Influenza

NHRC Laboratory-Confirmed Influenza Cases, US Military Basic Trainees

<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>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
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<td>0</td>
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<td>0</td>
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<td>35</td>
</tr>
<tr>
<td>Ft. Jackson</td>
<td></td>
<td></td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td></td>
<td>19</td>
</tr>
<tr>
<td>Ft. Leonard Wood</td>
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<td>0</td>
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<td>0</td>
<td>0</td>
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<td>4</td>
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<td>MCRD Parris Island</td>
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<td><strong>Total</strong></td>
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<td>0</td>
<td>0</td>
<td>0</td>
<td>158</td>
</tr>
</tbody>
</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

**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.
**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 10 December 2016:

- **At or below expected value:**
  - Fort Benning
  - 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:**
  - Marine Corps Recruit Depot, Parris Island
NHRC Respiratory Illness Update

Week Ending: 10 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)

Samples Received

<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>
</tr>
</thead>
<tbody>
<tr>
<td>Samples</td>
<td>33</td>
<td>20</td>
<td>44</td>
<td>50</td>
<td>53</td>
<td>20</td>
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<td>21</td>
<td>11</td>
</tr>
<tr>
<td>Adenoviruses</td>
<td>5%</td>
<td>2%</td>
<td>5%</td>
<td>4%</td>
<td>7%</td>
<td>5%</td>
<td>5%</td>
<td>9%</td>
<td>24%</td>
<td>26%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Influenza</td>
<td>5%</td>
<td>2%</td>
<td>5%</td>
<td>4%</td>
<td>7%</td>
<td>5%</td>
<td>5%</td>
<td>9%</td>
<td>24%</td>
<td>26%</td>
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<td></td>
</tr>
<tr>
<td>RSV</td>
<td>2%</td>
<td>5%</td>
<td>8%</td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C. pneumonia</td>
<td>4%</td>
<td>4%</td>
<td>15%</td>
<td>6%</td>
<td>7%</td>
<td>5%</td>
<td>8%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M. pneumonia</td>
<td>4%</td>
<td>4%</td>
<td>15%</td>
<td>6%</td>
<td>7%</td>
<td>5%</td>
<td>8%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rhinovirus</td>
<td>18%</td>
<td>40%</td>
<td>24%</td>
<td>9%</td>
<td>10%</td>
<td>19%</td>
<td>29%</td>
<td>36%</td>
<td>35%</td>
<td>24%</td>
<td>36%</td>
<td>29%</td>
</tr>
<tr>
<td>Subtype</td>
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<td>100%</td>
<td>0%</td>
<td>0%</td>
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<td></td>
</tr>
<tr>
<td>A/H3</td>
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<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
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<td>0%</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>A/Ph1</td>
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<td>0%</td>
<td>0%</td>
<td>0%</td>
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<td></td>
</tr>
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<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Back to FRI Report

- Observed FRI rate (expected rate = dashed line)
- Moderately elevated
- Substantially elevated
- Pneumonia rate (incl. afebrile)
**NHRC Respiratory Illness Update**

**Week Ending: 10 December 2016**

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### Ft. Leonard Wood FRI Rates and Diagnostic Test Results

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

**Rate (cases/100 trainees/week)**

<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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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Samples Received</td>
<td>26</td>
<td>13</td>
<td>20</td>
<td>9</td>
<td>25</td>
<td>22</td>
<td>10</td>
<td>13</td>
<td>20</td>
<td>42</td>
<td>15</td>
<td>24</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>4%</td>
<td>5%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Influenza</td>
<td>24%</td>
<td>7%</td>
<td>4%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSV</td>
<td>8%</td>
<td>38%</td>
<td>25%</td>
<td>30%</td>
<td>11%</td>
<td>4%</td>
<td>9%</td>
<td>40%</td>
<td>15%</td>
<td>10%</td>
<td>10%</td>
<td>7%</td>
</tr>
<tr>
<td>C. pneumo</td>
<td>8%</td>
<td>5%</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M. pneumo</td>
<td>38%</td>
<td>23%</td>
<td>30%</td>
<td>20%</td>
<td>22%</td>
<td>16%</td>
<td>9%</td>
<td>10%</td>
<td>8%</td>
<td>15%</td>
<td>24%</td>
<td>27%</td>
</tr>
</tbody>
</table>

---

### Great Lakes FRI Rates and Diagnostic Test Results

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

**Rate (cases/100 trainees/week)**

<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>
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<td></td>
<td></td>
<td></td>
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</tr>
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<td>Samples Received</td>
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<td>1</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>10</td>
<td>3</td>
<td>6</td>
<td>7</td>
<td>2</td>
<td>3</td>
<td>20</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>25%</td>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>Influenza</td>
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<td>10%</td>
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<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RSV</td>
<td>8%</td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C. pneumo</td>
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<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>M. pneumo</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Rhinovirus</td>
<td>100%</td>
<td>40%</td>
<td>10%</td>
<td>33%</td>
<td>17%</td>
<td>14%</td>
<td>25%</td>
<td>27%</td>
<td>60%</td>
<td>47%</td>
<td>41%</td>
<td>69%</td>
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</table>

---

### NHRC Respiratory Illness Update

**Back to FRI Report**

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

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* - 4 -
Back to FRI Report

Back to FRI Report

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

### Laboratory testing results - DoD beneficiaries, 2016 -2017

<table>
<thead>
<tr>
<th>Week</th>
<th>No. Specimens</th>
<th>Flu A (H3)</th>
<th>Flu A (pH1N1)</th>
<th>Flu B</th>
<th>Rhinovirus</th>
<th>M.pneumo</th>
<th>Adenovirus</th>
<th>C.pneumo</th>
<th>RSV</th>
<th>R. pneumonia</th>
<th>No Pathogen Identified</th>
<th>Flu Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>52</td>
<td>21</td>
<td>10</td>
<td>5</td>
<td>6</td>
<td>10</td>
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<td>10</td>
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<td>15</td>
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<td>20%</td>
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<td>55</td>
<td>24</td>
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<td>16</td>
<td>11</td>
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<td>11</td>
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<td>13</td>
<td>17</td>
<td>13</td>
<td>17</td>
<td>13</td>
<td>17</td>
<td>30%</td>
</tr>
</tbody>
</table>

**Legend:**
- Flu A (H3)
- Flu A (pH1N1)
- Flu B
- Rhinovirus
- M. pneumoniae
- Adenovirus
- C. pneumoniae
- RSV
- R. pneumonia
- No Pathogen Identified
- Flu Rate

*Note: The diagram illustrates the distribution of laboratory testing results for various pathogens among DoD beneficiaries from 2016 to 2017. The Y-axis represents the number of specimens tested, while the X-axis represents the weeks of testing.*
**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.

**U.S.-Mexico Border ILLI, 2016-17**

**U.S.-Mexico Border SARI, 2016-17**
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>
</tr>
<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.\(^2\) 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>Mutation</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
</tr>
</thead>
<tbody>
<tr>
<td>HA</td>
<td>S162N</td>
<td></td>
</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>
</tr>
<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. 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.

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%

**Influenza A/H3N2**
- H3N2 3C.3a 50%
- H3N2 3C.2a 50%

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


Amino Acid Substitution per 100 residues

A/South Carolina/NHRC_75452/2016* [S47P (LOSS GLY)]
A/South Carolina/NHRC_75458/2016*
A/South Carolina/NHRC_75444/2016
A/South Carolina/NHRC_75450/2016
A/South Carolina/NHRC_75458/2016*
A/South Carolina/NHRC_75461/2016*
A/South Carolina/NHRC_75402/2016*
A/California/NHRC_F021905/2016
A/California/NHRC_BRD241212N/2016 [Q454L, N498K]
A/California/NHRC_BRD12210N/2016 [L420I]
A/California/NHRC_BRD44334N/2016
A/California/NHRC_BRD90554N/2016
A/California/NHRC_F024539/2016
A/California/NHRC_C0V0006/2016 [H121D]
A/California/NHRC_SAR14446N/2016
A/Missouri/NHRC_36888/2016
A/California/NHRC_BRD21370N/2016
A/California/NHRC_BRD41318N/2016
A/California/NHRC_BRD41264N/2016
A/California/NHRC_F021931/2016
A/California/NHRC_SAR14354N/2016 [F193S]
A/California/NHRC_BRD1168N/2016
A/California/NHRC_BRD4126N/2016
A/California/NHRC_BRD90496N/2016
A/California/NHRC_SAR14353N/2016
A/Pennsylvania/47/2014
A/Switzerland/8715293/2013 [2015-2016]
A/Shanxi/Changzhi/1432/2014
A/Stockholm/06/2014
A/Stockholm/28/2014
A/NewYork/39/2012
A/Samara/73/2013 [140K]
A/HongKong/6/2014
A/Nebraska/04/2014
A/Pennsylvania/50/2016
A/NewJersey/NHRC_93395/2016*
A/NewJersey/NHRC_93398/2016*
A/NewJersey/NHRC_93400/2016*
A/NewJersey/NHRC_93408/2016*
A/NewJersey/NHRC_93410/2016*
A/NewJersey/NHRC_93418/2016*
A/NewJersey/NHRC_93420/2016*
A/NewJersey/NHRC_93422/2016*
A/NewJersey/NHRC_93433/2016*
A/NewJersey/NHRC_93442/2016*
A/NewJersey/NHRC_93457/2016*
A/NewJersey/NHRC_93462/2016*
A/HongKong/4801/2014 [2016-2017] [N968, L194P]
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

Amino Acid Substitution per 100 residues
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

Yamagata Lineage

Victoria Lineage

1A

1B
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=20)

B/Ohio/01/2005
B/South Australia/81/2012
B/Iceland/63/2014
B/Utah/09/2014
B/Florida/4/2006
B/New Jersey/NHRC_93364/2016
B/New Jersey/NHRC_93275/2016
B/New Jersey/NHRC_93279/2016
B/Texas/NHRC_55426/2016
B/Missouri/NHRC_36997/2016
B/Missouri/NHRC_36991/2016
B/Georgia/NHRC_68447/2016
B/Georgia/NHRC_68429/2016
B/Georgia/NHRC_68417/2016
B/Brisbane/18/2013
B/Illinois/NHRC_FDX51735/2016
B/Illinois/NHRC_FDX51734/2016
B/California/NHRC_BRD12168N/2016
B/California/NHRC_BRD12149N/2016
B/California/NHRC_BRD12149N/2016
B/California/NHRC_BRD80552N/2016
B/California/NHRC_BRD80550N/2016
B/California/NHRC_BRD80551N/2016
B/California/NHRC_BRD80549N/2016
B/California/NHRC_BRD80548N/2016
B/California/NHRC_BRD80484N/2016
B/California/NHRC_BRD80480N/2016
B/California/NHRC_BRD12129N/2016
B/California/NHRC_BRD12105N/2016
B/California/NHRC_BRD12105N/2016
B/California/NHRC_BRD12104N/2016
B/California/NHRC_BRD12103N/2016
B/California/NHRC_BRD12102N/2016
B/California/NHRC_BRD12101N/2016
B/California/NHRC_BRD12091N/2016
B/California/NHRC_BRD12081N/2016
B/California/NHRC_BRD12071N/2016
B/California/NHRC_BRD12061N/2016
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B/California/NHRC_BRD12031N/2016
B/California/NHRC_BRD12021N/2016
B/California/NHRC_BRD12011N/2016
B/California/NHRC_BRD12001N/2016
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