**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>
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<th>A/H1</th>
<th>B</th>
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<td>22</td>
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<td>76</td>
<td>6</td>
<td>30</td>
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</tbody>
</table>

*Cases presented 1/11 – 2/23. Only 6 of 56 cases had been vaccinated more than 14 days prior to illness.*

- 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, 2014-18**

![Graph showing vaccination status of confirmed influenza cases]

**Items of Note**

- Elevated FRI rate at MCRD Parris Island
- Large number of influenza and RSV cases among civilians in Imperial Co., CA (pg. 8)

**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 2012-18. 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 March 2018:
- At or below expected value:
  Fort Benning
  Fort Jackson
  Fort Leonard Wood
  Naval Recruit Training Command, Great Lakes (data through 16 September)
  Marine Corps Recruit Depot, San Diego
  Coast Guard Training Center, Cape May

- Moderately elevated:
  Marine Corps Recruit Depot, Parris Island

- Substantially elevated:
  Lackland Air Force Base (data through 13 January)
### Ft. Benning 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>
<th>Oct</th>
<th>Nov</th>
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<th>Oct</th>
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<th>Dec</th>
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</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>
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</tbody>
</table>

Samples Received:
- **Adenovirus**: 12
- **Influenza**: 9
- **RSV**: 4
- **C. pneumonia**: 4
- **M. pneumonia**: 11
- **Rhinovirus**: 7

### Ft. Jackson 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>
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<th>Jun</th>
<th>Jul</th>
<th>Aug</th>
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</thead>
<tbody>
<tr>
<td>Rate (cases/100 trainees/week)</td>
<td>2.0</td>
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</tbody>
</table>

Samples Received:
- **Adenovirus**: 21
- **Influenza**: 13
- **RSV**: 14
- **C. pneumonia**: 34
- **M. pneumonia**: 41
- **Rhinovirus**: 46

### Back to FRI Report
Back to FRI Report

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**Observed FRI rate** (expected rate = dashed line)  
- Moderately elevated  
- Substantially elevated  
- Pneumonia rate (incl. afebrile)
Fort Benning FRI Rate Status

Fort Jackson FRI Rate Status

Back to FRI Report

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)

<table>
<thead>
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<th>Month</th>
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### Cape May FRI Rates and Diagnostic Test Results
Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)

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</tbody>
</table>

### NHRC Respiratory Illness Update
Week Ending: 10 March 2018

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

- NHRC conducts FRI surveillance among DoD beneficiaries at 12 military facilities including Naval Medical Center San Diego (NMCSD), Naval Branch Health Clinic Kearny Mesa (NBHCKM), Naval Branch Health Clinic, Naval Training Center (NTC), Naval Hospital Camp Pendleton (NHCP), Branch Health Clinic Yuma (BHCY), James A. Lovell Federal Health Care Center (JALFHCC), United States Naval Hospital, Japan (PRSH), Naval Medical Center Portsmouth (NMCP), Boone Branch Health Clinic (BBHC), Oceana Branch Health Clinic (OBHC), Naval Hospital Lemoore (NHL), and Robert E. Bush Naval Hospital (RBNH).

- For questions regarding surveillance in this population, please contact the principal investigator (Chris Myers, christopher.a.myers48.civ@mail.mil) or the study coordinator (Michelle Ricketts, michelle.n.ricketts.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 (H3N2) HA and NA Protein Sequences

- Twenty seven analyzed H3N2 HA and NA sequences were derived from whole genome sequencing.
- All sequences were in subclade 3C.2a. Of those 3C.2a sequences, five were further classified as 3C.2a1, defined by the mutations N171K, I406V (HA2: I77V), and G484E (HA2: G155E).
- 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 A/Texas/50/2012 for NA sequences.

Summary of Influenza A (H3N2) Protein Homology When Compared with 2017-2018 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>27</td>
<td>A/HongKong/4801/2014</td>
<td>97.5-98.9%</td>
</tr>
<tr>
<td>H3N2 NA</td>
<td>27</td>
<td>A/HongKong/4801/2014</td>
<td>97.0-98.5%</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/](http://www.cbs.dtu.dk/services/NetNGlyc/)

<table>
<thead>
<tr>
<th>Mutation</th>
<th>ADD GLY</th>
<th>LOSS GLY</th>
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</thead>
<tbody>
<tr>
<td>HA</td>
<td>K135T, K160T</td>
<td>T10A, S1241, T128I, T135K</td>
</tr>
<tr>
<td>NA</td>
<td>S245N</td>
<td>D329S</td>
</tr>
</tbody>
</table>

Evolutionary Relationships Among Influenza A (H3N2) Hemagglutinin (HA) Genes 2017-2018 Influenza Season

Vaccine Strain

WHO Recommended 2018-19 Vaccine Strain

Reference Strain
2016-2017 Consensus (75 strains total)
Sept 2017 (2 strains)
Oct 2017 (6 strains)
Nov 2017 (16 strains)
Dec 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
SEA: US Special Forces

A/California/NHRC_BRD80830N/2017 [S124I LOSS GLY]
A/California/NHRC_28317/2017
A/California/NHRC_28324/2017
A/California/NHRC_28273/2017
A/California/NHRC_28278/2017
A/California/NHRC_28288/2017
A/California/NHRC_28303/2017
A/California/NHRC_BRD80816N/2017
A/California/NHRC_28270/2017
A/SouthCarolina/NHRC_75690/2017
2016-2017 Group 3C2a (18 strains)
A/Singapore/KK0164/2017

A/California/NHRC_BRD41684N/2017 [S279Y]
A/California/NHRC_BRD80860N/2017
A/California/NHRC_BRD21611N/2017
A/California/NHRC_BRD21615N/2017
A/California/NHRC_BRD41625N/2017
A/California/NHRC_BRD41640N/2017 [T10A LOSS GLY]
A/California/NHRC_BRD41657N/2017
A/California/NHRC_BRD80844N/2017
A/California/NHRC_BRD80852N/2017
A/California/NHRC_SAR20930N/2017
A/California/NHRC_SAR41846N/2017
A/California/NHRC_BRD80835N/2017 [T128I LOSS GLY]

A/California/NHRC_BRD12446N/2017 [F193S]
A/California/NHRC_BRD80823N/2017
A/Singapore/INFMH-16-0019/2016
A/Malaysia/1358/2016
2016-2017 Group 3C2a1 (56 strains)
A/California/NHRC_BRD41618N/2017
A/Singapore/TT0189/2017
A/HongKong/4801/2014 [N96S, L194P]
A/Switzerland/9715293/2013
2016-2017 Group 3C3a (1 strain)
A/Perth/16/2009
A/Victoria/361/2011

Amino Acid Substitution per 100 residues

3C.2a1

3C.2a

3C.2a1

3C.3a

3C.3a

3C.1

4.6

4

2

0
Evolutionary Relationships Among Influenza A (H3N2) Neuraminidase (NA) Genes 2017-2018 Influenza Season

Vaccine Strain

WHO Recommended 2018-19 Vaccine Strain

Reference Strain

2016-2017 Consensus (9 whole genome strains)
Sept 2017 (2 strains)
Oct 2017 (6 strains)
Nov 2017 (16 strains)
Dec 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
SEA: US Special Forces

A/California/NHRC_BRD80860N/2017
A/California/NHRC_BRD41684N/2017
A/California/NHRC_BRD21611N/2017
A/California/NHRC_BRD21615N/2017
A/California/NHRC_BRD41640N/2017
A/California/NHRC_BRD41657N/2017
A/California/NHRC_BRD41684N/2017
A/California/NHRC_BRD80835N/2017
A/California/NHRC_BRD80844N/2017
A/California/NHRC_BRD80852N/2017 [M241V]
A/California/NHRC_SAR20930N/2017
A/California/NHRC_SAR41846N/2017 [N385K]
A/California/NHRC_BRD80816N/2017 [S44P]
A/SouthCarolina/NHRC_75690/2017
A/California/NHRC_BRD41618N/2017
A/California/NHRC_28317/2017
A/California/NHRC_28324/2017
A/California/NHRC_28273/2017
A/California/NHRC_28278/2017
A/California/NHRC_28288/2017
A/California/NHRC_28303/2017
A/California/NHRC_28270/2017
A/California/NHRC_BRD80830N/2017 [P386S]
A/Arizona/NHRC_MAP6073A/2017
A/California/NHRC_SAR20944N/2017 [I302V]
A/Victoria/646/2017

2016-2017 H3NA Consensus (9 whole genome strains)

A/Singapore/INFIMH-16-0019/2016 [V212I]
A/Alaska/232/2015
A/California/NHRC_BRD80823N/2017 [F377L]
A/California/NHRC_BRD12446N/2017
A/Switzerland/9715293/2013
A/HongKong/4801/2014 [V231I]
A/Texas/50/2012 [R150H, D221E]
Phylogenetic Comparison of Influenza B (Yamagata and Victoria) HA and NA Protein Sequences

- **One** HA sequence belonged to the Y3 clade of the Yamagata lineage and **six** HA sequences belonged to the V1A clade of the Victoria lineage.
- **One** NA sequence belonged to the Yamagata lineage and **six** NA sequences belonged to the Victoria lineage. **Three** NA Victoria sequences and **one** NA Yamagata sequence were derived from whole genome sequencing.
- Of note, **five of the six** Victoria sequences contained the double amino acid deletion at positions 162 and 163.
- 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>2017-2018 Vaccine Strain</th>
<th>Protein Homology</th>
</tr>
</thead>
<tbody>
<tr>
<td>B/Yamagata HA</td>
<td>1</td>
<td>B/Phuket/3073/2013</td>
<td>99.5%</td>
</tr>
<tr>
<td>B/Yamagata NA</td>
<td>1</td>
<td>B/Phuket/3073/2013</td>
<td>98.3%</td>
</tr>
<tr>
<td>B/Victoria HA</td>
<td>6</td>
<td>B/Brisbane/60/2008</td>
<td>98.4-98.6%</td>
</tr>
<tr>
<td>B/Victoria NA</td>
<td>6</td>
<td>B/Brisbane/60/2008</td>
<td>98.1%</td>
</tr>
</tbody>
</table>
Evolutionary Relationships
Among Influenza B
Hemagglutinin (HA) Genes
2017-2018 Influenza Season

Yamagata Lineage

Victoria Lineage

Amino Acid Substitution per 100 residues

Reference Strain
2016-2017 Consensus
(16 whole genome strains)
Oct 2017 (1 strain)
Nov 2017 (4 strains)
Dec 2017 (1 strain)

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
FOX: DoD beneficiaries
JX or no prefix: US Recruit
SEA: US Special Forces
Evolutionary Relationships
Among Influenza B
Neuraminidase (NA) Genes
2017-2018 Influenza Season

Vaccine Strain
Reference Strain

2016-2017 Consensus
(28 whole genome strains)
Oct 2017 (1 strain)
Nov 2017 (4 strains)
Dec 2017 (1 strain)

Yamagata Lineage
2016-2017 B/Yamagata consensus (13 strains)

B/California/NHRC_SAR20941N/2017
B/Sydney/7/2014 [T461, G70E]
B/Wisconsin/05/2015 [I49M]
B/Phuket/3073/2013
B/Wisconsin/01/2010 [D340N]

1.9 Amino Acid Substitution per 100 residues 0

Victoria Lineage
2016-2017 B/Victoria consensus (15 strains)

B/California/NHRC_BRD12451N/2017
B/California/NHRC_BRD12452N/2017
B/California/NHRC_BRD12453N/2017
B/California/NHRC_BRD12454N/2017
B/California/NHRC_BRD12436N/2017
B/Wyoming/24/2015
B/South Australia/81/2012 [S99N]
B/Brisbane/60/2008

1.0 0

Amino Acid Substitution per 100 residues