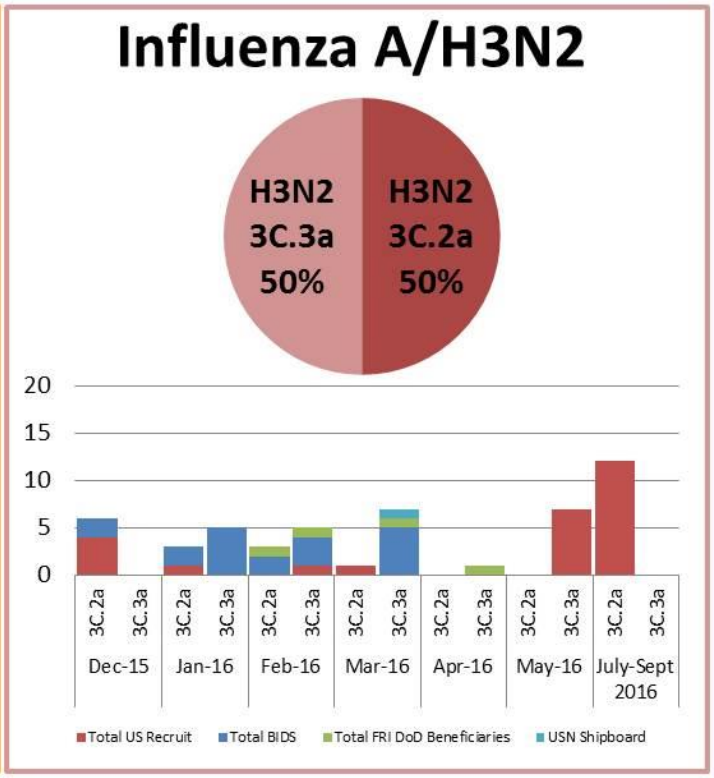
- Loss or gain of N-linked glycosylation sites affect host innate immune system recognition and the ability to induce adaptive immune response thus altering its viral antigenicity.[1] Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server http://www.cbs.dtu.dk/services/NetNGlyc/

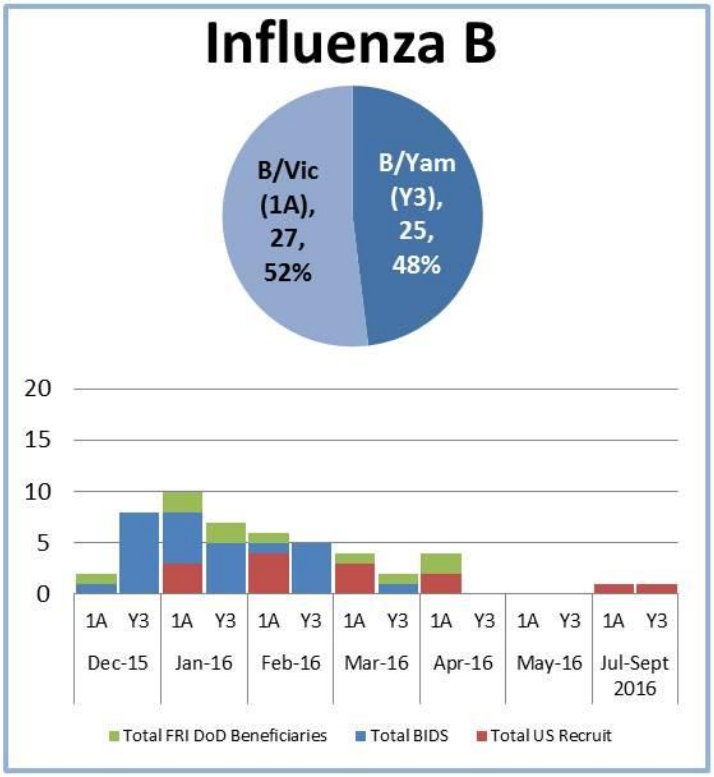
| | Mutation | |
|---|---|---|
| INF B Segment | ADD GLY | LOSS GLY |
| **HA** | A198T | N196D T198N |
| **NA** | D463N, S295N | |

1. Sun X. Jayaraman A. Mainprasad P. Raman R. Houser K. Pappas C. ...Tumpey T. (2013).
N-Linked Glycosylation of the Hemagglutin Protein Influences Virulence and Antigenicity of the 1918 Pandemic and Seasonal H1N1 Influenza A Viruses. *Journal of Virology* 8756-8766.
2. Lee H. Tang J. Kong D. Loh T. Chiang D. Lam T. Koay E. (2013). Comparison of Mutation Patterns in Full-Genome A/H3N2 Influenza Sequences Obtained Directly from Clinical Samples and the Same Samples after a Single MDCK Passage. *PLoS One*.

## Summary of Influenza A/pH1N1, A/H3N2 and Influenza B Hemagglutinin (HA) Genetic Groups



# Evolutionary Relationships Among Influenza A (pH1N1) Hemagglutinin (HA) Genes 2015-2016 Influenza Season

**Vaccine Strain**

**Reference Strain**

**2013-2014 consensus***

**December 2015**

**January 2016**

**February 2016**

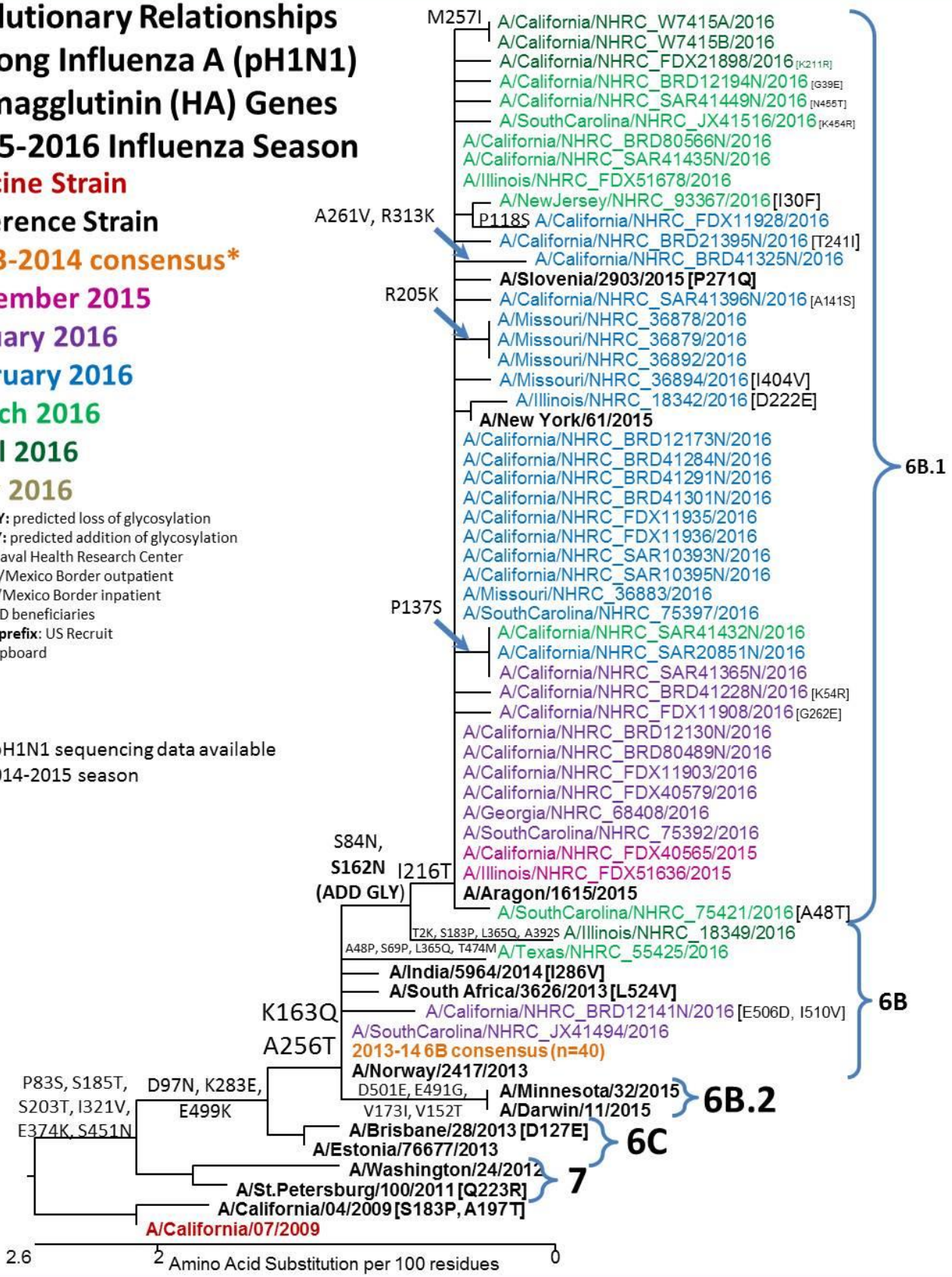
**March 2016**

**April 2016**

**May 2016**

**LOSS GLY:** predicted loss of glycosylation
**ADD GLY:** predicted addition of glycosylation
**NHRC:** Naval Health Research Center
**BRD:** US/Mexico Border outpatient
**SAR:** US/Mexico Border inpatient
**FDX:** DoD beneficiaries
**JX or no prefix**: US Recruit
**Ship:** Shipboard

*No pH1N1 sequencing data available for 2014-2015 season



# Evolutionary Relationships Among Influenza A (pH1N1) Neuraminidase (NA) Genes 2015-2016 Influenza Season

**Vaccine Strain**

**Reference Strain**

**2013-2014 consensus***

**December 2015**

**January 2016**

**February 2016**

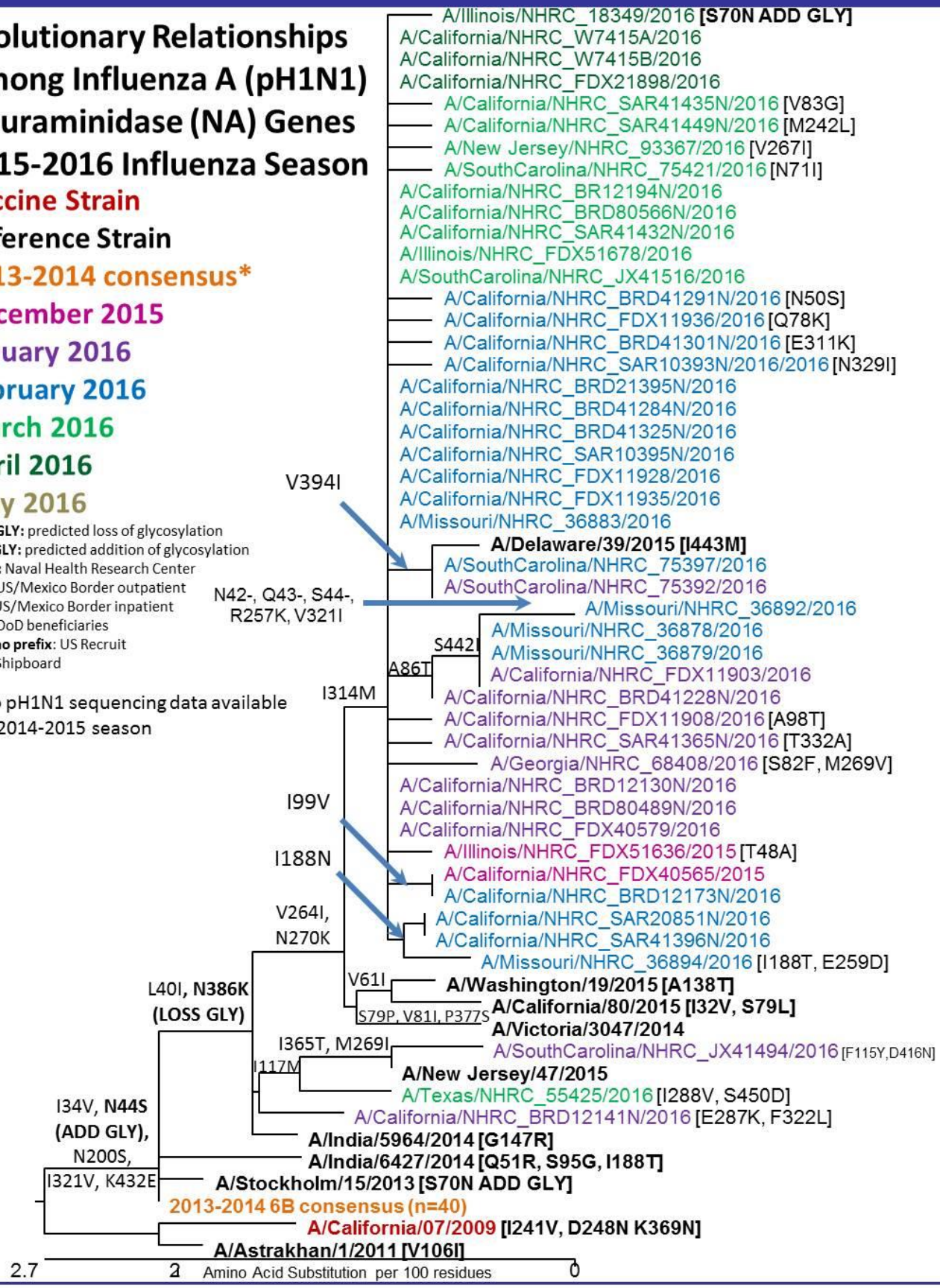
**March 2016**

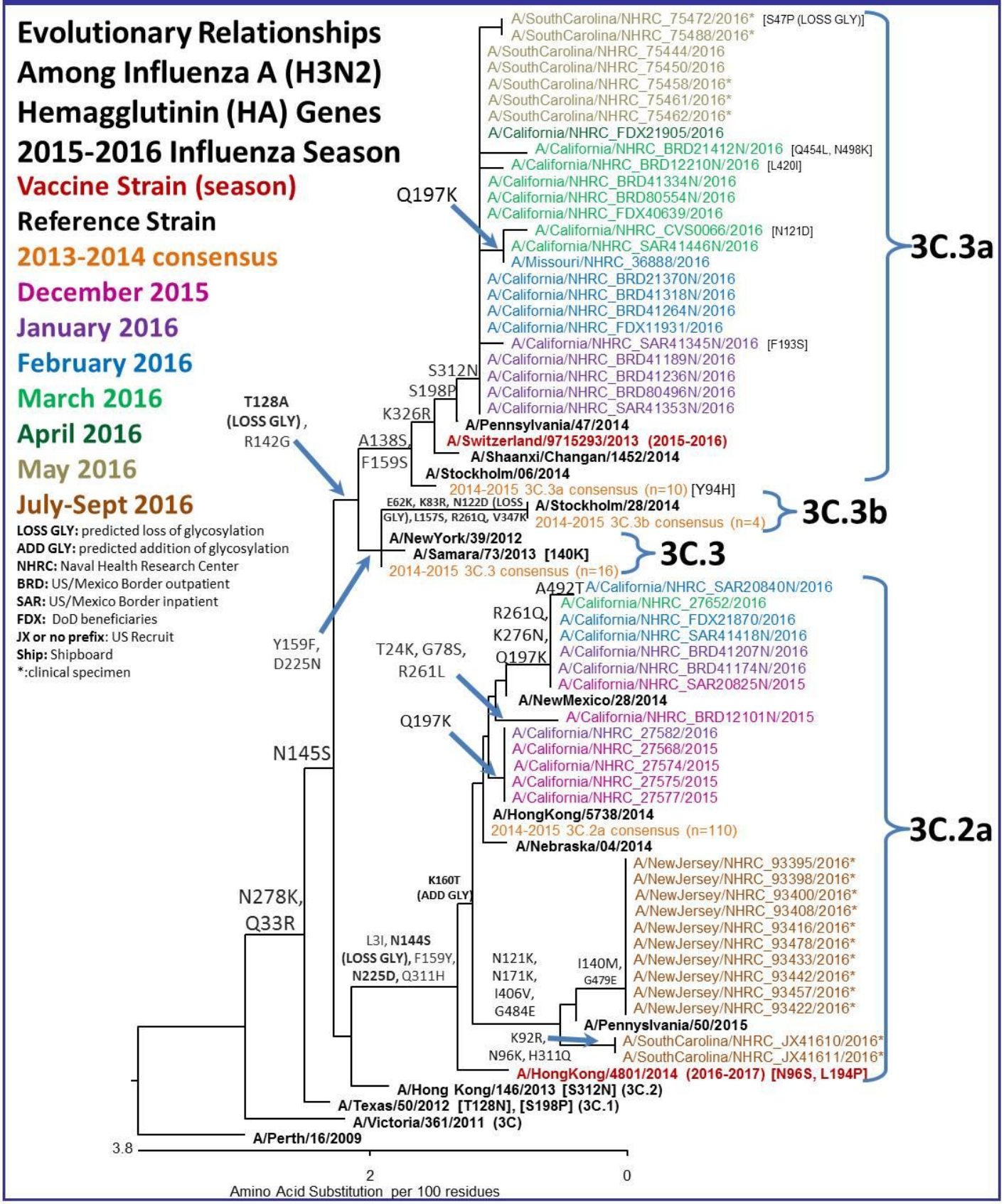
**April 2016**

**May 2016**

**LOSS GLY:** predicted loss of glycosylation
**ADD GLY:** predicted addition of glycosylation
**NHRC:** Naval Health Research Center
**BRD:** US/Mexico Border outpatient
**SAR:** US/Mexico Border inpatient
**FDX:** DoD beneficiaries
**JX or no prefix**: US Recruit
**Ship:** Shipboard

*No pH1N1 sequencing data available for 2014-2015 season

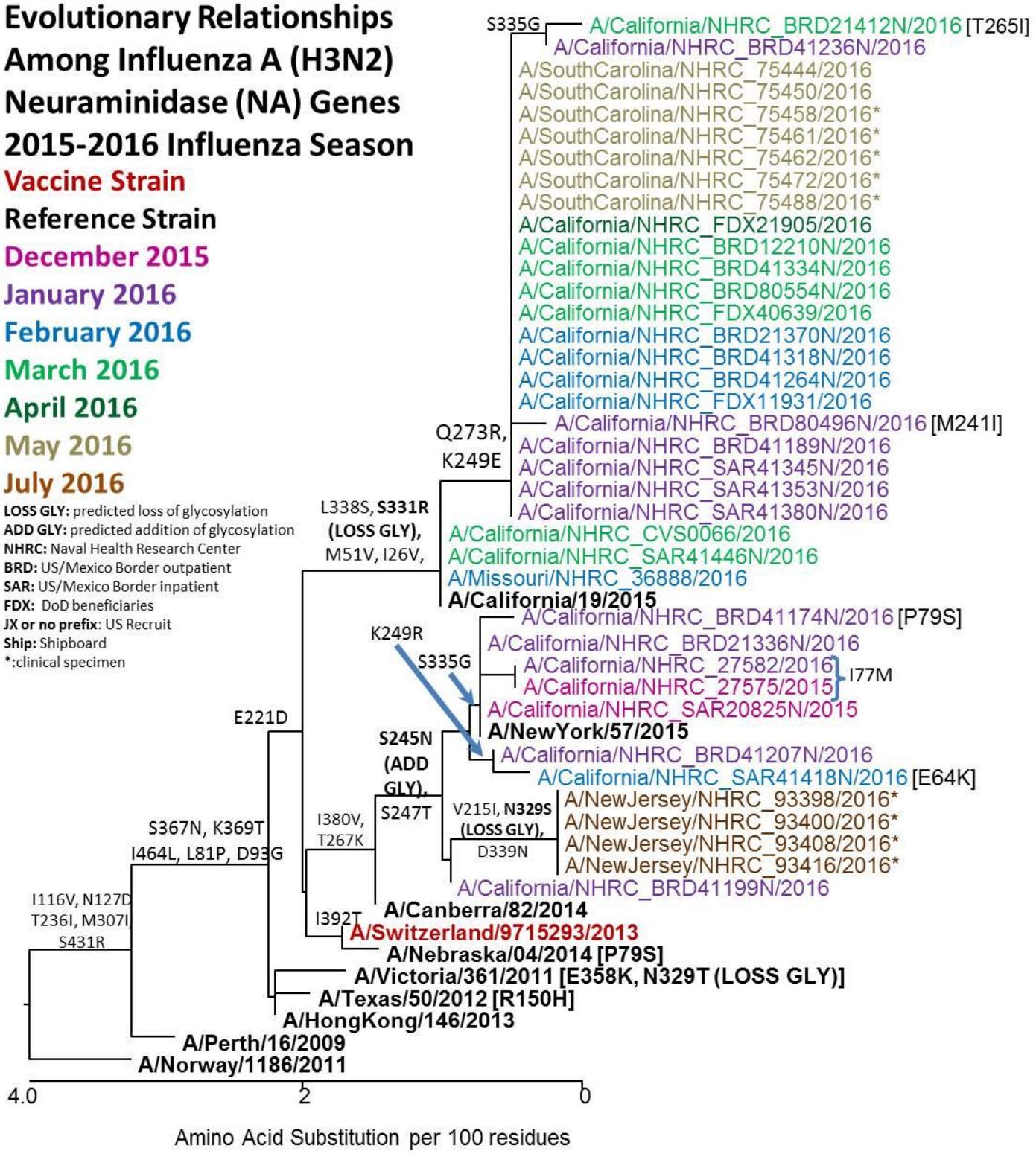



Evolutionary Relationships Among Influenza A (H3N2) Hemagglutinin (HA) Genes 2015-2016 Influenza Season
Vaccine Strain (season)
Reference Strain
2013-2014 consensus
December 2015
January 2016
February 2016
March 2016
April 2016
May 2016
July-Sept 2016
LOSS GLY: predicted loss of glycosylation
ADD GLY: predicted addition of glycosylation
NHRC: Naval Health Research Center
BRD: US/Mexico Border outpatient
SAR: US/Mexico Border inpatient
FDX: DoD beneficiaries
JX or no prefix: US Recruit
Ship: Shipboard
*:clinical specimen
A/SouthCarolina/NHRC_75472/2016* [S47P (LOSS GLY)]
A/SouthCarolina/NHRC_75488/2016*
A/SouthCarolina/NHRC_75444/2016
A/SouthCarolina/NHRC_75450/2016
A/SouthCarolina/NHRC_75458/2016*
A/SouthCarolina/NHRC_75461/2016*
A/SouthCarolina/NHRC_75462/2016*
A/California/NHRC_FDX21905/2016
A/California/NHRC_BRD21412N/2016 [Q454L, N498K]
A/California/NHRC_BRD12210N/2016 [L420I]
A/California/NHRC_BRD41334N/2016
A/California/NHRC_BRD80554N/2016
A/California/NHRC_FDX40639/2016
A/California/NHRC_CVS0066/2016 [N121D]
A/California/NHRC_SAR41446N/2016
A/Missouri/NHRC_36888/2016
A/California/NHRC_BRD21370N/2016
A/California/NHRC_BRD41318N/2016
A/California/NHRC_BRD41264N/2016
A/California/NHRC_FDX11931/2016
A/California/NHRC_SAR41345N/2016 [F193S]
A/California/NHRC_BRD41189N/2016
A/California/NHRC_BRD41236N/2016
A/California/NHRC_BRD80496N/2016
A/California/NHRC_SAR41353N/2016
Q197K
S312N
S198P
K326R
T128A (LOSS GLY), R142G
A138S, F159S
A/Pennsylvania/47/2014
A/Switzerland/9715293/2013 (2015-2016)
A/Shaanxi/Changan/1452/2014
A/Stockholm/06/2014
2014-2015 3C.3a consensus (n=10) [Y94H]
3C.3a
E62K, K83R, N122D (LOSS GLY), L157S, R261Q, V347K
A/Stockholm/28/2014
2014-2015 3C.3b consensus (n=4)
3C.3b
A/NewYork/39/2012
A/Samara/73/2013 [140K]
2014-2015 3C.3 consensus (n=16)
3C.3
Y159F, D225N
A492T
A/California/NHRC_SAR20840N/2016
A/California/NHRC_27652/2016
A/California/NHRC_FDX21870/2016
A/California/NHRC_SAR41418N/2016
A/California/NHRC_BRD41207N/2016
A/California/NHRC_BRD41174N/2016
A/California/NHRC_SAR20825N/2015
R261Q, K276N, Q197K
T24K, G78S, R261L
A/NewMexico/28/2014
A/California/NHRC_BRD12101N/2015
Q197K
A/California/NHRC_27582/2016
A/California/NHRC_27568/2015
A/California/NHRC_27574/2015
A/California/NHRC_27575/2015
A/California/NHRC_27577/2015
N145S
A/HongKong/5738/2014
2014-2015 3C.2a consensus (n=110)
A/Nebraska/04/2014
3C.2a
A/NewJersey/NHRC_93395/2016*
A/NewJersey/NHRC_93398/2016*
A/NewJersey/NHRC_93400/2016*
A/NewJersey/NHRC_93408/2016*
A/NewJersey/NHRC_93416/2016*
A/NewJersey/NHRC_93478/2016*
A/NewJersey/NHRC_93433/2016*
A/NewJersey/NHRC_93442/2016*
A/NewJersey/NHRC_93457/2016*
A/NewJersey/NHRC_93422/2016*
K160T (ADD GLY)
N278K, Q33R
L3I, N144S (LOSS GLY), F159Y, N225D, Q311H
N121K, N171K, I406V, G484E
I140M, G479E
A/Pennsylvania/50/2015
K92R, N96K, H311Q
A/SouthCarolina/NHRC_JX41610/2016*
A/SouthCarolina/NHRC_JX41611/2016*
A/HongKong/4801/2014 (2016-2017) [N96S, L194P]
A/Hong Kong/146/2013 [S312N] (3C.2)
A/Texas/50/2012 [T128N], [S198P] (3C.1)
A/Victoria/361/2011 (3C)
A/Perth/16/2009
3.8
2
0
Amino Acid Substitution per 100 residues

# Evolutionary Relationships Among Influenza A (H3N2) Neuraminidase (NA) Genes 2015-2016 Influenza Season

Vaccine Strain
Reference Strain
December 2015
January 2016
February 2016
March 2016
April 2016
May 2016
July 2016

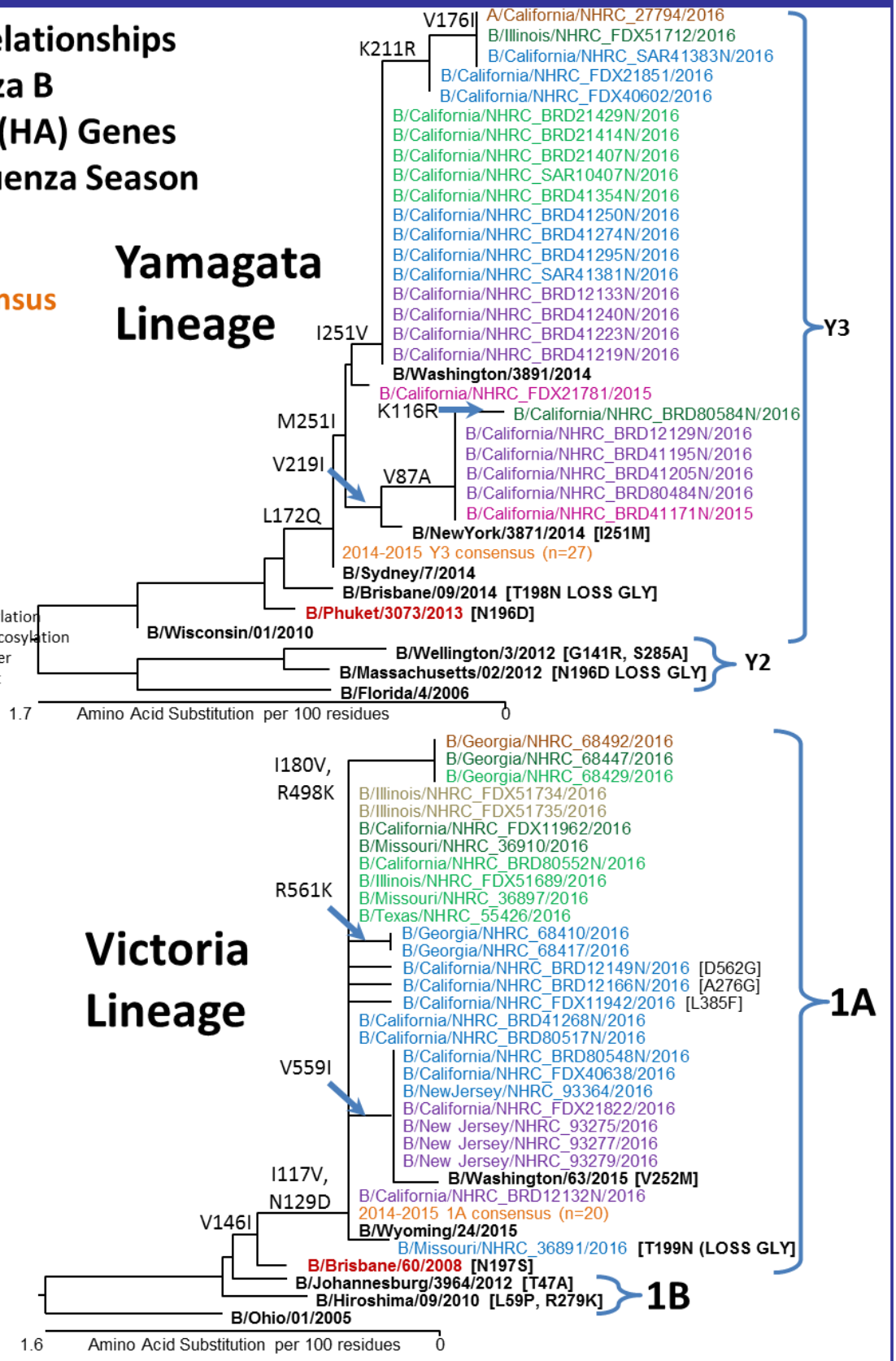
**LOSS GLY:** predicted loss of glycosylation
**ADD GLY:** predicted addition of glycosylation
**NHRC:** Naval Health Research Center
**BRD:** US/Mexico Border outpatient
**SAR:** US/Mexico Border inpatient
**FDX:** DoD beneficiaries
**JX or no prefix**: US Recruit
**Ship:** Shipboard
*:clinical specimen

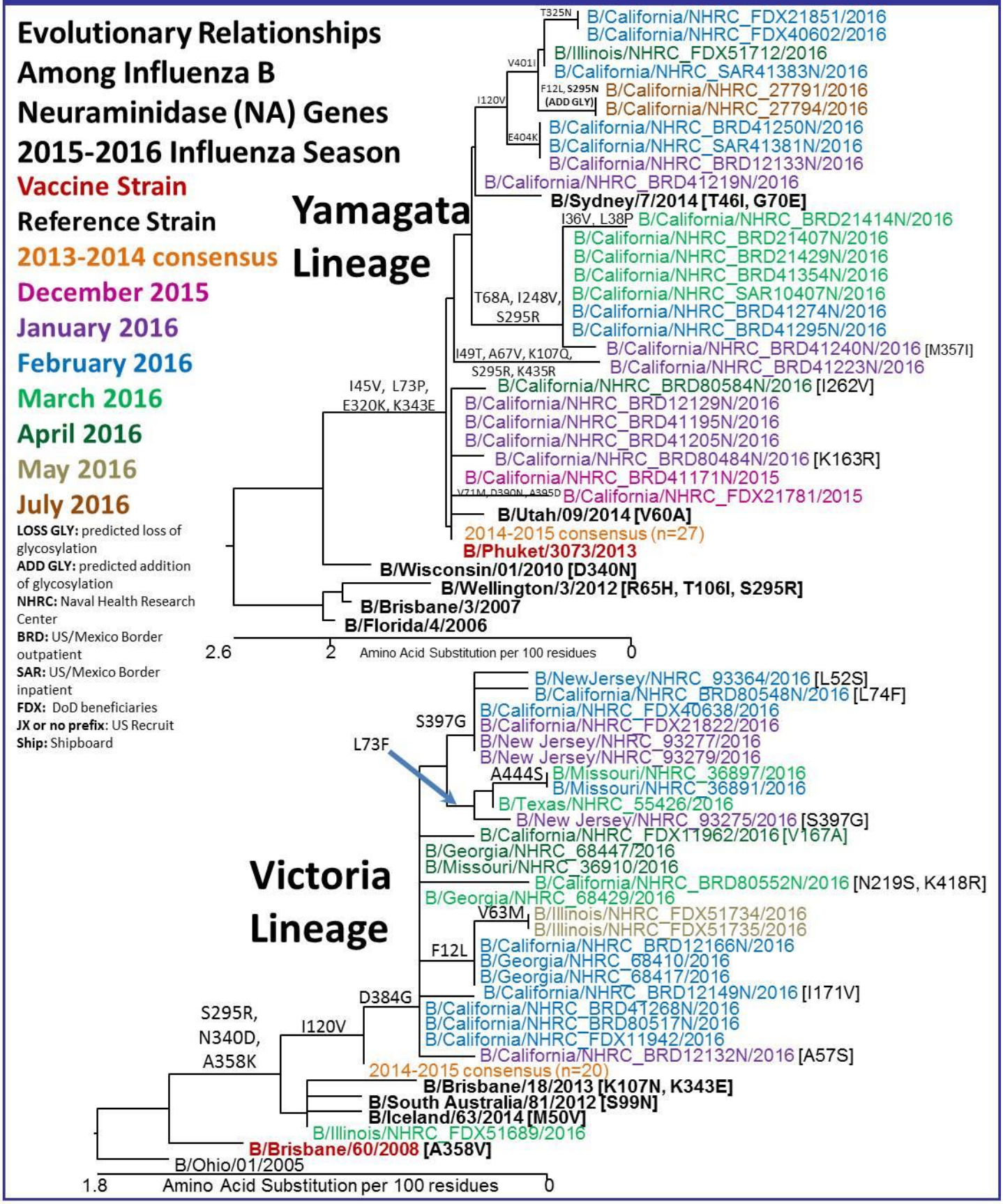


# Evolutionary Relationships Among Influenza B Hemagglutinin (HA) Genes 2015-2016 Influenza Season

**Vaccine Strain**
**Reference Strain**
**2013-2014 consensus**
**December 2015**
**January 2016**
**February 2016**
**March 2016**
**April 2016**
**May 2016**
**July 2016**

**LOSS GLY:** predicted loss of glycosylation
**ADD GLY:** predicted addition of glycosylation
**NHRC:** Naval Health Research Center
**BRD:** US/Mexico Border outpatient
**SAR:** US/Mexico Border inpatient
**FDX:** DoD beneficiaries
**JX or no prefix:** US Recruit
**Ship:** Shipboard




Evolutionary Relationships Among Influenza B Neuraminidase (NA) Genes 2015-2016 Influenza Season
Vaccine Strain
Reference Strain
2013-2014 consensus
December 2015
January 2016
February 2016
March 2016
April 2016
May 2016
July 2016
LOSS GLY: predicted loss of glycosylation
ADD GLY: predicted addition of glycosylation
NHRC: Naval Health Research Center
BRD: US/Mexico Border outpatient
SAR: US/Mexico Border inpatient
FDX: DoD beneficiaries
JX or no prefix: US Recruit
Ship: Shipboard
Yamagata Lineage
T325N
B/California/NHRC_FDX21851/2016
B/California/NHRC_FDX40602/2016
V401I
B/Illinois/NHRC_FDX51712/2016
B/California/NHRC_SAR41383N/2016
F12L, S295N (ADD GLY)
B/California/NHRC_27791/2016
B/California/NHRC_27794/2016
I120V
E404K
B/California/NHRC_BRD41250N/2016
B/California/NHRC_SAR41381N/2016
B/California/NHRC_BRD12133N/2016
B/California/NHRC_BRD41219N/2016
B/Sydney/7/2014 [T46I, G70E]
I36V, L38P
B/California/NHRC_BRD21414N/2016
B/California/NHRC_BRD21407N/2016
B/California/NHRC_BRD21429N/2016
B/California/NHRC_BRD41354N/2016
T68A, I248V, S295R
B/California/NHRC_SAR10407N/2016
B/California/NHRC_BRD41274N/2016
B/California/NHRC_BRD41295N/2016
I49T, A67V, K107Q, S295R, K435R
B/California/NHRC_BRD41240N/2016 [M357I]
B/California/NHRC_BRD41223N/2016
I45V, L73P, E320K, K343E
B/California/NHRC_BRD80584N/2016 [I262V]
B/California/NHRC_BRD12129N/2016
B/California/NHRC_BRD41195N/2016
B/California/NHRC_BRD41205N/2016
B/California/NHRC_BRD80484N/2016 [K163R]
B/California/NHRC_BRD41171N/2015
V71M, D390N, A395D
B/California/NHRC_FDX21781/2015
B/Utah/09/2014 [V60A]
2014-2015 consensus (n=27)
B/Phuket/3073/2013
B/Wisconsin/01/2010 [D340N]
B/Wellington/3/2012 [R65H, T106I, S295R]
B/Brisbane/3/2007
B/Florida/4/2006
2.6
2
Amino Acid Substitution per 100 residues
0
Victoria Lineage
B/NewJersey/NHRC_93364/2016 [L52S]
B/California/NHRC_BRD80548N/2016 [L74F]
S397G
B/California/NHRC_FDX40638/2016
B/California/NHRC_FDX21822/2016
L73F
B/New Jersey/NHRC_93277/2016
B/New Jersey/NHRC_93279/2016
A444S
B/Missouri/NHRC_36897/2016
B/Missouri/NHRC_36891/2016
B/Texas/NHRC_55426/2016
B/New Jersey/NHRC_93275/2016 [S397G]
B/California/NHRC_FDX11962/2016 [V167A]
B/Georgia/NHRC_68447/2016
B/Missouri/NHRC_36910/2016
B/California/NHRC_BRD80552N/2016 [N219S, K418R]
B/Georgia/NHRC_68429/2016
V63M
B/Illinois/NHRC_FDX51734/2016
B/Illinois/NHRC_FDX51735/2016
F12L
B/California/NHRC_BRD12166N/2016
B/Georgia/NHRC_68410/2016
B/Georgia/NHRC_68417/2016
B/California/NHRC_BRD12149N/2016 [I171V]
D384G
B/California/NHRC_BRD41268N/2016
B/California/NHRC_BRD80517N/2016
B/California/NHRC_FDX11942/2016
B/California/NHRC_BRD12132N/2016 [A57S]
S295R, N340D, A358K
I120V
2014-2015 consensus (n=20)
B/Brisbane/18/2013 [K107N, K343E]
B/South Australia/81/2012 [S99N]
B/Iceland/63/2014 [M50V]
B/Illinois/NHRC_FDX51689/2016
B/Brisbane/60/2008 [A358V]
B/Ohio/01/2005
1.8
Amino Acid Substitution per 100 residues
0

w