



Cumulative Results

Locations	77
Collected	2,266
Tested	2,122

Influenza A 541

A(H1N1)pdm09	4
A(H3N2)	536
A(H3N2) & RSV	1
A/not subtyped	0

Influenza B* 40

B	40
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Other Respiratory Pathogens 627

Adenovirus	38
<i>Bordetella pertussis</i>	0
<i>Chlamydomphila pneumoniae</i>	2
Coronavirus	62
Human Metapneumovirus	27
<i>Mycoplasma pneumoniae</i>	27
Parainfluenza	113
RSV	108
Rhino/Enterovirus	169
Non-influenza Viral Coinfections	73
Non-influenza Bacterial Coinfections	8
-M. pneumo coinfections (8)	

Lab data are current as of 6 February 2017.
Results are preliminary and may change as
more results are received.
*Influenza B lineages will be reported in the
periodic molecular sequencing reports.

Respiratory Highlights

22 January - 4 February 2017 (Surveillance Weeks 4 & 5)

- During 22 January - 4 February 2017, a total of 460 specimens were collected from 52 locations. Results were finalized for 357 specimens from 51 locations. During Week 4, two influenza A(H1N1)pdm09, 92 influenza A(H3N2), and ten influenza B viruses were identified. During Week 5, 75 influenza A(H3N2) and ten influenza B viruses were identified. Approximately 40% of specimens tested positive for influenza during Week 4. Approximately 43% of specimens tested positive for influenza during Week 5. The influenza percent positive for the season is approximately 27%.
- According to the CDC, influenza activity has continued to increase in the United States. Twenty influenza-associated pediatric deaths have been reported for the 2016-2017 season. The proportion of people who sought medical care for influenza-like illness (ILI) has been at or above the national baseline of 2.2% for eight consecutive weeks (CDC, [FluView Report Week 5](#), cited 10 February 2017).

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DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1. Results by region and location for specimens collected during Weeks 4 & 5

Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	Coronavirus	hMPV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona & RSV	Adeno & Rhino/Entero	Corona & RSV	Corona & RSV & Rhino/Entero	hMPV & Rhino/Entero	Para & RSV	RSV & Rhino/Entero	No Pathogen	Total
Deployed	Country 1, Location B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	4	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
EUCOM	Incirlik AB, Turkey	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
PACOM	Eielson AFB, AK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	4	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1	6
Region 1	Hanscom AFB, MA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	USCG Academy, CT	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
Region 2	Ft Drum, NY	-	-	5	-	-	1	-	-	-	-	-	-	-	-	-	-	-	6
	JB McGuire-Dix-Lakehurst, NJ	-	9	-	-	-	2	-	-	2	-	-	-	-	-	-	1	8	22
	USMA - West Point, NY	-	12	-	-	2	-	1	1	-	-	-	-	-	-	-	-	10	26
Region 3	Dover AFB, DE	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	7
	JB Anacostia-Bolling, DC	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	JB Andrews, MD	-	6	1	-	-	-	-	-	-	-	-	-	-	-	-	-	4	11
	JB Langley-Eustis, VA	-	7	-	-	1	-	-	4	-	-	-	-	-	-	-	-	10	22
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 4	Columbus AFB, MS	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2
	Eglin AFB, FL	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	Ft Bragg, NC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	8
	Ft Campbell, KY	1	6	1	1	-	-	-	-	-	-	-	-	-	1	-	-	4	14
	Hurlburt Field, FL	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Keesler AFB, MS	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
	Maxwell AFB, AL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Moody AFB, GA	-	5	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	7
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Robins AFB, GA	-	5	2	-	-	-	-	-	-	-	-	-	-	-	-	-	3	10
	Seymour Johnson AFB, NC	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Shaw AFB, SC	-	4	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	7

(Cont'd from page 3)

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

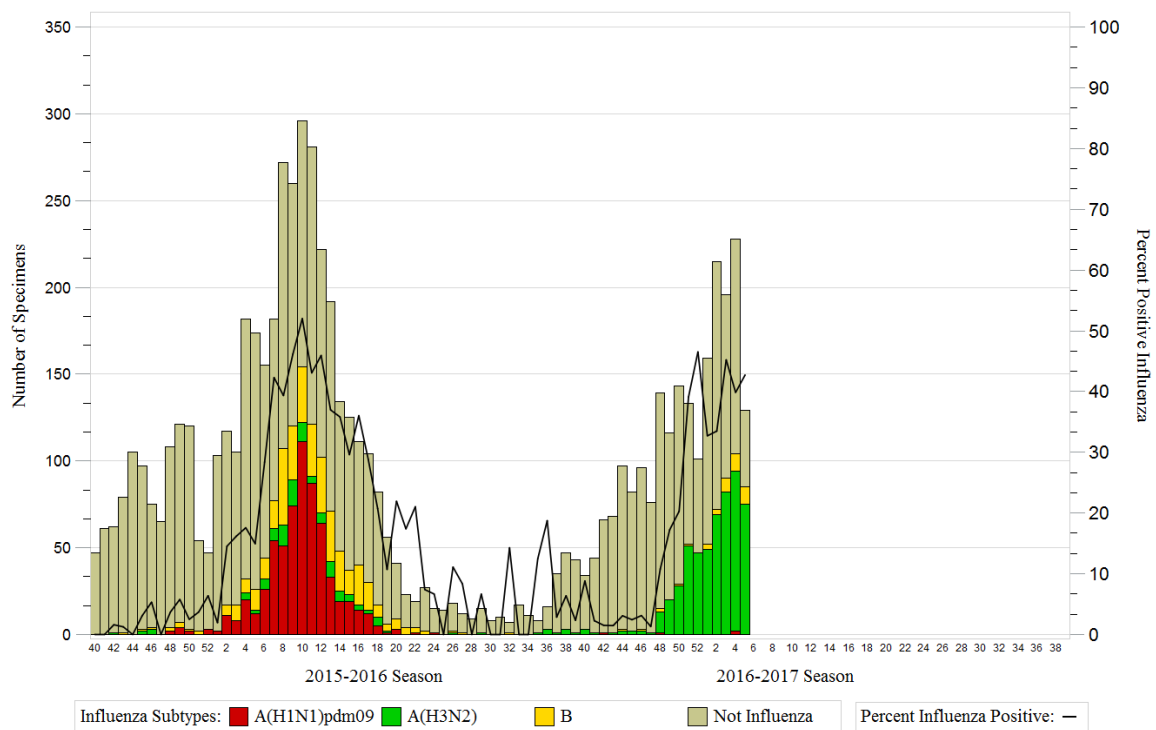
Table 1. Results by region and location for specimens collected during Weeks 4 & 5
(Cont'd from page 2)

Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	Coronavirus	hMPV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona & RSV	Adeno & Rhino/Entero	Corona & RSV	Corona & RSV & Rhino/Entero	hMPV & Rhino/Entero	Para & RSV	RSV & Rhino/Entero	No Pathogen	Total
Region 5	Wright-Patterson AFB, OH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	2
Region 6	Altus AFB, OK	-	4	-	-	-	-	-	2	-	1	-	-	-	-	-	1	3	11
	Barksdale AFB, LA	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	1
	Cannon AFB, NM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Ft Polk, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Little Rock AFB, AR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Sheppard AFB, TX	-	20	-	-	-	-	1	-	1	-	-	-	-	-	-	-	5	27
	Tinker AFB, OK	-	14	1	-	1	-	-	-	-	-	-	-	-	-	-	-	6	22
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 7	M cConnell AFB, KS	-	3	-	-	2	-	-	1	-	-	-	-	-	-	-	-	1	7
	Offutt AFB, NE	1	11	2	-	1	-	-	-	1	-	-	-	-	-	-	-	2	18
Region 8	Ellsworth AFB, SD	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	FE Warren AFB, WY	-	8	1	-	2	-	1	2	1	-	-	-	-	-	-	-	3	18
	Hill AFB, UT	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2
	Malmstrom AFB, MT	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Minot AFB, ND	-	5	-	-	-	-	-	1	-	-	1	-	-	-	-	-	1	8
	Peterson AFB, CO	-	4	1	-	1	-	-	3	-	-	-	-	-	-	-	-	1	10
Region 9	Beale AFB, CA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Davis-Monthan AFB, AZ	-	1	-	-	-	-	-	-	1	-	-	1	1	-	-	1	-	5
	Nellis AFB, NV	-	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	2	4
	Travis AFB, CA	-	5	-	-	-	1	-	3	-	-	-	-	-	-	-	-	2	11
Region 10	Fairchild AFB, WA	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	Mountain Home AFB, ID	-	4	-	-	-	-	3	2	-	-	-	2	-	-	-	-	3	14
Total		2	167	20	2	11	5	7	20	10	1	1	3	1	1	1	3	102	357

*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 5 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.

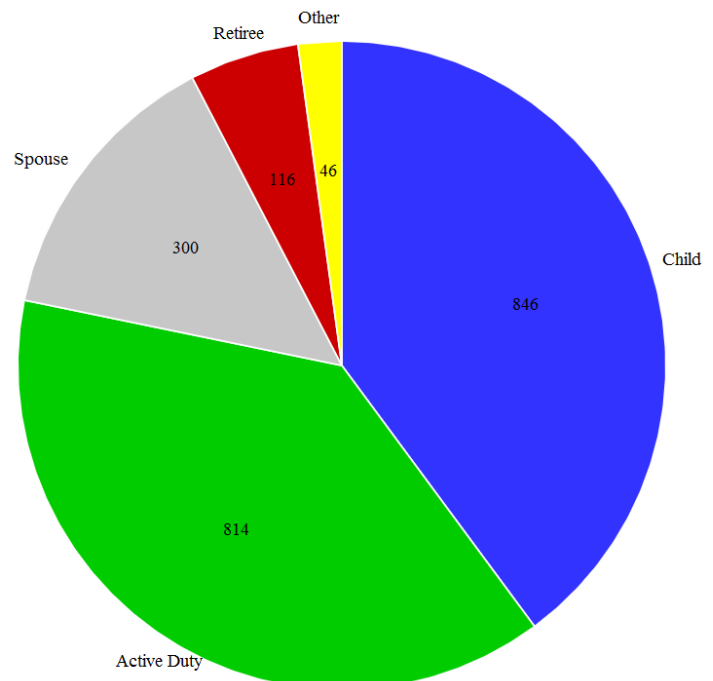
Table 2. ILI by age group for the 2016-2017 surveillance year through Week 5

Age Group	Frequency	Percent
0-5	488	23.00
6-9	136	6.41
10-17	223	10.51
18-24	331	15.60
25-44	699	32.94
45-64	189	8.91
65+	56	2.64

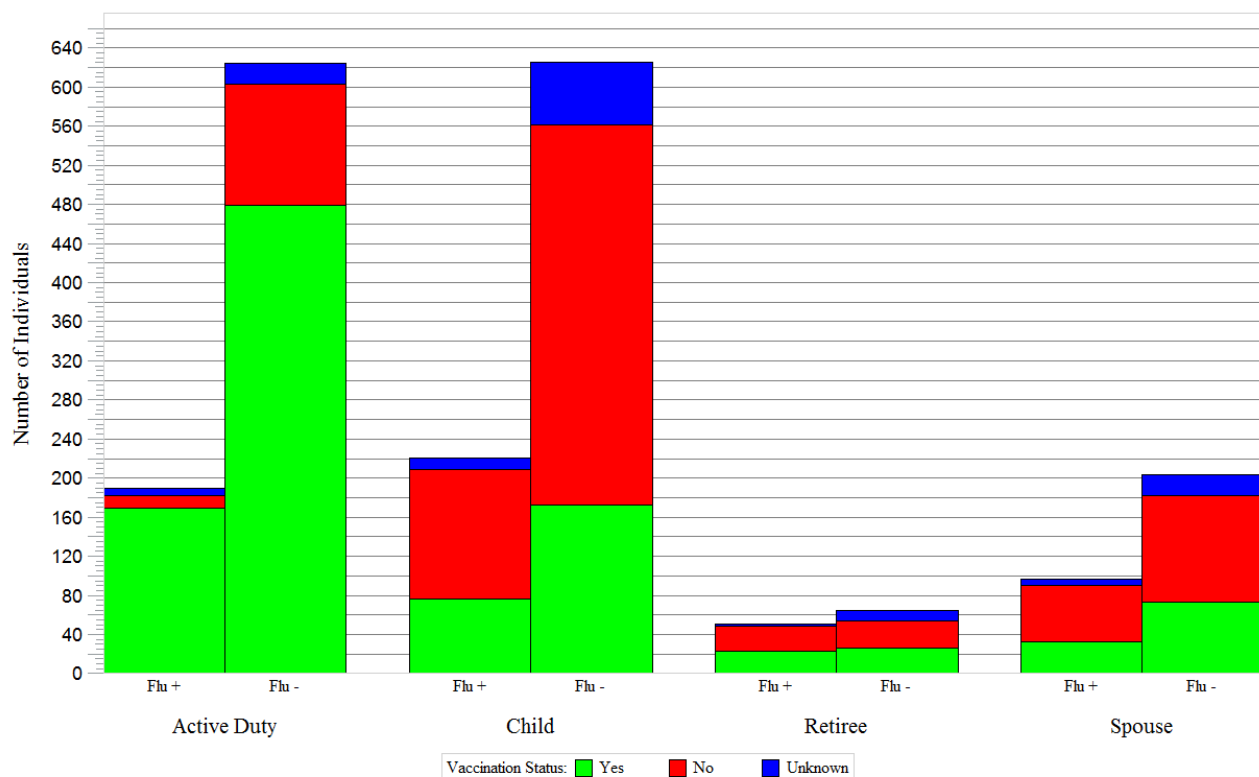
Demographic Summary

Of 2,122 ILI cases, 814 (38.4%) are service members, 846 (39.9%) are children, 300 (14.1%) are spouses, and 162 (7.6%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=2,122) is 22 (range 0, 96).

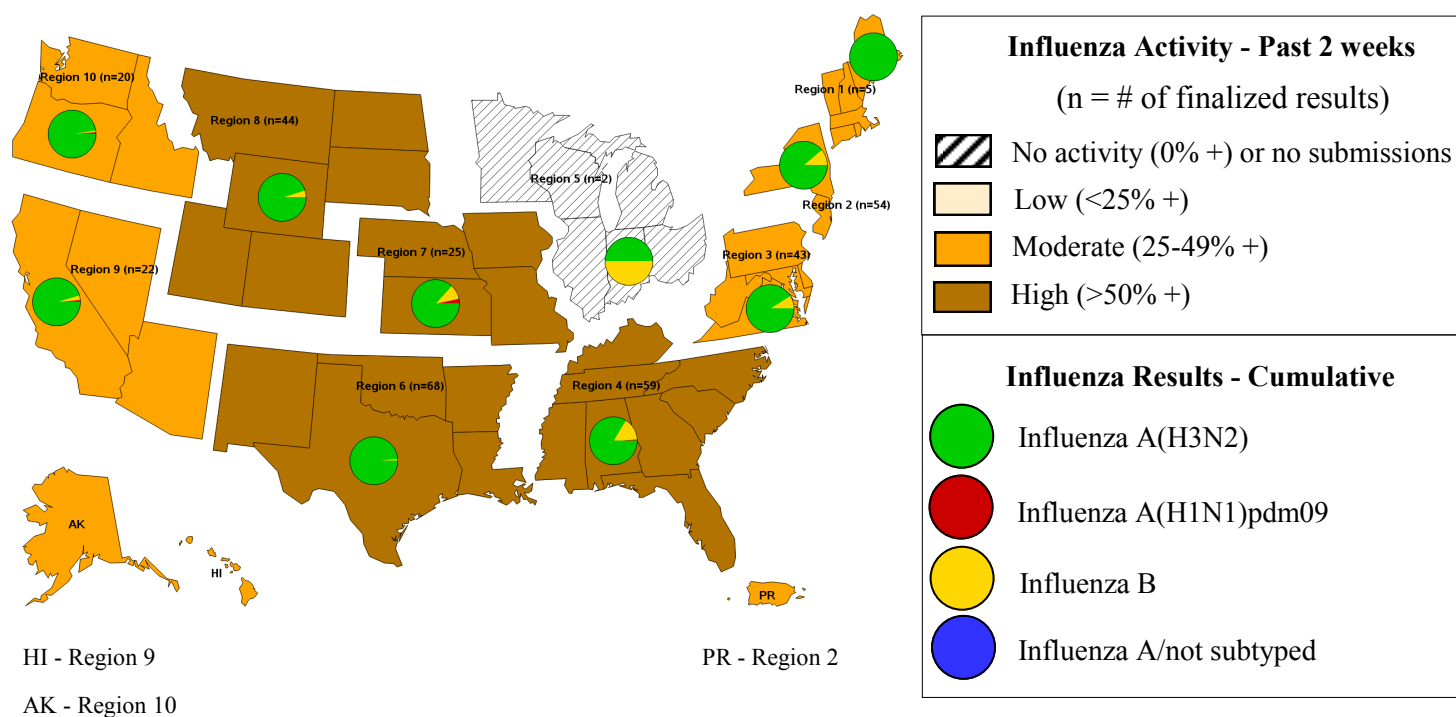
Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 5



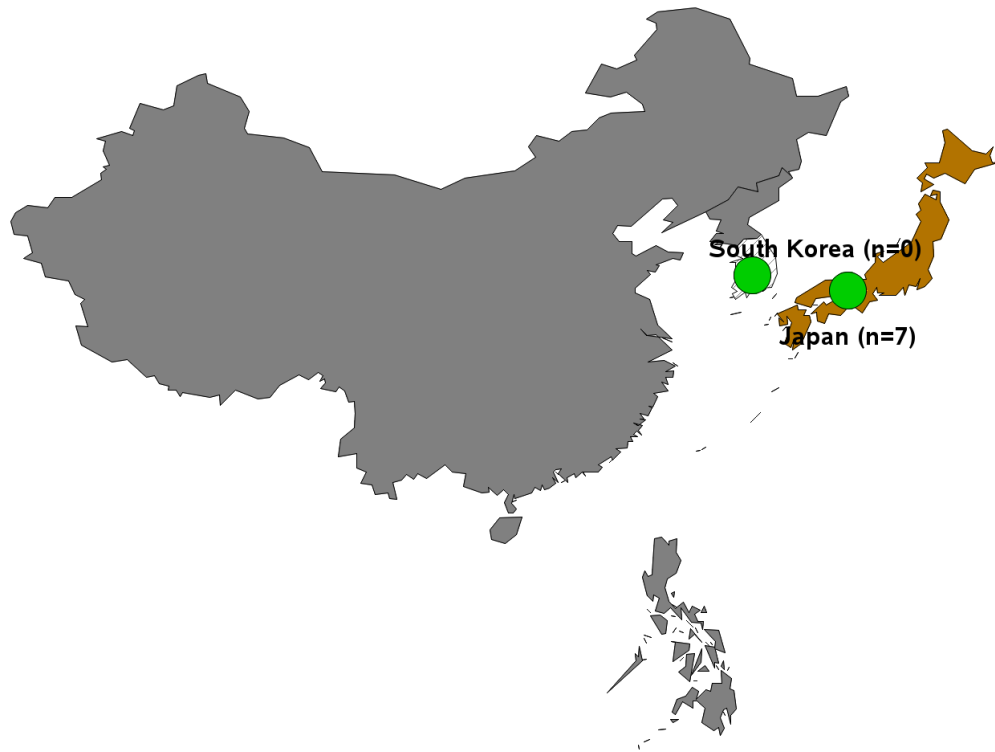
Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 5



Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 5

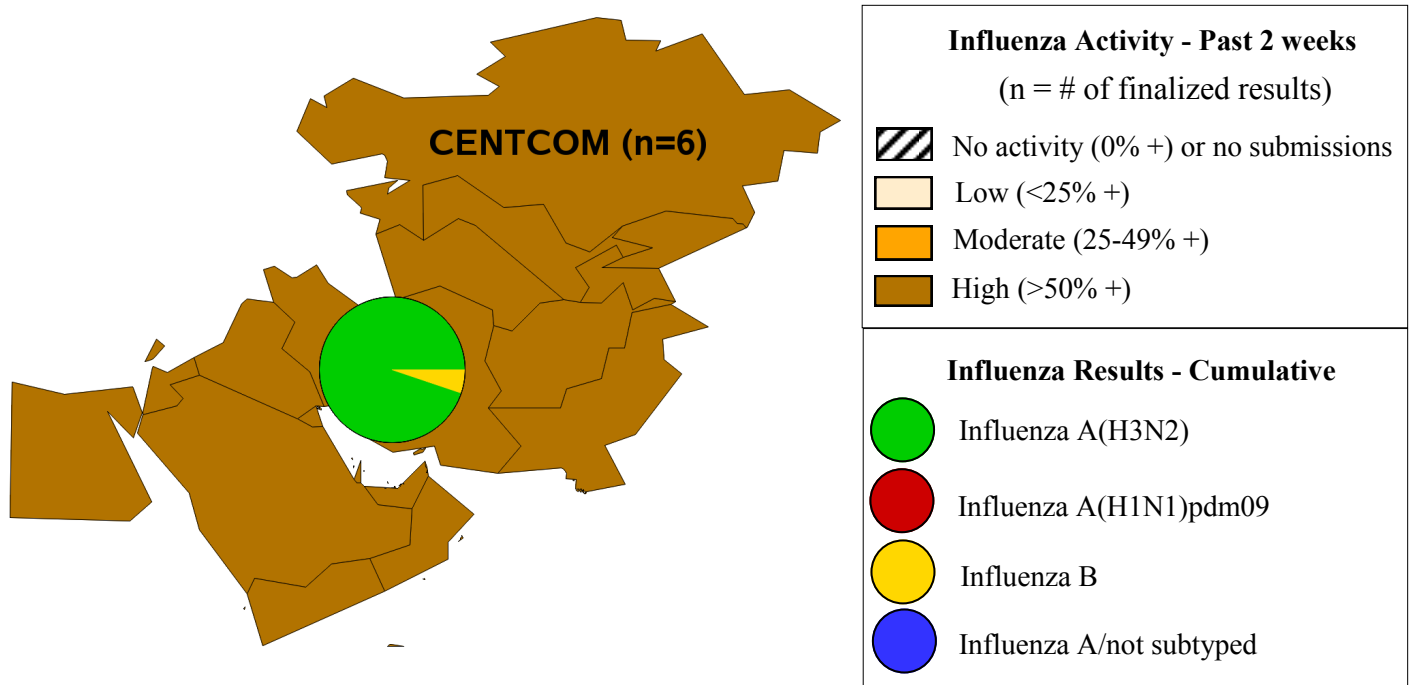


Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 5 (Pacific)



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 5



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 5

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	-	6	-	1	-	-	1	-	-	-	1	-	1	-	5	15
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	27	-	1	-	-	5	-	-	-	-	4	2	-	10	49
EUCOM	Incirlik AB, Turkey	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	3
PACOM	CFA Okinawa, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Eielson AFB, AK	-	-	-	-	-	-	-	-	1	-	-	-	-	-	5	6
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	1	-	-	1	3
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Kadena AB, Japan	-	3	-	-	-	-	-	-	-	2	-	2	-	1	18	26
	Kunsan AB, South Korea	-	2	-	-	-	-	1	-	-	-	-	1	-	-	1	5
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Osan AB, South Korea	-	3	-	-	-	-	-	-	-	-	-	-	-	-	6	9
	Tripler AM C, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	14	-	-	1	-	2	1	2	-	2	7	3	-	42	74
Region 1	Hanscom AFB, MA	-	1	-	-	-	-	-	-	1	1	-	-	1	-	2	6
	USCG Academy, CT	-	4	-	-	-	-	-	-	1	-	-	3	-	2	4	14
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	-	1	-	8	4	-	1	7	1	6	4	1	2	-	10	45
	JB McGuire-Dix-Lakehurst, NJ	-	30	-	-	2	-	5	3	2	7	5	9	4	-	51	118
	USMA - West Point, NY	-	40	-	1	10	-	4	2	1	5	9	4	4	-	80	160
Region 3	Dover AFB, DE	-	5	-	-	1	-	1	-	1	-	1	1	-	-	15	25
	JB Anacostia-Bolling, DC	-	2	-	-	-	-	-	-	-	-	1	-	-	-	-	3
	JB Andrews, MD	-	10	-	1	-	-	1	-	-	-	2	1	2	-	19	36
	JB Langley-Eustis, VA	-	12	-	2	-	-	2	2	2	4	17	22	8	-	57	128
	NM C Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 4	Columbus AFB, MS	-	3	-	-	-	-	1	-	-	-	-	1	-	-	7	12
	Eglin AFB, FL	-	8	-	1	2	-	1	-	-	-	4	9	3	-	16	44
	Ft Bragg, NC	-	4	-	3	-	-	1	-	1	3	2	6	3	3	21	47
	Ft Campbell, KY	1	14	-	2	1	-	-	1	-	-	3	-	5	-	10	37
	Hurlburt Field, FL	-	7	-	-	-	-	-	-	-	1	-	-	-	-	7	15
	JB Charleston (AF), SC	-	3	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	1	2	1	1	-	7	12
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	4
	Maxwell AFB, AL	-	2	-	-	-	-	-	-	-	1	-	1	-	-	8	12
	Moody AFB, GA	-	11	-	2	1	-	1	-	-	1	5	4	7	1	16	49
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NH Camp Lejeune, NC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	10	-	2	-	-	-	-	1	-	1	-	-	-	7	21
	Seymour Johnson AFB, NC	-	2	-	-	1	-	-	-	1	1	-	1	-	-	3	9
	Shaw AFB, SC	-	11	-	4	1	-	5	1	1	3	1	3	-	-	27	57

(Cont'd on page 8)

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

Laboratory Results—Through Current Surveillance Week 5

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

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
Region 5	Scott AFB, IL	-	-	-	1	-	-	-	-	1	2	1	1	-	1	6	13
	Wright-Patterson AFB, OH	-	1	-	-	-	-	-	-	1	1	-	1	2	-	10	16
Region 6	Altus AFB, OK	-	4	-	-	1	-	-	1	-	-	3	4	2	-	22	37
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	2	-	1	-	-	4	7
	Cannon AFB, NM	-	2	-	-	-	-	1	-	1	1	-	3	-	-	14	22
	Ft Polk, LA	-	1	-	-	-	-	-	-	1	-	-	-	-	-	1	3
	Laughlin AFB, TX	-	-	-	-	-	-	-	2	-	-	-	-	-	-	1	3
	Little Rock AFB, AR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Sheppard AFB, TX	-	34	-	-	-	-	3	1	-	6	-	6	-	-	30	80
	Tinker AFB, OK	-	33	1	1	-	-	2	-	1	5	4	6	-	-	40	93
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10	10
		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Region 7	McConnell AFB, KS	-	10	-	-	-	-	3	-	1	2	1	4	-	-	15	36
	Offutt AFB, NE	1	16	-	3	1	-	3	-	-	-	-	5	1	-	24	54
Region 8	Ellsworth AFB, SD	-	7	-	-	-	-	2	-	-	3	-	3	-	-	14	29
	FE Warren AFB, WY	-	16	-	1	2	-	2	-	1	2	4	3	-	-	16	47
	Hill AFB, UT	-	17	-	-	-	-	2	-	-	4	3	4	-	-	22	52
	Malmstrom AFB, MT	-	4	-	1	-	-	-	-	1	-	-	1	-	-	3	10
	Minot AFB, ND	-	5	-	-	-	-	1	1	1	-	1	2	1	-	6	18
	Peterson AFB, CO	-	9	-	1	-	-	2	-	-	1	6	3	4	-	10	36
	USAF Academy, CO	-	1	-	-	-	-	-	1	-	-	1	1	-	-	2	6
		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	-	6	-	-	-	-	-	-	-	5	-	4	3	-	14	32
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	2	-	-	-	1	-	1	-	4	8
	Nellis AFB, NV	1	2	-	2	2	-	1	-	-	4	3	5	6	-	15	41
	Travis AFB, CA	-	49	-	-	-	1	1	4	-	6	5	8	1	-	29	104
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Fairchild AFB, WA	1	13	-	1	2	-	3	-	-	4	2	4	-	-	38	68
	JB Lewis-McChord, WA	-	2	-	-	1	-	-	-	-	-	-	-	-	-	-	3
	Mt Home AFB, ID	-	19	-	-	1	1	1	-	1	23	8	12	4	-	56	126
	NH Bremerton, WA	-	33	-	-	4	-	-	-	-	6	4	4	2	-	14	67
Total		4	536	1	40	38	2	62	27	27	113	108	169	73	8	914	2122

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

Molecular Sequence Analysis Report #3

USAFSAM Epidemiology Laboratory Service

This is the third USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 75 specimens collected between 12 July 2016 and 9 January 2017, with 66 specimens analyzed by USAFSAM, six hemagglutinin sequences provided by the Naval Medical Research Unit 6 (NAMRU-6) in Peru, and three hemagglutinin sequences provided by the Walter Reed Army Institute of Research (WRAIR). Among the specimens analyzed, two (2.7%) were influenza A(H1N1)pdm09, 65 (86.7%) were influenza A(H3N2), four (5.3%) were influenza B/Victoria lineage, and four (5.3%) were influenza B/Yamagata lineage. 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 2-5 display the phylogenetic relationships among HA sequences for influenza A(H1N1)pdm09, A(H3N2), and influenza B/Victoria and B/Yamagata lineages, respectively.

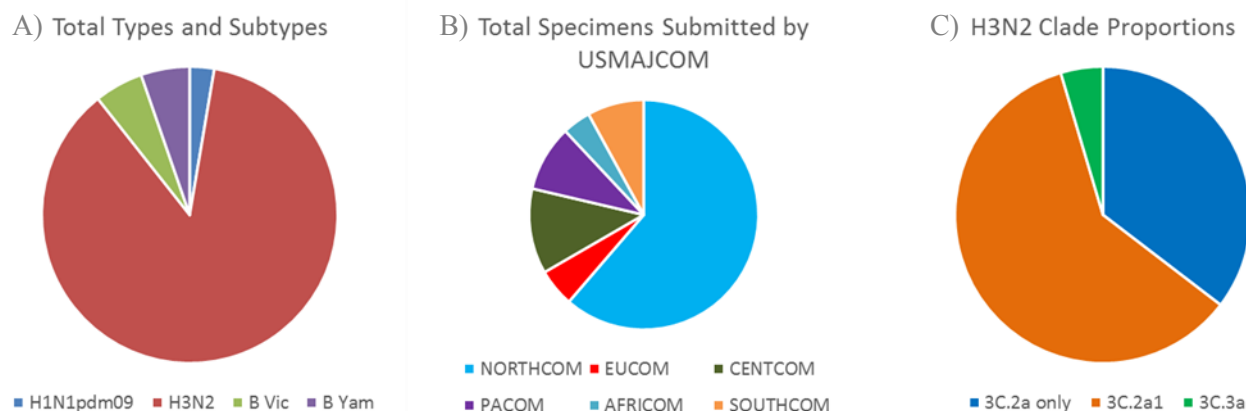


Figure 1: A) Proportion of influenza hemagglutinin sequence subtypes and lineages submitted to USAFSAM for this report, B) Number of influenza positive specimens submitted by sentinel sites separated by USMAJCOM (AFRICOM data from WRAIR, SOUTHCOM data from NAMRU-6), C) Proportion of specimens in each influenza A(H3N2) clade represented in this report.

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

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

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
CONUS					
California					
Travis AFB		9			9
Colorado					
Peterson AFB		1			1
Florida					
Eglin AFB		1			1
Georgia					
Moody AFB		1			1
Robins AFB		1			1
Idaho					
Mt Home AFB		2			2
Kansas					
McConnell AFB		1			1
Maryland					
JB Andrews		1			1
Nebraska					
Offutt AFB		1			1
New York					
USMA - West Point		2			2
North Carolina					
Ft Bragg		2			2
Ohio					
Wright-Patterson AFB	1	1	2	1	5
Oklahoma					
Tinker AFB		3			3
South Carolina					
Shaw AFB		1			1
Texas					
SAMMC		4	1		5
Sheppard AFB		2			2
Utah					
Hill AFB		4			4
Virginia					
JB Langley-Eustis				1	1
Washington					
Fairchild AFB		2			2
JB Lewis-McChord		1			1

(Cont'd on page 11)

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

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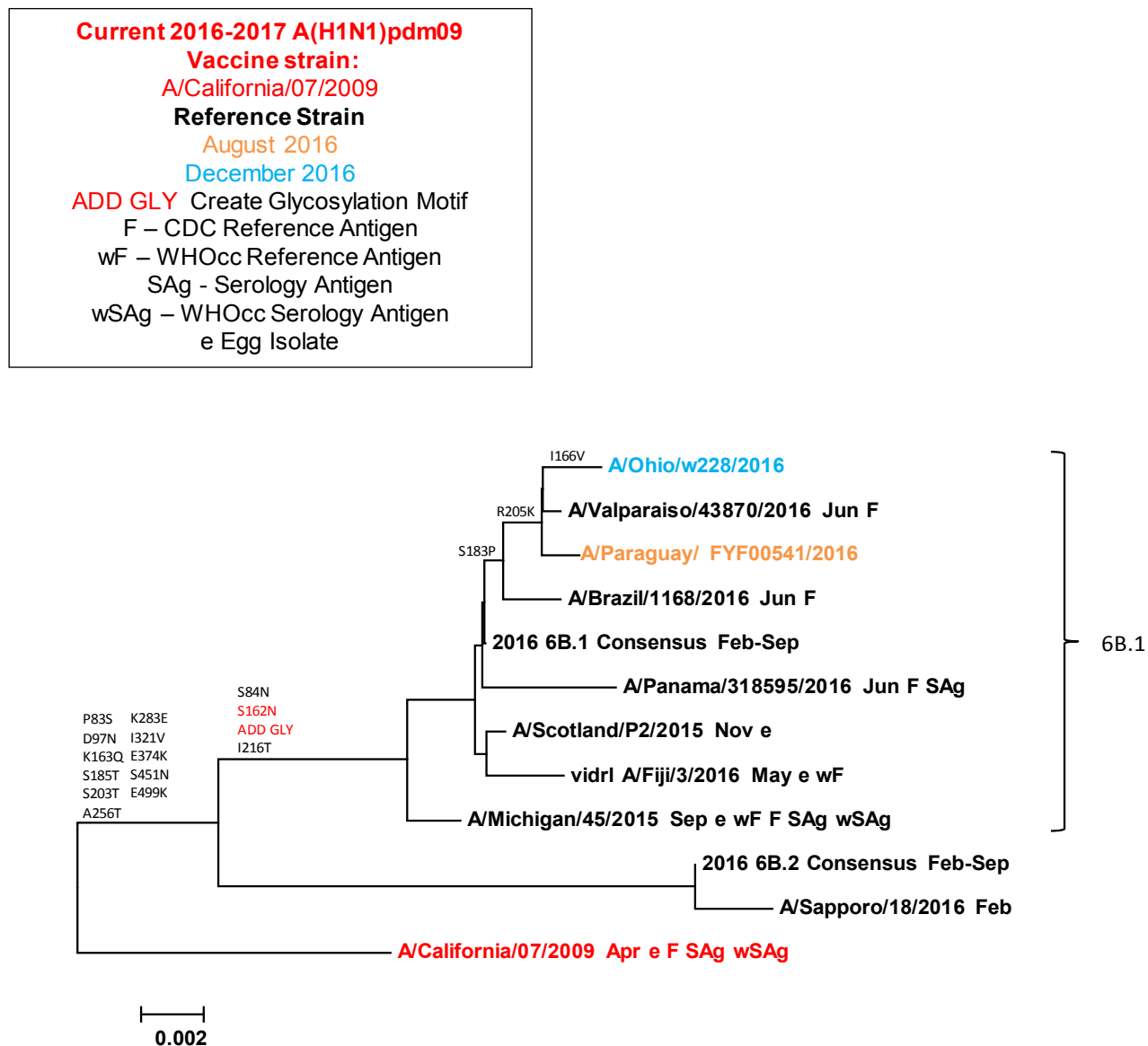
	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
OCNUS					
Country1					
Location A	2				2
Country2					
Location A	7				7
Germany					
Landstuhl RMC	2		1		3
Vilseck AHC	1				1
Japan					
Yokota AB	2				2
Nigeria					
WRAIR	3				3
Paraguay					
NAMRU-6	1		1		2
Peru					
NAMRU-6	3		1		4
South Korea					
Brian Allgood ACH	4				4
Kunsan AB	1				1
Grand Total	2	65	4	4	75

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.^{1,3,4} Sequence data was constructed and analyzed using multiple software programs. Genetic and predicted antigenic information that resulted from this analysis is shared with 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 67 influenza A isolates, two (3.0%) 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 exhibited an overall protein homology of 97.2%-97.3% 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 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.⁴ 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 17 mutations present in the A(H1N1)pdm09 isolates, five occurred at predicted antigenic sites (zero at site A, one at site B, zero at site C, two at site D, and two at site E) and two occurred at the receptor binding site.^{2,5}

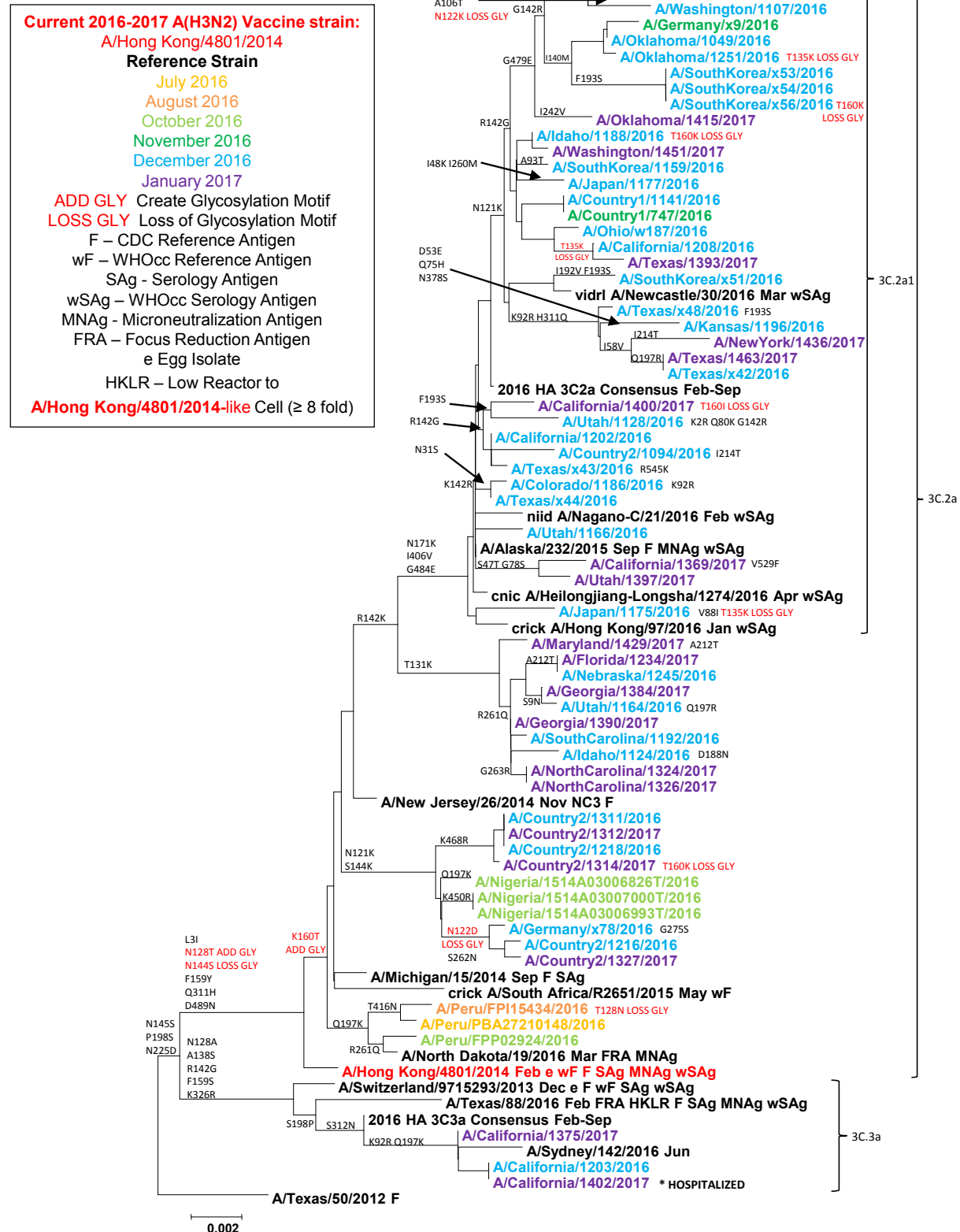
Figure 2. Influenza A(H1N1)pdm09 HA Phylogenetic Analysis



Influenza A(H3N2)

- Among the 67 influenza A isolates, 65 (97.0%) 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 97.3%-99.1% (average 98.2%) 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. Sixty-two (95.4%) of the influenza A(H3N2) sequences classified as subclade 3C.2a and 3 (4.6%) classified as subclade 3C.3a. Thirty-nine of the 62 3C.2a isolates (62.9%) 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 28 (71.8%) of the 3C.2a1 isolates (43.1% of the total H3N2).
- Among the influenza A(H3N2) isolates characterized in this report, seven mutations: N122K (asparagine to lysine), N122D (asparagine to aspartic acid), T128N (threonine to asparagine), T135K (threonine to lysine), N144S (asparagine to serine), 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 59 mutations present in the A(H3N2) specimens, 21 occurred at predicted antigenic sites (six at site A, four at site B, three at site C, three at site D, and five at site E) and two occurred at the receptor binding site.^{2,5}
- A/California/1402/2017 was collected from a hospitalized patient who was not vaccinated. Records show that the patient exhibited flu-like symptoms which included fever (102.5°F), cough, fatigue, body aches, chills, runny nose, and headache at the time this specimen was collected.

Figure 3. Influenza A(H3N2) HA Phylogenetic Analysis



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) and the B/Yamagata isolates (Figure 5).
- 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.¹ Four (50.0%) of the influenza B isolates characterized in this report fell into the Victoria lineage and four (50.0%) fell into the Yamagata lineage.
- The influenza B/Victoria isolates characterized for this report exhibited a protein homology of 98.7% when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-like virus. The influenza B/Yamagata isolates characterized for this report exhibited a protein homology of 98.9%-99.1% (average 90.0%) when compared to the 2016-2017 B/Yamagata vaccine component, B/Phuket/3073/2013-like virus.
- All of the influenza B/Victoria isolates fall into clade V1A and all of the B/Yamagata isolates fall into clade Y3.
- For B/Victoria, one mutation, A199T (alanine to threonine), adds a glycosylation motif. For B/Yamagata, one mutation, D197N (aspartic acid to asparagine), adds a glycosylation motif.

Figure 4. Influenza B Victoria HA Phylogenetic Analysis

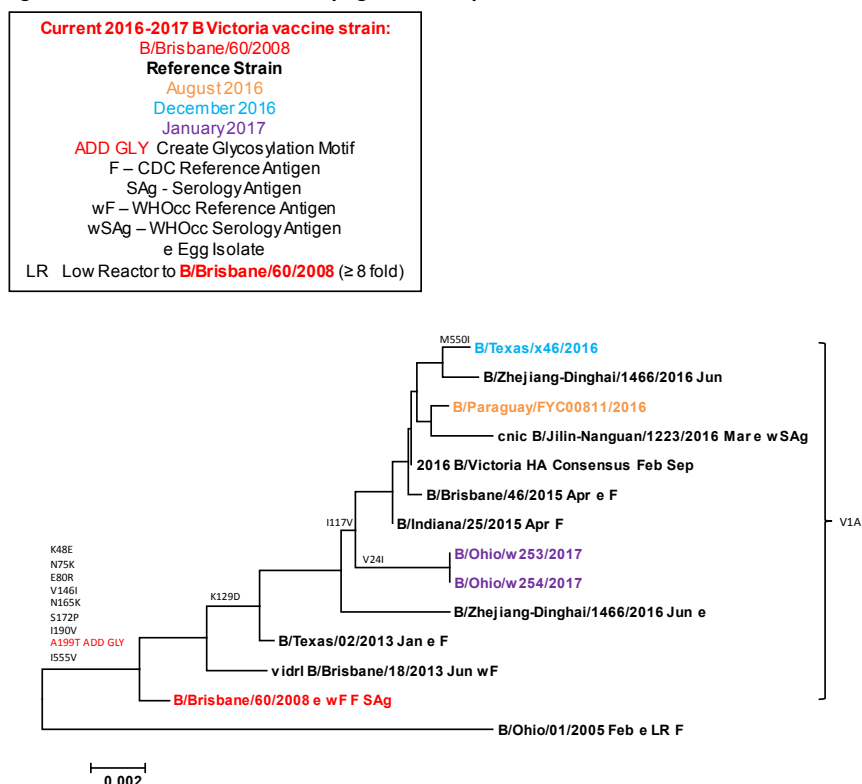
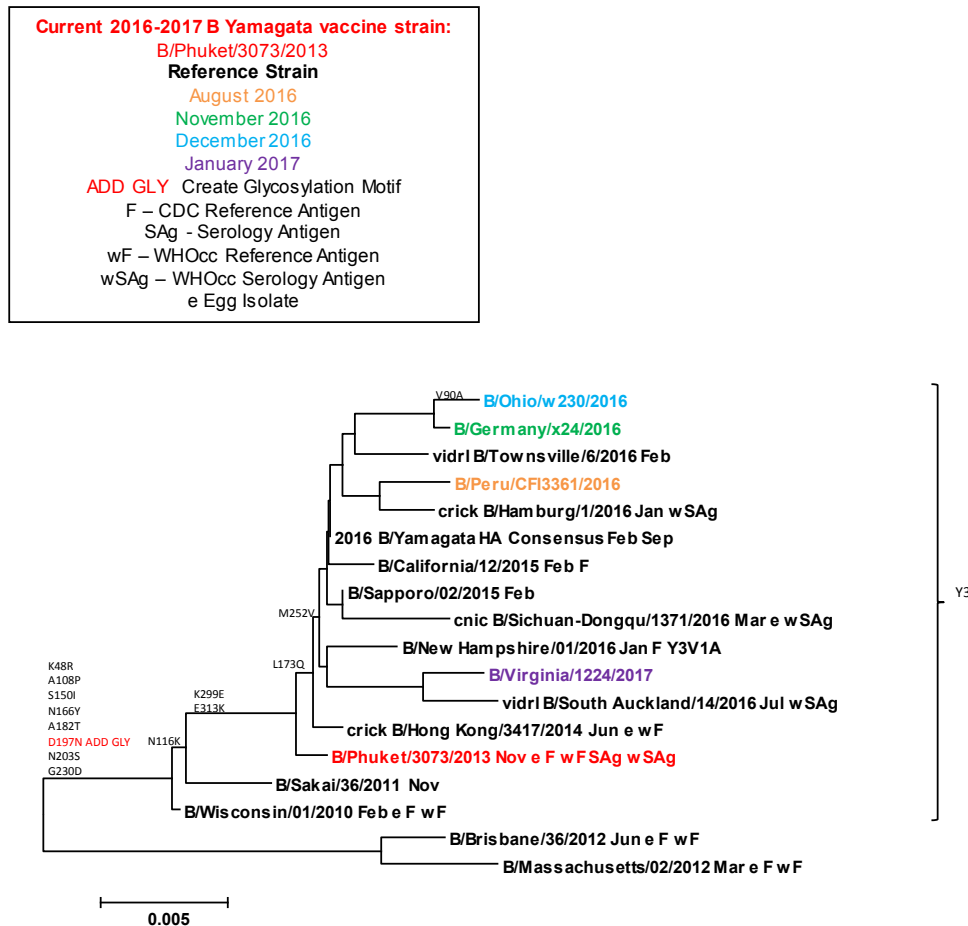


Figure 5. Influenza B Yamagata HA Phylogenetic Analysis



References:

1. Wright, P., Neumann, G., and Kawaoka, Y. (2007). Orthomyxoviruses In: Knipe, D.M., Howley, P.M. (Eds.), Fields Virology. Wolters Kluwer, Lippincott Williams & Wilkins, Philadelphia, pp.1692-1740.
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.

References:

1. Wright, P., Neumann, G., and Kqaoka, Y. (2007). Orthomyxoviruses In: Knipe, D.M., Howley, P.M. (Eds.), Fields Virology. Wolters Kluwer, Lippincott Williams & Wilkins, Philadelphia, pp.1692-1740.
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.
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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).

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.

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