Influenza

NHRC Laboratory-Confirmed Influenza Cases, US Military Basic Trainees

Current Week*  Since Oct.1, 2016  No. Tested

<table>
<thead>
<tr>
<th>Site</th>
<th>A/Untyp.</th>
<th>A/H3</th>
<th>A/H1</th>
<th>B</th>
<th>A/Untyp.</th>
<th>A/H3</th>
<th>A/H1</th>
<th>B</th>
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<td>CGTC Cape May</td>
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</table>

- 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

- 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
- 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.
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
NHRC Respiratory Illness Update  
Week Ending: 3 December 2016

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

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

Back to FRI Report

- Observed FRI rate (expected rate = dashed line)  • Moderately elevated  • Substantially elevated  — Pneumonia rate (incl. afebrile)
Fl. Leonard Wood FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)

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

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NHRC Respiratory Illness Update

Week Ending: 3 December 2016

Back to FRI Report

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

<table>
<thead>
<tr>
<th>Samples Received</th>
<th>34</th>
<th>42</th>
<th>56</th>
<th>62</th>
<th>57</th>
<th>50</th>
<th>28</th>
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<th>33</th>
<th>53</th>
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<th>55</th>
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<td>Adenovirus</td>
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<td>Influenza</td>
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<tr>
<td>RSV</td>
<td>21%</td>
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<td>16%</td>
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<tr>
<td>C. pneumo</td>
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<td>M. pneumo</td>
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Rhinovirus

<table>
<thead>
<tr>
<th>Month</th>
<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
<th>Oct</th>
<th>Nov</th>
<th>Dec</th>
<th>Jan</th>
<th>Feb</th>
<th>Mar</th>
<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rate (cases/100 trainees/week)</td>
<td></td>
<td></td>
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Samples Received

<table>
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<tr>
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<th>2015</th>
<th>2016</th>
<th>2017</th>
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<tr>
<td>Adenovirus</td>
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<td>4%</td>
<td>11%</td>
</tr>
<tr>
<td>Influenza</td>
<td>5%</td>
<td>13%</td>
<td>11%</td>
</tr>
<tr>
<td>RSV</td>
<td>4%</td>
<td>3%</td>
<td>2%</td>
</tr>
<tr>
<td>C. pneumo</td>
<td>4%</td>
<td>13%</td>
<td>7%</td>
</tr>
<tr>
<td>M. pneumo</td>
<td>6%</td>
<td>2%</td>
<td>5%</td>
</tr>
<tr>
<td>Rhinovirus</td>
<td>39%</td>
<td>27%</td>
<td>13%</td>
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Influenza Subtype

<table>
<thead>
<tr>
<th>Influenza Subtype</th>
<th>B</th>
<th>A/H3</th>
<th>A/pH1</th>
<th>Untyped</th>
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<tr>
<td>2015</td>
<td>76%</td>
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<td>2016</td>
<td>89%</td>
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</tr>
<tr>
<td>2017</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
</tr>
</tbody>
</table>

Back to FRI Report

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 | 14 | 4 | 25 | 7 | 19 | 23 | 18 | 8 | 59 | 20 | 6 | 8 | 3 |
|------------------|----|----|----|----|----|---|----|---|----|----|----|---|----|----|---|----|----|---|
| Adenovirus       |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| Influenza        |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| RSV              | 21%| 10%| 16%|    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| C. pneumo        |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| M. pneumo        |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| Rhinovirus       | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% | 4% |

Rhinovirus

<table>
<thead>
<tr>
<th>Month</th>
<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
<th>Oct</th>
<th>Nov</th>
<th>Dec</th>
<th>Jan</th>
<th>Feb</th>
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<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rate (cases/100 trainees/week)</td>
<td></td>
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Samples Received

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<thead>
<tr>
<th></th>
<th>2015</th>
<th>2016</th>
<th>2017</th>
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<tr>
<td>Adenovirus</td>
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<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td>Influenza</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td>RSV</td>
<td>100%</td>
<td>100%</td>
<td>100%</td>
</tr>
<tr>
<td>C. pneumo</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td>M. pneumo</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td>Rhinovirus</td>
<td>0%</td>
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Influenza Subtype

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<thead>
<tr>
<th>Influenza Subtype</th>
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<th>A/H3</th>
<th>A/pH1</th>
<th>Untyped</th>
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<td>2015</td>
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</tr>
<tr>
<td>2017</td>
<td>0%</td>
<td>100%</td>
<td>0%</td>
<td>0%</td>
</tr>
</tbody>
</table>

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~ Observed FRI rate (expected rate = dashed) • 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)

<table>
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<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
<th>Oct</th>
<th>Nov</th>
<th>Dec</th>
<th>Jan</th>
<th>Feb</th>
<th>Mar</th>
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<tbody>
<tr>
<td>Year</td>
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<td></td>
</tr>
<tr>
<td>Samples Received</td>
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<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>5</td>
<td>13</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
</tbody>
</table>

- **Adenovirus**: 100%
- **Influenza**: 40%
- **RSV** 46%
- **C. pneumo**: 11%
- **M. pneumo**: 50%
- **Rhinovirus**: 50%

### Cape May FRI Rates and Diagnostic Test Results

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

<table>
<thead>
<tr>
<th>Month</th>
<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
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<td></td>
</tr>
<tr>
<td>Samples Received</td>
<td>9</td>
<td>6</td>
<td>9</td>
<td>13</td>
<td>15</td>
<td>21</td>
<td>17</td>
<td>4</td>
<td>7</td>
<td>13</td>
<td>5</td>
<td>6</td>
</tr>
</tbody>
</table>

- **Adenovirus**: 11%
- **Influenza**: 7%
- **RSV**: 10%
- **C. pneumo**: 38%
- **M. pneumo**: 33%
- **Rhinovirus**: 44%

### Influenza Subtype

<table>
<thead>
<tr>
<th>Month</th>
<th>Apr</th>
<th>May</th>
<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
<th>Sep</th>
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<td></td>
<td></td>
</tr>
<tr>
<td>Samples Received</td>
<td>9</td>
<td>6</td>
<td>9</td>
<td>13</td>
<td>15</td>
<td>21</td>
<td>17</td>
<td>4</td>
<td>7</td>
<td>13</td>
<td>5</td>
<td>6</td>
</tr>
</tbody>
</table>

- **A/H1**: 100%
- **A/h3**: 0%
- **A/pH1**: 100%
- **Untyped**: 0%

### Back to FRI Report
NHRC Respiratory Illness Update

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.

Laboratory testing results - DoD beneficiaries, 2015-16
**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

<table>
<thead>
<tr>
<th>Segment</th>
<th>No. Isolates</th>
<th>2015-2016 Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/pH1N1 HA</td>
<td>47</td>
<td>A/California/07/2009</td>
<td>97.0-98.0%</td>
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<tr>
<td>A/pH1N1 NA</td>
<td>46</td>
<td>A/California/07/2009</td>
<td>96.1-97.3%</td>
</tr>
</tbody>
</table>

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. 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/](http://www.cbs.dtu.dk/services/NetNGlyc/)

<table>
<thead>
<tr>
<th>A/pH1N1 Segment</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
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<tr>
<td>HA</td>
<td>S162N</td>
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</tr>
<tr>
<td>NA</td>
<td>N44S, S70N</td>
<td>N386K</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Segment</th>
<th>No.</th>
<th>2015-2016 Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>H3N2 HA</td>
<td>50</td>
<td>A/Switzerland/9715293/2013</td>
<td>96.8-99.6%</td>
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<tr>
<td>H3N2 NA</td>
<td>37</td>
<td>A/Switzerland/9715293/2013</td>
<td>97.9-98.6%</td>
</tr>
</tbody>
</table>

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/

<table>
<thead>
<tr>
<th>A/H3N2 Segment</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
</tr>
</thead>
<tbody>
<tr>
<td>HA</td>
<td>K160T</td>
<td>S47P N122D T128A N144S N158K N158H T160K T160I</td>
</tr>
<tr>
<td>NA</td>
<td>S245N N329I S331R</td>
<td>S247T N329S N329T</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Segment</th>
<th>No. Isolates</th>
<th>2015-2016 Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>B/Victoria HA</td>
<td>27</td>
<td>B/Brisbane/60/2008</td>
<td>99.1-99.5%</td>
</tr>
<tr>
<td>B/Victoria NA</td>
<td>27</td>
<td>B/Brisbane/60/2008</td>
<td>98.3-98.54%</td>
</tr>
<tr>
<td>B/Yamagata HA</td>
<td>25</td>
<td>B/Phuket/3073/2013</td>
<td>99.1-99.5%</td>
</tr>
<tr>
<td>B/Yamagata NA</td>
<td>26</td>
<td>B/Phuket/3073/2013</td>
<td>98.7-100.0%</td>
</tr>
</tbody>
</table>

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. Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server [link](http://www.cbs.dtu.dk/services/NetNGlyc/)

<table>
<thead>
<tr>
<th>INF B Segment</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
</tr>
</thead>
<tbody>
<tr>
<td>HA</td>
<td>A198T</td>
<td>N196D T198N</td>
</tr>
<tr>
<td>NA</td>
<td>D463N, S295N</td>
<td></td>
</tr>
</tbody>
</table>

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

**Influenza A/pH1N1**

- **6B.1, 43, 91%**
- **6B, 4, 9%**

Dec-15 | Jan-16 | Feb-16 | Mar-16 | Apr-16 | May-16
--- | --- | --- | --- | --- | ---

**Influenza A/H3N2**

- **H3N2 3C.3a 50%**
- **H3N2 3C.2a 50%**

Dec-15 | Jan-16 | Feb-16 | Mar-16 | Apr-16 | May-16 | July-Sept 2016
--- | --- | --- | --- | --- | --- | ---
3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a | 3C.2a

**Influenza B**

- **B/Vic (1A), 27, 52%**
- **B/Yam (Y3), 25, 48%**

Dec-15 | Jan-16 | Feb-16 | Mar-16 | Apr-16 | May-16 | Jul-Sept 2016
--- | --- | --- | --- | --- | --- | ---
1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3 | 1A | Y3

- Total FRI DoD Beneficiaries
- Total BIDS
- Total US Recruited
- Individual
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 Recruiter
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
JK or no prefix: US Recruit
Ship: Shipboard
*clinical specimen

Amino Acid Substitution per 100 residues
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

Victoria Lineage

Amino Acid Substitution per 100 residues

2014-2015 consensus (n=27)
2014-2015 consensus (n=20)
2014-2015 consensus (n=29)