



**Cumulative Results**

Locations	75
Collected	1,720
Tested	1,575

<b>Influenza A</b>	<b>339</b>
A(H1N1)pdm09	2
A(H3N2)	336
A(H3N2) & RSV	1
A/not subtyped	0
<b>Influenza B*</b>	<b>16</b>
B	16

<b>Other Respiratory Pathogens</b>	<b>535</b>
Adenovirus	32
<i>Bordetella pertussis</i>	0
<i>Chlamydomphila pneumoniae</i>	2
Coronavirus	50
Human Metapneumovirus	20
<i>Mycoplasma pneumoniae</i>	27
Parainfluenza	101
RSV	79
Rhino/Enterovirus	156
Non-influenza Viral Coinfections	60
Non-influenza Bacterial Coinfections	8
- <i>M. pneumo</i> coinfections (8)	

Lab data are current as of 23 January 2017.  
Some results are preliminary and may change  
as finalized results are received.  
\*Influenza B lineages will be reported in the  
periodic molecular sequencing reports.

**Respiratory Highlights**

**8 - 21 January 2017 (Surveillance Weeks 2 & 3)**

- During 8 - 21 January 2017, a total of 336 specimens were collected from 56 locations. Results were finalized for 226 specimens from 49 locations. During Week 2, 67 influenza A(H3N2) and three influenza B viruses were identified. During Week 3, 52 influenza A(H3N2) and four influenza B viruses were identified. Approximately 34% of specimens tested positive for influenza during Week 2. Approximately 46% of specimens tested positive for influenza during Week 3. The influenza percent positive for the season is approximately 23%.
- According to the CDC, there has been an increase of 3.3% of individuals seeing their health care provider for influenza-like illness (ILI) nationwide. New York, Missouri, New Jersey, Oklahoma, South Carolina, and Tennessee have been experiencing high ILI activity. Other states like Alabama, Georgia, Louisiana, Alaska, Pennsylvania, Utah, Virginia, Wyoming, and Puerto Rico have been experiencing moderate ILI illness (CDC, [FluView Report Week 2](#), cited 25 January 2017).

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# DoD Global, Laboratory-Based, Influenza Surveillance Program

**Table 1.** Results by region and location for specimens collected during Weeks 2 & 3

Region*		A (H3N2)	B	Adenovirus	Coronavirus	hMNV	<i>M. pneumoniae</i>	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & Corona & Rhino/Entero	Adeno & Corona & RSV	Adeno & RSV	Adeno & RSV & Rhino/Entero	Corona & RSV	hMNV & <i>M. pneumo</i>	Para & RSV	RSV & Rhino/Entero	No Pathogen	Total
Deployed	Country 2, Location A	-	-	-	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2	6
EUCOM	Incirlik AB, Turkey	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
PACOM	JB Elmendorf-Richardson, AK	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1
	Osan AB, South Korea	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Yokota AB, Japan	2	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	4
Region 1	USCG Academy, CT	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
Region 2	Ft Drum, NY	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	2
	JB McGuire-Dix-Lakehurst, NJ	12	-	-	-	-	-	1	3	-	-	-	-	-	-	-	-	-	-	4	20
	USMA - West Point, NY	9	-	1	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	3	15
Region 3	Dover AFB, DE	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	JB Andrews, MD	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	2	5
	JB Langley-Eustis, VA	2	-	-	1	1	1	-	1	-	-	-	-	-	-	-	-	-	-	2	8
Region 4	Columbus AFB, MS	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Eglin AFB, FL	2	-	1	-	-	-	-	3	1	-	1	-	-	-	-	-	1	-	1	10
	Ft Bragg, NC	-	3	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	4
	Ft Campbell, KY	7	1	-	-	-	-	-	1	-	-	-	1	1	-	-	-	-	-	1	12
	Hurlburt Field, FL	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	JB Charleston (AF), SC	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	Maxwell AFB, AL	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Moody AFB, GA	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	NH Camp Lejeune, NC	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Robins AFB, GA	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Shaw AFB, SC	4	1	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	8

(Cont'd on page 3)

\*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.

# DoD Global, Laboratory-Based, Influenza Surveillance Program

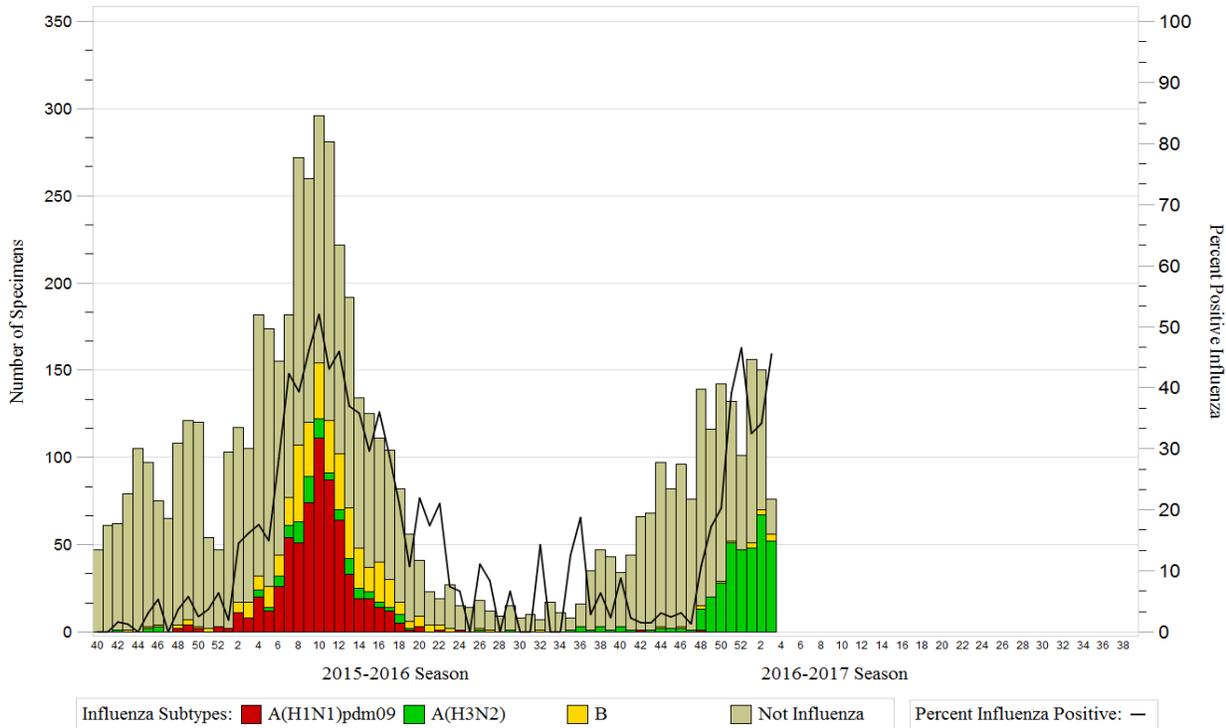
**Table 1.** Results by region and location for specimens collected during Weeks 2 & 3  
(Cont'd from page 2)

Region*		A(H3N2)	B	Adenovirus	Coronavirus	hMPV	<i>M. pneumoniae</i>	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & Corona & Rhino/Entero	Adeno & Corona & RSV	Adeno & RSV	Adeno & RSV & Rhino/Entero	Corona & RSV	hMPV & <i>M. pneumoniae</i>	Para & RSV	RSV & Rhino/Entero	No Pathogen	Total
Region 5	Wright-Patterson AFB, OH	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 6	Altus AFB, OK	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Cannon AFB, NM	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Sheppard AFB, TX	8	-	-	1	-	-	-	-	2	-	-	-	-	-	-	-	-	-	6	17
	Tinker AFB, OK	7	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	1	10
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
Region 7	McConnell AFB, KS	2	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	3
	Offutt AFB, NE	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	5
Region 8	Ellsworth AFB, SD	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	FE Warren AFB, WY	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Hill AFB, UT	2	-	-	1	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	5
	Malmstrom AFB, MT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Minot AFB, ND	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Peterson AFB, CO	1	-	-	-	-	-	-	3	-	-	-	-	-	1	-	-	-	-	-	5
Region 9	Beale AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Davis-Monthan AFB, AZ	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Nellis AFB, NV	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1
	Travis AFB, CA	12	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	13
Region 10	CGS North Bend, OR	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Fairchild AFB, WA	4	-	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	1	7
	JB Lewis-McChord, WA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	1	-	-	1	-	-	1	4	-	-	-	-	-	-	-	-	-	-	1	8
	NH Bremerton, WA	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6
<b>Total</b>	<b>119</b>	<b>7</b>	<b>2</b>	<b>14</b>	<b>3</b>	<b>2</b>	<b>7</b>	<b>20</b>	<b>4</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>39</b>	<b>226</b>

\*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.

## Laboratory Results - Cumulative for Season

**Graph 1.** Percent influenza positive by week: 2015-2016 surveillance year and through Week 3 of the 2016-2017 surveillance year



Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

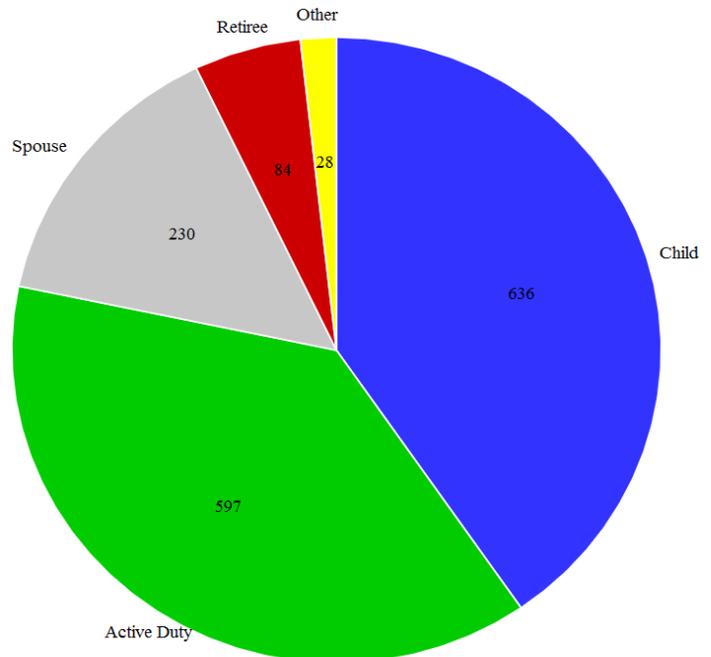
**Table 2.** ILI by age group for the 2016-2017 surveillance year through Week 3

Age Group	Frequency	Percent
0-5	371	23.56
6-9	106	6.73
10-17	159	10.10
18-24	243	15.43
25-44	515	32.70
45-64	132	8.38
65+	49	3.11

### Demographic Summary

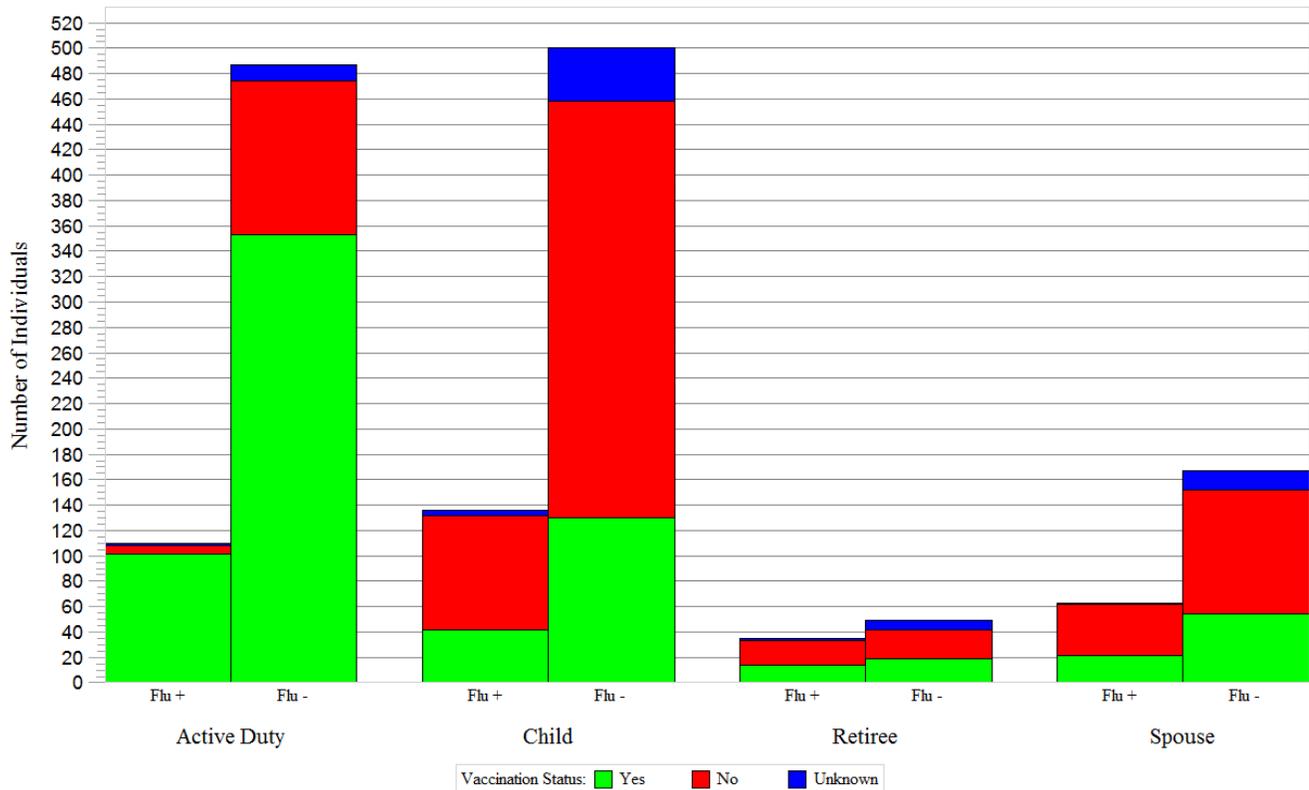
Of 1,575 ILI cases, 597 (37.9%) are service members, 636 (40.4%) are children, 230 (14.6%) are spouses, and 112 (7.1%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=1,575) is 22 (range 0, 91).

**Graph 2.** ILI by beneficiary status for the 2016-2017 surveillance year through Week 3

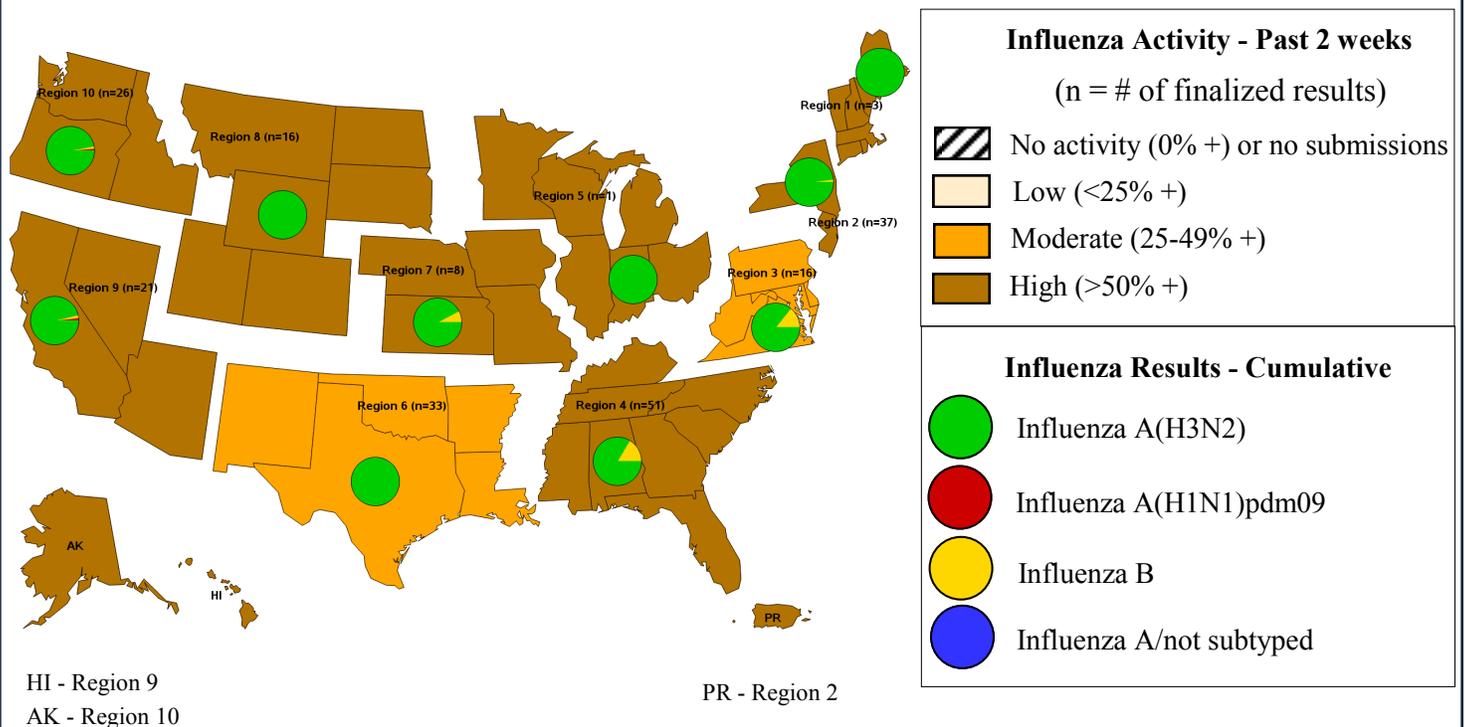


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**Graph 3.** Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 3

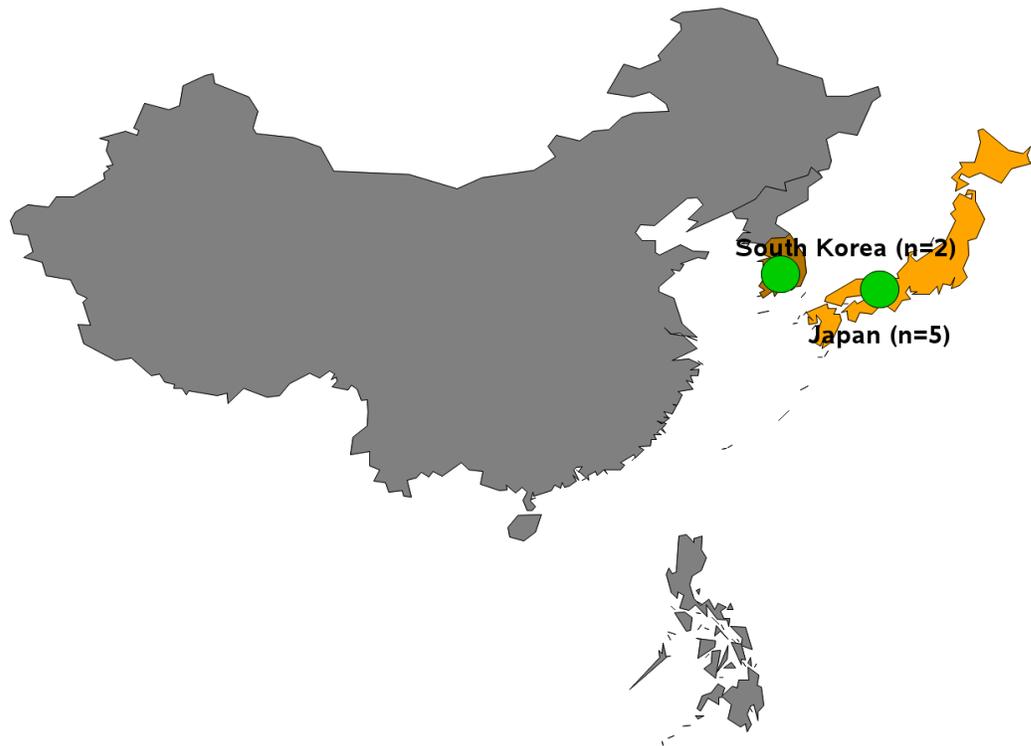


**Map 1.** Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 3



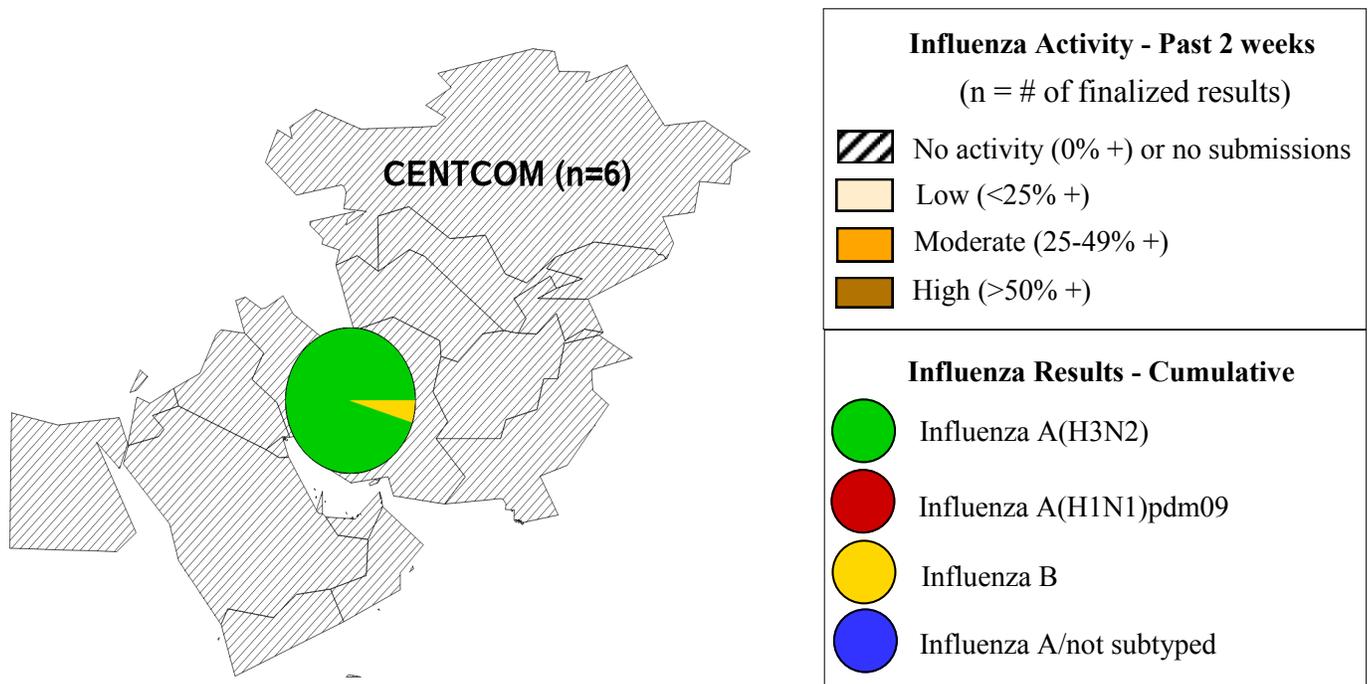
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**Map 2.** Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 3 (Pacific)



Note - Countries shaded in gray do not contain sentinel sites and are only displayed for geographical perspective.

**Map 3.** Influenza subtypes and activity level for CENTCOM for the 2016-2017 surveillance year through Week 3



Note - Specimens for CENTCOM were tested at USAFSAM or Landstuhl Regional Medical Center (LRMC).

# DoD Global, Laboratory-Based, Influenza Surveillance Program

## Laboratory Results—Through Current Surveillance Week 3

**Table 3.** Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

Region*		A(H1N1)pdm09	A(H3N2)	A(H3N2) & RSV	B	Adenovirus	C. pneumoniae	Coronavirus	hMPV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	Non-Influenza Bacterial Coinfection	No Pathogen	Total
Deployed	Country 1, Location A	-	3	-	-	-	-	1	-	-	-	1	-	-	-	7	12
	Country 1, Location B	-	1	-	1	-	-	1	-	-	-	1	-	-	-	1	5
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	16	-	-	-	-	5	-	-	-	-	2	2	-	8	33
EUCOM	Incirlik AB, Turkey	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
PACOM	Eielson AFB, AK	-	-	-	-	-	-	-	-	1	-	-	-	-	-	4	5
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	1	-	-	1	3
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Kadena AB, Japan	-	3	-	-	-	-	-	-	-	2	-	2	-	1	16	24
	Kunsan AB, South Korea	-	2	-	-	-	-	1	-	-	-	-	1	-	-	-	4
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Osan AB, South Korea	-	3	-	-	-	-	-	-	-	-	-	-	-	-	5	8
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	8	-	-	-	-	2	-	2	-	2	7	3	-	38	62
	Region 1	Hanscom AFB, MA	-	-	-	-	-	-	-	1	1	-	-	1	-	1	4
USCG Academy, CT		-	3	-	-	-	-	-	-	1	-	-	3	-	2	2	11
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	-	-	-	1	4	-	1	6	1	5	3	1	2	-	10	34
	JB McGuire-Dix-Lakehurst, NJ	-	21	-	-	2	-	5	1	2	7	4	7	3	-	31	83
	USMA - West Point, NY	-	26	-	-	8	-	2	2	1	4	8	4	4	-	59	118
Region 3	Dover AFB, DE	-	3	-	-	1	-	1	-	1	-	1	1	-	-	9	17
	JB Anacostia-Bolling, DC	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
	JB Andrews, MD	-	4	-	-	-	-	-	-	-	-	2	1	2	-	7	16
	JB Langley-Eustis, VA	-	5	-	2	-	-	1	2	2	4	13	22	8	-	47	106
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
Region 4	Columbus AFB, MS	-	2	-	-	-	-	-	-	-	-	-	1	-	-	6	9
	Eglin AFB, FL	-	5	-	1	2	-	1	-	-	-	4	8	3	-	16	40
	Ft Bragg, NC	-	3	-	3	-	-	1	-	1	3	1	6	3	3	11	35
	Ft Campbell, KY	-	7	-	1	-	-	-	1	-	-	3	-	4	-	3	19
	Hurlburt Field, FL	-	5	-	-	-	-	-	-	-	1	-	-	-	-	3	9
	JB Charleston (AF), SC	-	3	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	1	2	-	1	-	6	10
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	4
	Maxwell AFB, AL	-	2	-	-	-	-	-	-	-	1	-	1	-	-	6	10
	Moody AFB, GA	-	6	-	2	1	-	1	-	1	5	2	7	1	13	39	
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NH Camp Lejeune, NC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	5	-	-	-	-	-	-	1	-	1	-	-	-	4	11
	Seymour Johnson AFB, NC	-	-	-	-	1	-	-	-	1	1	-	1	-	-	3	7
	Shaw AFB, SC	-	7	-	2	1	-	5	1	1	3	-	3	-	-	21	44

(Cont'd on page 8)

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# DoD Global, Laboratory-Based, Influenza Surveillance Program

## Laboratory Results—Through Current Surveillance Week 3

**Table 3.** Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year  
(Cont'd from page 7)

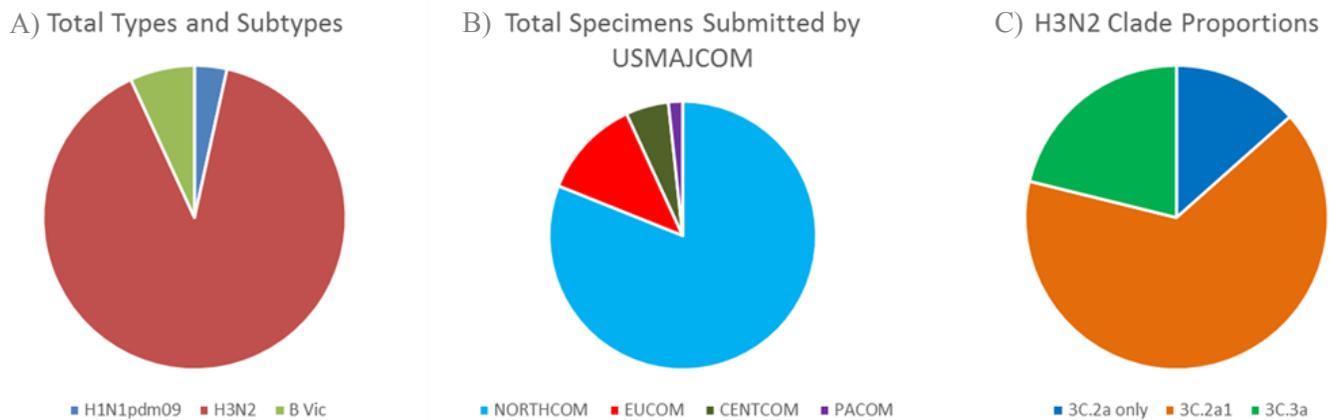
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Region 5	Scott AFB, IL	-	-	-	-	-	-	-	-	1	2	1	1	-	1	6	12
	Wright-Patterson AFB, OH	-	1	-	-	-	-	-	-	1	1	-	1	1	-	8	13
Region 6	Altus AFB, OK	-	-	-	-	1	-	-	1	-	-	-	4	-	-	15	21
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	1	-	1	-	-	3	5
	Cannon AFB, NM	-	2	-	-	-	-	1	-	1	1	-	3	-	-	8	16
	Ft Polk, LA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Laughlin AFB, TX	-	-	-	-	-	-	-	2	-	-	-	-	-	-	1	3
	Sheppard AFB, TX	-	14	-	-	-	-	3	1	-	4	-	5	-	-	19	46
	Tinker AFB, OK	-	15	1	-	-	-	1	-	1	4	3	6	-	-	27	58
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	8
Region 7	McConnell AFB, KS	-	7	-	-	-	-	1	-	1	2	-	4	-	-	13	28
	Offutt AFB, NE	-	5	-	1	1	-	2	-	-	-	-	4	1	-	11	25
Region 8	Ellsworth AFB, SD	-	3	-	-	-	-	2	-	-	3	-	3	-	-	7	18
	FE Warren AFB, WY	-	1	-	-	2	-	-	-	1	1	1	2	-	-	10	18
	Hill AFB, UT	-	15	-	-	-	-	2	-	-	4	2	4	-	-	22	49
	Malmstrom AFB, MT	-	3	-	-	-	-	-	-	1	-	-	1	-	-	3	8
	Minot AFB, ND	-	-	-	-	-	-	1	-	1	-	-	2	-	-	4	8
	Petersen AFB, CO	-	5	-	-	-	-	1	-	-	1	3	3	4	-	8	25
	USAF Academy, CO	-	1	-	-	-	-	-	1	-	-	1	1	-	-	1	5
Region 9	Beale AFB, CA	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	Davis-Monthan AFB, AZ	-	5	-	-	-	-	-	-	-	5	-	3	-	-	12	25
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	2	-	-	-	1	-	1	-	4	8
	Nellis AFB, NV	1	2	-	1	2	-	1	-	-	4	3	4	6	-	12	36
	Travis AFB, CA	-	44	-	-	-	1	1	2	-	5	1	8	-	-	27	89
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Fairchild AFB, WA	1	11	-	1	1	-	3	-	-	4	2	4	-	-	29	56
	JB Lewis-McChord, WA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Mt Home AFB, ID	-	15	-	-	1	1	1	-	1	20	5	12	2	-	49	107
	NH Bremerton, WA	-	33	-	-	4	-	-	-	-	5	4	4	2	-	13	65
<b>Total</b>		<b>2</b>	<b>336</b>	<b>1</b>	<b>16</b>	<b>32</b>	<b>2</b>	<b>50</b>	<b>20</b>	<b>27</b>	<b>101</b>	<b>79</b>	<b>156</b>	<b>60</b>	<b>8</b>	<b>685</b>	<b>1575</b>

\*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.

**Molecular Sequence Analysis Report #2**

**USAFSAM Epidemiology Laboratory Service**

This is the second USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 58 specimens collected between 18 November 2016 and 21 December 2016 and subsequently analyzed at USAFSAM. Among the specimens analyzed, two (3.4%) were influenza A(H1N1)pdm09, 52 (89.7%) were influenza A(H3N2), and four (6.9%) were influenza B/Victoria lineage. No influenza B/Yamagata lineage viruses were identified for this report. Figure 1 shows the proportion of hemagglutinin (HA) sequences analyzed for this report by type/subtype, USMAJCOM, and influenza A(H3N2)-specific clade designations. Sequences for each type and subtype included in this report are shown for each sentinel site in Table 1. Figures 2-4 display the phylogenetic relationships among HA sequences for influenza A(H1N1)pdm09, A(H3N2), and influenza B, respectively.



**Figure 1:** A) Proportion of influenza hemagglutinin sequence subtypes and lineages submitted to USAFSAM for this report, B) number of influenza positive specimens submitted by sentinel sites separated by USMAJCOM, C) proportion of specimens in each influenza A(H3N2) clade represented in this report.

**Table 1:** Influenza subtypes and lineages from corresponding sentinel sites included in the analyses for this report.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	Grand Total
<b>CONUS</b>				
<b>Arizona</b>				
Davis Monthan AFB		1		1
<b>California</b>				
Beale AFB		1		1
Travis AFB		5		5
<b>Colorado</b>				
USAF Academy		1		1
<b>Florida</b>				
Eglin AFB		1		1
Hurlburt Field		1		1
<b>Georgia</b>				
Moody AFB			1	1
<b>Idaho</b>				
Mountain Home AFB		7		7
<b>Kansas</b>				
McConnell AFB		3		3
<b>Mississippi</b>				
Keesler AFB	1			1
<b>Nevada</b>				
Nellis AFB		1		1
<b>New Jersey</b>				
JB McGuire-Dix-Lakehurst		1		1
<b>New Mexico</b>				
Cannon AFB		1		1
<b>New York</b>				
USMA - West Point		8		8
<b>Ohio</b>				
Wright-Patterson AFB		1		1

*(Cont'd on page 11)*

**Table 1:** Influenza subtypes and lineages from corresponding sentinel sites included in the analyses for this report.  
*(Cont'd from page 10)*

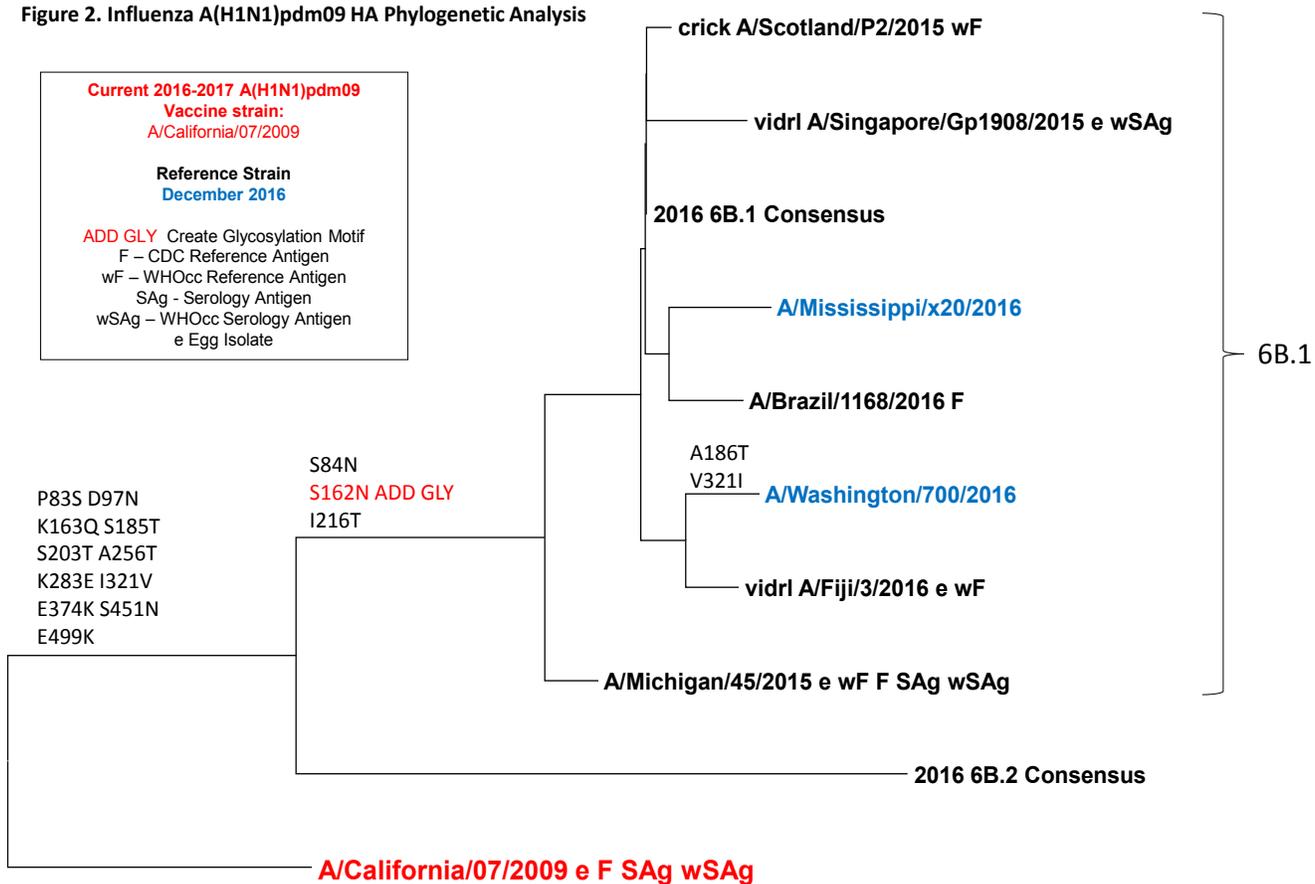
	A(H1N1)pdm09	A(H3N2)	B/Victoria	Grand Total
<b>CONUS</b>				
Oklahoma				
Tinker AFB		3		3
South Carolina				
Shaw AFB			1	1
Texas				
SAMMC		2	2	4
Sheppard AFB		1		1
Utah				
Hill AFB		2		2
Virginia				
Langley AFB		1		1
Washington				
Fairchild AFB	1			1
<b>OCONUS</b>				
Country 2				
Location A		3		3
Germany				
Landstuhl RMC		3		3
Ramstein AB		1		1
USAG Grafenwoehr		1		1
USAG Stuttgart		2		2
Japan				
Kadena AB		1		1
<b>Grand Total</b>	<b>2</b>	<b>52</b>	<b>4</b>	<b>58</b>

The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously published experimental evidence.<sup>1,3,4</sup> Sequence data was constructed and analyzed using multiple software programs. Genetic and predicted antigenic information that resulted from this analysis is shared with the United States Centers for Disease Control and Prevention (CDC), World Health Organization (WHO) and contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

### Influenza A(H1N1)pdm09

- Among the 54 influenza A isolates, two (3.7%) were influenza A(H1N1)pdm09. The influenza A(H1N1)pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009-like virus (Figure 2).
- The A(H1N1)pdm09 isolates characterized for this report both exhibited an overall protein homology of 97.1% compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus.
- Both of the A(H1N1)pdm09 HA sequences for this report contain mutations consistent with the predominating subgroup, referred to as group 6B, and all classified as clade 6B.1 (distinguished by the mutations S162N and I216T).
- Gain or loss of *N*-linked glycosylation sites has been shown to alter HA protein surface topology. A gain in glycosylation could be advantageous to the virus by virtue of a masking effect on important antibody recognition sites, thus potentially modulating viral antigenicity.<sup>4</sup> Observations are based solely on sequence motifs. For the influenza A(H1N1)pdm09 isolates characterized in this report, one mutation, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif.
- Of the 15 mutations present in the A(H1N1)pdm09 isolates, six occurred at predicted antigenic sites (zero at site A, two at site B, zero at site C, two at site D, and two at site E) and two occurred at the receptor binding site.<sup>2,5</sup>

**Figure 2. Influenza A(H1N1)pdm09 HA Phylogenetic Analysis**



**Influenza A(H3N2)**

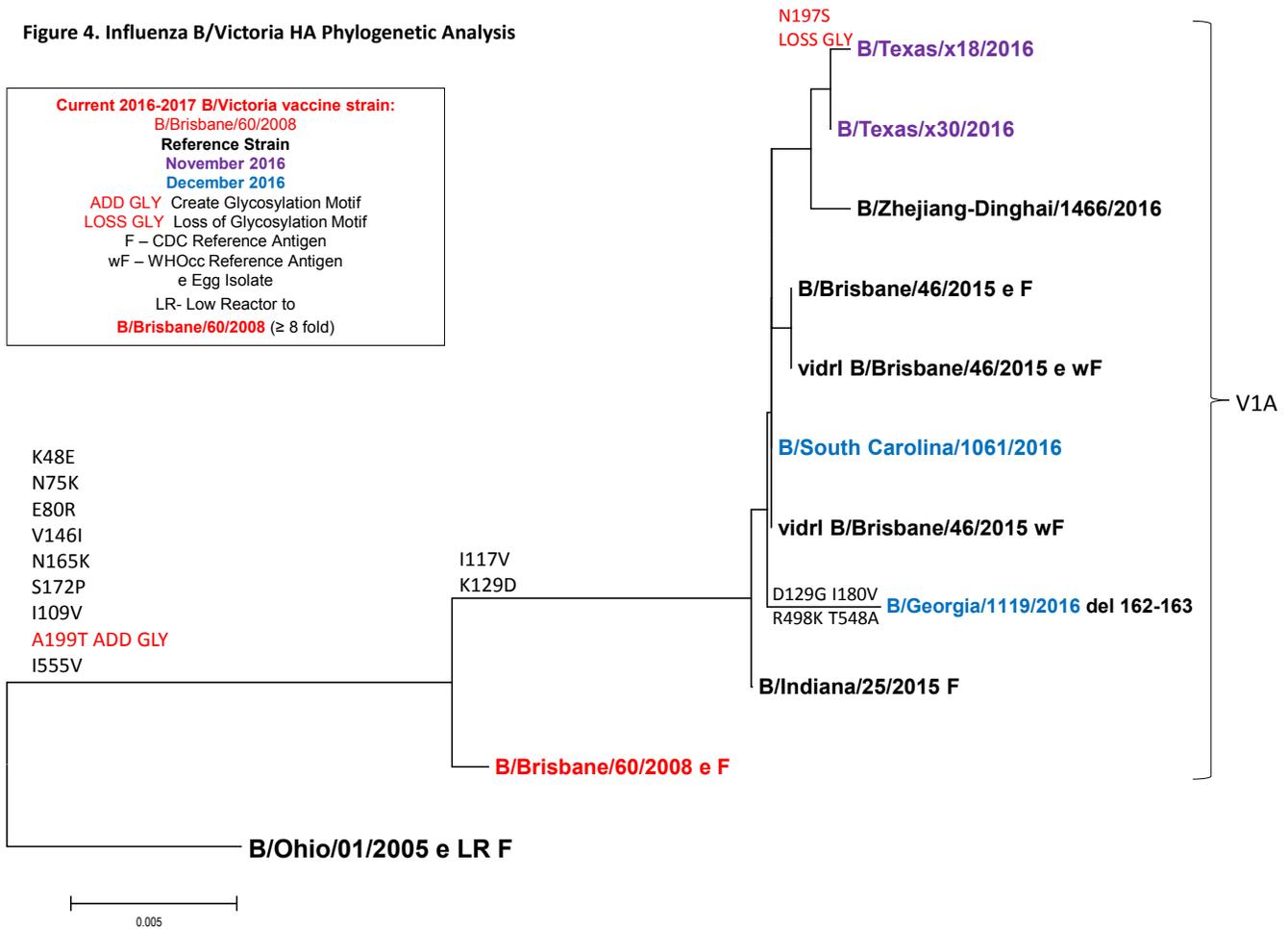
- Among the 54 influenza A isolates, 52 (96.3%) were influenza A(H3N2). The influenza A(H3N2) HA sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from a previous vaccine strain, A/Texas/50/2012 (Figure 3).
- The A(H3N2) isolates characterized for this report exhibited an overall protein homology of 97.1-98.9% (average 98.3%) compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014-like virus.
- All of the influenza A(H3N2) isolates sequenced for this report were in clade 3C. Forty-one (78.8%) of the influenza A(H3N2) sequences classified as subclade 3C.2a and 11 (21.2%) classified as subclade 3C.3a. Thirty-four of the 41 3C.2a isolates (82.9%) further classified as the newly distinguished subclade within 3C.2a, 3C.2a1 (determined by the mutations N171K, I406V, and G484E). Another mutation of interest, N121K, was present in 25 (73.5%) of the 3C.2a1 isolates (48.1% of the total H3N2) but not in any of the other clades, although this mutation has previously been shown to appear sporadically among the influenza A(H3N2) viruses.
- Among the influenza A(H3N2) isolates characterized in this report, five mutations; T135K (threonine to lysine), N144S (asparagine to serine), N144K (asparagine to lysine), T160I (threonine to isoleucine), and T160K (threonine to lysine) were observed that could cause the loss of a glycosylation motif. Two other mutations, N128T (asparagine to threonine) and K160T (lysine to threonine), were observed that could cause the gain of a glycosylation motif.
- Of the 38 mutations present in the A(H3N2) specimens, 15 occurred at predicted antigenic sites (five at site A, three at site B, two at site C, one at site D, and four at site E) and two occurred at the receptor binding site.<sup>2,5</sup>



## **Influenza B**

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains and are midpoint rooted for both the B/Victoria isolates (Figure 4).
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.<sup>1</sup> All four of the influenza B isolates characterized in this report fell into the Victoria lineage.
- The influenza B/Victoria isolates characterized for this report exhibited a protein homology of 98.6-99.5% (average 99.3%) when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-like virus.
- All of the influenza B/Victoria isolates fall into clade V1A.
- One mutation, N197S (asparagine to serine) was observed that causes the loss of a glycosylation motif while another mutation, A199T (alanine to threonine), was observed that adds a glycosylation motif.
- Interestingly, the HA sequence for the isolate B/Georgia/1119/2016 contained a six base pair deletion at nucleotide positions 484-489 (amino acid positions 162-163) of the cleaved functional sequence. This deletion corresponds to the three nucleotide deletion observed in influenza B/Yamagata lineage HA sequences, however the remainder of the B/Georgia/1119/2016 HA sequence aligned with other influenza B/Victoria isolates and references. When this sequence was aligned in a BLAST search query, one other influenza B/Victoria HA sequence that was submitted by the Centers for Disease Control and Prevention (CDC), B/New York/52/2016 (GenBank accession CY209594.1), showed the same six nucleotide deletion.

**Figure 4. Influenza B/Victoria HA Phylogenetic Analysis**



**References:**

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2. Kongchanagul, A., Suptawiwat, O., Kanrai, P., Uprasertkul, M., Puthavathana, P., and Auewarakul P. (2008). Positive selection at the receptor-binding site of hemagglutinin H5 in viral sequences derived from human tissues. *Journal of Gen. Vir.* **89**, 1805-1810.
3. Cherry, J.L., Lipman, D.J., Nikolskaya, A., and Wolf, Y.I. (2009). Evolutionary Dynamics of N-Glycosylation Sites of Influenza Virus Hemagglutinin. *PLoS Curr Influenza*. August 18: RRN1001.
4. Deem, M., and Pan, K. (2009). The epitope regions of H1-subtype influenza A, with application to vaccine efficacy. *Protein Engineering, Design and Selection*. **22**, no. 9. 543-546.
5. Wolf, Y.I., Viboud, C., Holmes, E.C., Koonin, E.V., and Lipman, D.J. (2006). Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol Direct.*; 1: 34. doi: 10.1186/1745-6150-1-34.

## Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the Defense Health Agency/Armed Forces Health Surveillance Branch—Air Force Satellite Cell (DHA/AFHSB-AF) and U.S. Air Force School of Aerospace Medicine (USAFSAM) (sentinel site respiratory surveillance), the Naval Health Research Center (recruit and shipboard population-based respiratory surveillance), the Naval Medical Research Unit (NAMRU-3) in Cairo, Egypt, the Naval Medical Research Unit (NAMRU-2) in Phnom Penh, Cambodia, the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Bangkok, Thailand, the Naval Medical Research Unit (NAMRU-6) in Lima, Peru, and the United States Army Medical Research Unit-Kenya (USAMRU-K) located in Nairobi, Kenya. This work is supported by the Air Force and GEIS Operations, a Division of the Armed Forces Health Surveillance Branch (AFHSB).

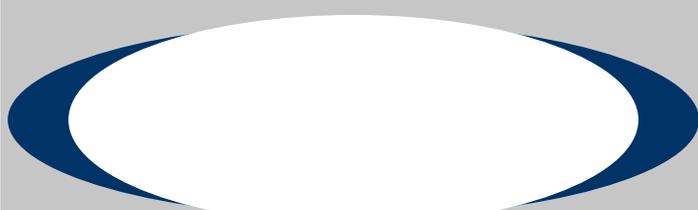
## Sentinel Site Surveillance

In 1976, the U.S. Air Force Medical Service began conducting routine, global, laboratory-based influenza surveillance. Air Force efforts expanded to DoD-wide in 1997. DHA/AFHSB-AF and USAFSAM manages the surveillance program that includes global surveillance among DoD beneficiaries at over 95 sentinel sites (including deployed locations) and many non-sentinel sites (please see map below). Collaborating partner laboratories include five DoD overseas medical research laboratories (AFRIMS, NAMRU-2, NAMRU-3, NAMRU-6, USAMRU-K) who collect specimens from local residents in surrounding countries that may not otherwise be covered in existing surveillance efforts. Additionally, the Naval Health Research Center (NHRC) in San Diego, CA collects specimens from DoD recruit training centers and conducts surveillance along the Mexico border.

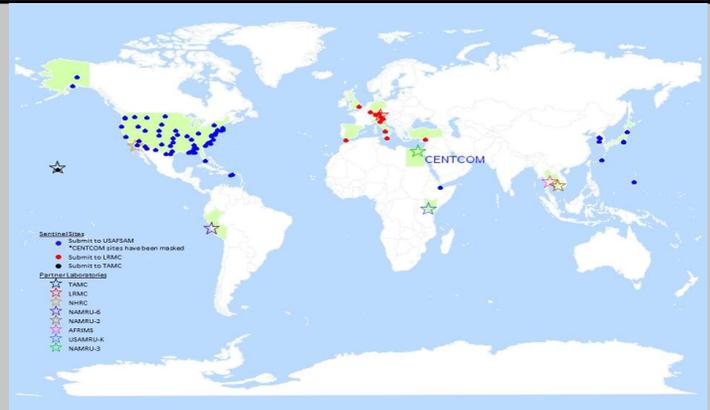
Landstuhl Regional Medical Center (LRMC) and Tripler Army Medical Center (TAMC) assist the program by processing DoD specimens for the EUCOM region and the State of Hawaii, respectively. This process seeks to provide more timely results and efficient transport of specimens.

Available on our website (listed below) is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and a dashboard containing respiratory data for our sentinel sites.

*Errata:*



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## Collaborating Partners

In addition to all participating DoD military sentinel sites, collaborating laboratories and medical centers (described above) may be further understood by reviewing the sites' website. Click on the sites' icon to be directed to their webpage.

