2017 Week 34 (through 26 August 2017)

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>No. Tested</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ft. Benning</td>
<td>9</td>
<td>1</td>
<td></td>
<td></td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td>188</td>
</tr>
<tr>
<td>Ft. Jackson</td>
<td>16</td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>321</td>
</tr>
<tr>
<td>Ft. Leonard Wood</td>
<td>6</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
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<td>105</td>
</tr>
<tr>
<td>NRTC Great Lakes</td>
<td>19</td>
<td></td>
<td></td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>223</td>
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<tr>
<td>Lackland AFB</td>
<td>1</td>
<td></td>
<td></td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>32</td>
</tr>
<tr>
<td>MCRD Parris Island</td>
<td></td>
<td>20</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>123</td>
</tr>
<tr>
<td>MCRD San Diego</td>
<td></td>
<td>21</td>
<td>1</td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>319</td>
</tr>
<tr>
<td>CGTC Cape May</td>
<td></td>
<td>1</td>
<td>29</td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>238</td>
</tr>
<tr>
<td>Total</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>120</td>
<td>2</td>
<td>18</td>
<td>1549</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.

Items of Note

- FRI rates at all basic training centers are at or below expected values

- Nine confirmed cases of adenovirus serotype 14 at MCRD Parris Island, June-August 2017

- NHRC is able to test for novel influenza strains, MERS coronavirus, enterovirus EV-68, Ebola virus, and Zika virus

Contact Information

Address:
Commanding Officer
Attn: Code 166
Naval Health Research Center
140 Sylvester Rd.
San Diego, CA 92106

Web:
NHRC Operational Infectious Diseases

Email:
NHRC FRI Surveillance Program

Vaccination Status of Confirmed Influenza Cases Among US Military Basic Trainees, 2014-17

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 2012-17. 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 26 August 2017:
- **At or below expected value:**
  - Fort Benning
  - Fort Jackson
  - Fort Leonard Wood
  - Naval Recruit Training Command, Great Lakes
  - Marine Corps Recruit Depot, San Diego
  - Marine Corps Recruit Depot, Parris Island
  - Lackland Air Force Base (data through 12 August)
  - Coast Guard Training Center, Cape May
- **Moderately elevated:**
  - None
- **Substantially elevated:**
  - None
Ft. Leonard Wood 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>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>
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<th>Sep</th>
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<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>2.0</td>
<td>1.5</td>
<td>1.0</td>
<td>0.5</td>
<td>0.0</td>
<td>0.5</td>
<td>1.0</td>
<td>1.5</td>
<td>2.0</td>
<td></td>
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</tr>
</tbody>
</table>

Samples Received
22 10 3 6 7 2 3 20 26 25 30 32 15 12 8 24 12 28 25 34 36 23 20

Adenovirus 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5%
Influenza 24% 7% 4% 25% 33% 25% 7% 25% 33% 27% 25% 25% 33% 25% 25% 33% 27% 25% 25% 33% 27% 25% 25% 33%
RSV 9% 40% 15% 10% 10% 7% 4% 50% 6% 33% 27% 25% 13% 13% 20% 21% 20% 29% 15% 27% 15% 27% 15% 27%
C. pneumo 9% 40% 15% 10% 10% 7% 4% 50% 6% 33% 27% 25% 13% 13% 20% 21% 20% 29% 15% 27% 15% 27% 15% 27%
M. pneumo 23% 20% 15% 10% 2% 33% 33% 17% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5%
Rhinovirus 9% 10% 8% 15% 24% 27% 4% 33% 27% 33% 25% 25% 25% 25% 25% 25% 25% 25% 25% 25% 25% 25% 25% 25%

Great Lakes 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>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>
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<th>Sep</th>
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<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>2.0</td>
<td>1.5</td>
<td>1.0</td>
<td>0.5</td>
<td>0.0</td>
<td>0.5</td>
<td>1.0</td>
<td>1.5</td>
<td>2.0</td>
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<td></td>
</tr>
</tbody>
</table>

Samples Received
10 3 6 7 2 3 20 26 25 30 32 15 12 8 24 12 28 25 34 36 23 20

Adenovirus 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5% 5%
Influenza 14% 50% 10% 4% 8% 4% 42% 29% 24% 3% 6% 5% 6% 5% 6% 5% 6% 5% 6% 5% 6% 5% 6% 5%
RSV 10% 33% 17% 14% 25% 27% 60% 47% 41% 60% 42% 38% 38% 8% 24% 21% 22% 43% 15%
C. pneumo 10% 33% 17% 14% 25% 27% 60% 47% 41% 60% 42% 38% 38% 8% 24% 21% 22% 43% 15%
M. pneumo 10% 33% 17% 14% 25% 27% 60% 47% 41% 60% 42% 38% 38% 8% 24% 21% 22% 43% 15%
Rhinovirus 10% 33% 17% 14% 25% 27% 60% 47% 41% 60% 42% 38% 38% 8% 24% 21% 22% 43% 15%

Influenza Subtype
A/H3 0% 0% 100% 80% 100% 83% 100% 83% 100% 83% 100% 83% 100% 83% 100% 83% 100% 83% 100% 83% 100% 83% 100% 83%
A/pH1 100% 100% 50% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0%
Untyped 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0%

Back to FRI Report
NHRC Respiratory Illness Update

Week Ending: 26 August 2017

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

MCRD PI 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)
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 investigator (Chris Myers, christopher.a.myers48.civ@mail.mil) or the study coordinator (Erin Hansen, erin.a.hansen.ctr@mail.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(H1N1)pdm09 HA and NA Protein Sequences

- 2 analyzed Influenza A(H1N1)pdm09 HA sequences were derived from MDCK-SIAT1 isolates and 6 were derived by clinical specimens.
- All sequences belonged to the subclade 6B.1, defined by mutations S84N, S162T (ADD GLY) and I216T.
- 4 analyzed Influenza A(H1N1)pdm09 NA sequence was derived from MDCK-SIAT1 isolates and 7 were 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 (both HA and NA sequences) are with respect to A/California/07/2009.

Summary of Influenza A(H1N1)pdm09 Protein Homology When Compared with 2016-2017 Vaccine Strain and upcoming 2017-2018 Vaccine Strain

<table>
<thead>
<tr>
<th>Segment</th>
<th>No. Isolates</th>
<th>Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>A(H1N1)pdm09 HA</td>
<td>8</td>
<td>A/California/07/2009 (2016-17)</td>
<td>96.4-97.2%</td>
</tr>
<tr>
<td>A(H1N1)pdm09 HA</td>
<td>8</td>
<td>A/Michigan/45/2015 (2017-18)</td>
<td>99.0-100%</td>
</tr>
<tr>
<td>A(H1N1)pdm09 NA</td>
<td>11</td>
<td>A/California/07/2009 (2016-17)</td>
<td>96.5-97.3%</td>
</tr>
<tr>
<td>A(H1N1)pdm09 NA</td>
<td>11</td>
<td>A/Michigan/45/2015 (2017-18)</td>
<td>99.3-100%</td>
</tr>
</tbody>
</table>

Summary of Influenza A(H1N1)pdm09 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>Mutation</th>
<th>Segment</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/A(H1N1)pdm09</td>
<td>HA</td>
<td>S162N</td>
<td>N/A</td>
</tr>
<tr>
<td></td>
<td>NA</td>
<td>N44S, S70N</td>
<td>N386K</td>
</tr>
</tbody>
</table>

Evolutionary Relationships
Among Influenza A(H1N1)pdm09
Hemagglutinin (HA) Genes
2016-2017 Influenza Season

Vaccine Strain

Reference Strain

2015-16 Consensus (47 strains)
Dec 2016 (2 strains)
Jan 2017 (1 strain)
Feb 2017 (4 strains)
Mar 2017 (1 strain)

LOSSL GLY: predicted loss of glycosylation
ADD GLY: predicted addition of glycosylation
NHRC: Naval Health Research Center
BRD: US/Mexico Border outpatient
SARI: US/Mexico Border inpatient
FDX or NMCSD: DoD beneficiaries
JX or no prefix: US Recruit

*: clinical specimen

A/Missouri/NHRC_36962/2017* [A215G]
A/Fiji/3/2016 [Q223R]
A/California/NHRC_BRD41506N/2017*
A/California/NHRC_SAR20891N/2017*
A/North Dakota/03/2016
A/California/NHRC_BRD41490N/2017* [A215S]
A/California/NHRC_NMCSD0075/2016*
A/California/NHRC_BRD12309N/2017
A/California/NHRC_27982/2017
A/California/NHRC_NMCSD0076/2016*
2015-16 6B.1 Consensus (43 strains)
A/Michigan/45/2015 (2017-18 season)
A/Minnesota/32/2015
A/Darwin/11/2015
2015-16 6B Consensus (4 strains)
A/Norway/2417/2013
A/California/07/2009

Amino Acid Substitution per 100 residues
Evolutionary Relationships
Among Influenza A(H1N1)pdm09
Neuraminidase (NA) 2016-2017
Influenza Season

Vaccine Strain

Reference Strain

2015-16 Consensus (46 strains)

Dec 2016 (2 strains)
- A/Missouri/NHRC_36962/2017* [A75V, K260R]

Jan 2017 (1 strain)
- A/California/NHRC_BRD41523N/2017

Feb 2017 (5 strains)
- L127F, D199N
- A/California/NHRC_BRD41511N/2017
- A/California/NHRC_BRD41503N/2017*
- A/California/NHRC_BRD41506N/2017*
  - A/California/NHRC_SAR20891N/2017* [R173K]

Mar 2017 (3 strains)
- A/Delaware/39/2015 [V394I, I443M]
- A/California/NHRC_BRD12309N/2017 [V81I]
- A/California/NHRC_BRD41490N/2017*
  - A/California/NHRC_BRD41490N/2017
  - A/California/NHRC_NMCSD0076/2016* [S95N, I223R’]
  - A/California/NHRC_NMCSD0075/2016 [N68S]

2015-16 6B.1 Consensus (46 strains)
- A/Michigan/45/2015 (2017-18 season)
- A/California/80/2015 [I32V, V67I, S79L]
- A/Astrakhan/1/2011 [V106I]
- A/California/07/2009 [I241V, D248N K369N]

Amino Acid Substitution per 100 residues

1. Known marker for Neuraminidase inhibitor (NAI) resistance. NAI inhibition assay (NA Star) was performed using MDCK-SIAT1 isolate. With respect to the wild type NAI susceptible virus (A/CA/12/2012), IC50 fold change was 11.03 for Zanamivir and 19.02 for Oseltamivir. These fold changes both fall in the reduced inhibition range (RI).
http://www.who.int/influenza/gisrs_laboratory/antiviral_susceptibility/nai_overview/en/
Phylogenetic Comparison of Influenza A (H3N2) HA and NA Protein Sequences

- 5 analyzed H3N2 HA sequences were derived from MDCK isolates and 78 were derived from clinical specimen.
- 1 sequence belonged to 3C.3a and 82 were in subclade 3C.2a. Of those 3C.2a sequences, 49 were further classified as 3C.2a1, defined by the mutations N171K, I406V (HA2: I77V), and G484E (HA2: G155E).
- 2 analyzed H3N2 NA sequences were derived from MDCK isolates and 24 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 A/Perth/16/2009 for HA and NA sequences.

Summary of Influenza A (H3N2) Protein Homology When Compared with 2016-2017 Vaccine Strain

<table>
<thead>
<tr>
<th>Segment</th>
<th>No.</th>
<th>2016-2017 Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>H3N2 HA</td>
<td>83</td>
<td>A/HongKong/4801/2014</td>
<td>97.2-98.9%</td>
</tr>
<tr>
<td>H3N2 NA</td>
<td>26</td>
<td>A/HongKong/4801/2014</td>
<td>97.0-98.9%</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>NA</td>
<td>S245N</td>
<td>D329S</td>
</tr>
</tbody>
</table>

Evolutionary Relationships Among Influenza A (H3N2) Hemagglutinin (HA) Genes 2016-2017 Influenza Season

Vaccine Strain

Reference Strain

2015-16 Consensus (50 strains)

July-Sept 2016 (16 strains)

Oct-Dec 2016 (13 strains)

Jan 2017 (20 strains)

Feb 2017 (16 strains)

Mar 2017 (10 strains)

April 2017 (7 strains)

May 2017 (1 strain)

LOSS GLY: predicted loss of glycosylation
ADD GLY: predicted addition of glycosylation
NHRC: Naval Health Research Center
BMD: US/Mexico Border outpatient
SAR: US/Mexico Border inpatient
DX: DoD beneficiaries
JX or no prefix: US Recruit
SEA: US Special Forces
*clinical specimen
**: shipboard surveillance

A/Philippines/NHRC_MCY0131/2016* (2 strains)
A/Georgia/NHRC_68549/2016*
A/South Carolina/NHRC_XJ7557/2016*
A/South Carolina/NHRC_7558/2017* [H2: R186]
A/Missouri/NHRC_36948/2017*
A/California/NHRC_BRD12067/2016*
A/South Carolina/NHRC_7557/2016*
A/Alaska/232/2016*
A/California/NHRC_BRD1519/2017*
A/California/NHRC_SAR10481/2017* [S198P]
A/Clinical/NHRC_BRD14868/2017* [P239S, G240R]
A/Missouri/NHRC_36958/2017* [S91N]
A/South Carolina/NHRC_XJ41937/2017*
A/California/NHRC_SEA0/2017* [N2K LOSS GLY, S265G]
A/California/NHRC_2807/2017*
A/Alaska/240/2015 [D3SN, K92R, S114T]
2015-16 3C.2a Consensus (25 strains)
A/South Carolina/NHRC_79519/2017*
A/California/NHRC_BRD08071/2017*
A/California/NHRC_FDX09238/2017*
A/California/NHRC_RT012/2017*
A/Alabama/NHRC_FDX15625/2017*
A/South Carolina/NHRC_XJ41745/2017* [P273L]
A/Japan/NHRC_FDX701/2016*
A/Japan/NHRC_FDX70127/2017*
A/Hong Kong/480/2014 [N96S, L194F]
2015-16 3C.3a Consensus (25 strains)
A/Texas/56/2012 [T128N], [S199P] (3C.1)
A/Perth/16/2009
Evolutionary Relationships Among Influenza A (H3N2) Neuraminidase (NA) Genes 2016-2017 Influenza Season

Vaccine Strain

Reference Strain

2015-16 Consensus (37 strains)

July-Sept 2016 (14 strains)

Oct-Dec 2016 (5 strains)

January 2017 (1 strain)

March 2017 (4 strains)

April 2017 (3 strains)

**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

*: clinical specimen

—: shipboard surveillance

A/California/NHRC_FD90142/2016*
A/California/NHRC_SAR41594N/2016*
A/California/NHRC_BRD12267N/2016* [I62V]

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A/Alaska/232/2015
A/Illinois/NHRC_18564/2017* [F205I]
A/Georgia/NHRC_68549/2016* [K220N]
A/Philippines/NHRC_MCY0131/2016* (2 strains)

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A/NewJersey/NHRC_93692/2017*
A/SouthCarolina/NHRC_JX41822/2017*
A/NewJersey/NHRC_93675/2017*
A/California/NHRC_BRD12386N/2017*
A/NewJersey/NHRC_93422/2016* (9 strains) [V215I]

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A/Japan/NHRC_FD970127/2017* [K296R]
A/California/NHRC.CG5904/2017*
A/SouthCarolina/NHRC_JX41626/2016
A/SouthCarolina/NHRC_JX41638/2016
A/SouthCarolina/NHRC_JX41610/2016*
A/SouthCarolina/NHRC_JX41611/2016*

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A/Alaska/240/2015
A/NewYork/57/2015 [S335G]
A/Canberra/82/2014

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2015-16 H3NA Consensus (37 strains)
A/California/NHRC_BRD41554N/2017*

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A/HongKong/4801/2014 [V231I]
A/Switzerland/9715293/2013

---

A/Texas/50/2012
A/Perth/16/2009

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Amino Acid Substitution per 100 residues
Phylogenetic Comparison of Influenza B (Yamagata and Victoria) HA and NA Protein Sequences

- 9 sequences belonged to the Y3 clade of the Yamagata lineage and 7 sequence belonged to the V1A clade of the Victoria lineage.
- Two B/Victoria HA sequences contained the double amino acid deletion at positions 162 and 163. Viruses with these deletions are currently referred to as the “B/Victoria deletion variant subgroup” and are antigenically distinct from the vaccine strain.¹
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown with respect to B/Phuket/3073/2013 for B/Yamagata HA sequences, B/Wisconsin/01/2010 for B/Yamagata NA sequences, B/Ohio/01/2005 for B/Victoria HA sequences, and B/Brisbane/60/2008 for B/Victoria NA sequences.

Summary of Influenza B Protein Homology When Compared with 2016-2017 Vaccine Strain

<table>
<thead>
<tr>
<th>Segment</th>
<th>No. Isolates</th>
<th>2016-2017 Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>B/Yamagata HA</td>
<td>9</td>
<td>B/Phuket/3073/2013</td>
<td>99.3-99.5%</td>
</tr>
<tr>
<td>B/Yamagata NA</td>
<td>12</td>
<td>B/Phuket/3073/2013</td>
<td>98.9-99.3%</td>
</tr>
<tr>
<td>B/Victoria HA</td>
<td>7</td>
<td>B/Brisbane/60/2008</td>
<td>98.4-99.5%</td>
</tr>
<tr>
<td>B/Victoria NA</td>
<td>15</td>
<td>B/Brisbane/60/2008</td>
<td>98.0-98.7%</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.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>INF B Segment</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
</tr>
</thead>
<tbody>
<tr>
<td>HA</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>NA</td>
<td>N/A</td>
<td>N/A</td>
</tr>
</tbody>
</table>

Evolutionary Relationships Among Influenza B Hemagglutinin (HA) Genes 2016-2017 Influenza Season

Yamagata Lineage

- B/SouthCarolina/NHRC_JX41701/2017*
- B/Illinois/NHRC_FDX51909/2017
- B/California/NHRC_BRD80728N/2017*
- B/California/NHRC_SAR10492N/2017*
- B/California/NHRC_BRD12374N/2017*
- B/SouthCarolina/NHRC_75620/2017
- B/California/NHRC_BRD12337N/2017*
- B/Illinois/NHRC_FDX51839/2017*
- B/Illinois/NHRC_18462/2016

Victoria Lineage

- B/Illinois/NHRC_FDX51841/2017*[S510F]
- B/Illinois/NHRC_FDX51878/2017*
- B/Illinois/NHRC_18512/2017*
- B/California/NHRC_BRD41561N/2017*
- B/Washington/63/2015 [V252M, I559V]
- B/Illinois/NHRC_18545/2017*

- 2015-16 V1A Consensus (27 strains)

- B/Wyoming/24/2015
- B/California/NHRC_MAP2003A/2017*[T121I]
- B/Illinois/NHRC_FDX51883/2017[A154V]

- B/Texas/02/2013
- B/Ohio/01/2005

- 1.8 Amino Acid Substitution per 100 residues

**B/Victoria deletion variant subgroup**

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

*: clinical specimen
Evolutionary Relationships Among Influenza B Neuraminidase (NA) Genes 2016-2017 Influenza Season

Vaccine Strain
Reference Strain

2015-16 Consensus (26 strains)
June 2016 (1 strain)
Oct 2016 (1 strain)
Jan 2017 (4 strains)
Feb 2017 (8 strains)
March 2017 (3 strains)
April-June 2017 (8 strains)

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

*: clinical specimen
: shipboard surveillance

Yamagata Lineage

B/California/NHRC/SAR10463N/2017* [1262V]
B/California/NHRC_BRD12420N/2017*
B/California/NHRC_BRD880728N/2017*
B/California/NHRC_SAR10492N/2017*
B/SouthCarolina/NHRC_75620/2017*
B/California/NHRC_BRD12337N/2017*
B/Illinois/NHRC_FD51839/2017*
B/SouthCarolina/NHRC_JX41701/2017*
B/California/NHRC_BRD12301N/2017*
B/Illinois/NHRC_18462/2016 [M403V, E404G]
A/Philippines/NHRC_MCY0103/2016*
B/Illinois/NHRC_FD51909/2017*

B/Wisconsin/05/2015 [49M]
B/Sydney/7/2014 [T46I, G70E]

2015-16 B/YAM Consensus (26 strains)

B/Phuket/3073/2013
B/Wisconsin/01/2010 [D340N]

1.6 Amino Acid Substitution per 100 residues 0

Victoria Lineage

B/California/NHRC_BRD41581N/2017*
B/Illinois/NHRC_FD51883/2017*
B/California/NHRC_BRD12417N/2017* [S397R]
B/Illinois/NHRC_FD51851/2017* [K107R, D392G]
B/Illinois/NHRC_18545/2017* [F12V]
F40I, M50I, D366N
B/Illinois/NHRC_FD51827/2017*
B/Illinois/NHRC_FD51823/2017*
B/California/NHRC_28039/2017*
B/NewJersey/NHRC_93612/2017*
B/NewJersey/NHRC_93621/2017*
B/Texas/NHRC_55449/2017*
V40I
B/Illinois/NHRC_FD51878/2017*
B/Illinois/NHRC_FD51841/2017* [N235S]
T68A, R84H
B/Illinois/NHRC_18512/2017*
B/Virginia/NHRC_BAT0112/2017* [A67T]

2015-16 B/VIC Consensus (27 strains)
B/Wyoming/24/2015
B/South Australia/81/2012 [S99N]
B/Brisbane/60/2008 [A358V]

1.0 Amino Acid Substitution per 100 residues 0