USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2015-2016

Cumulative Results

Locations	79
Collected	4,297
Tested	4,243

Influenza A	**742**
A(H1N1)pdm09	635
A(H1N1)pdm09 & B	1
A(H1N1)pdm09 & Coronavirus	1
A(H1N1)pdm09 & Parainfluenza	1
A(H3N2)	103
A(H3N2) & B	1

Influenza B*	**368**
B	367
B & Adenovirus	1

Other Respiratory Pathogens	**1,030**
Adenovirus	161
Bordetella pertussis	1
Chlamydophila pneumoniae	2
Coronavirus	85
Human Metapneumovirus	85
Mycoplasma pneumoniae	55
Parainfluenza	108
RSV	129
Rhinovirus/Enterovirus	271
Non-influenza Viral Coinfections	117
Non-influenza Bacterial Coinfections	16
-B. pertussis (3)	
-B. pertussis & M. pneumo (1)	
-C. pneumo (2)	
-C. pneumo & M. pneumo (1)	
-M. pneumo (9)	

Lab data are current as of 31 May 2016. 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
15 - 28 May 2016 (Surveillance Weeks 20 & 21)

- During 15-28 May 2016, a total of 56 specimens were collected and received from 25 locations. Results were finalized for 52 specimens from 22 locations. During Week 20, three influenza A(H1N1)pdm09 and six influenza B viruses were identified. Four influenza B viruses were identified during Week 21. Approximately 22% of specimens tested positive for influenza during Week 20. The percent positive for Week 21 increased to approximately 28%, as fewer specimens were received. The influenza percent positive for the season is currently 26%.

- Flu activity continues to decrease in the United States. For this season, it has peaked nationally and is winding down. New York and Puerto Rico continue to report widespread flu activity. Influenza B viruses have been most common in recent weeks; however, A(H1N1)pdm09 has been predominant overall this season. Second waves of influenza B activity occur during many flu seasons. CDC continues to recommend influenza vaccination as long as influenza viruses are circulating. CDC also recommends that patients suspected of having influenza who are at high-risk of flu complications or who are very sick with flu-like symptoms should receive prompt treatment with influenza antiviral drugs without waiting for confirmatory testing (CDC Situation Update, Cited 2 June 2016).

- This report contains the eighth molecular sequence analysis report and includes 93 specimens collected between 9 December 2015 and 8 March 2016. See page 8 for further details.

- This report will be last weekly report for this season. Subsequent reports for the remainder of this season will be distributed monthly.

Table of Contents

88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Table 1. Results by region and location for specimens collected during Weeks 20 & 21

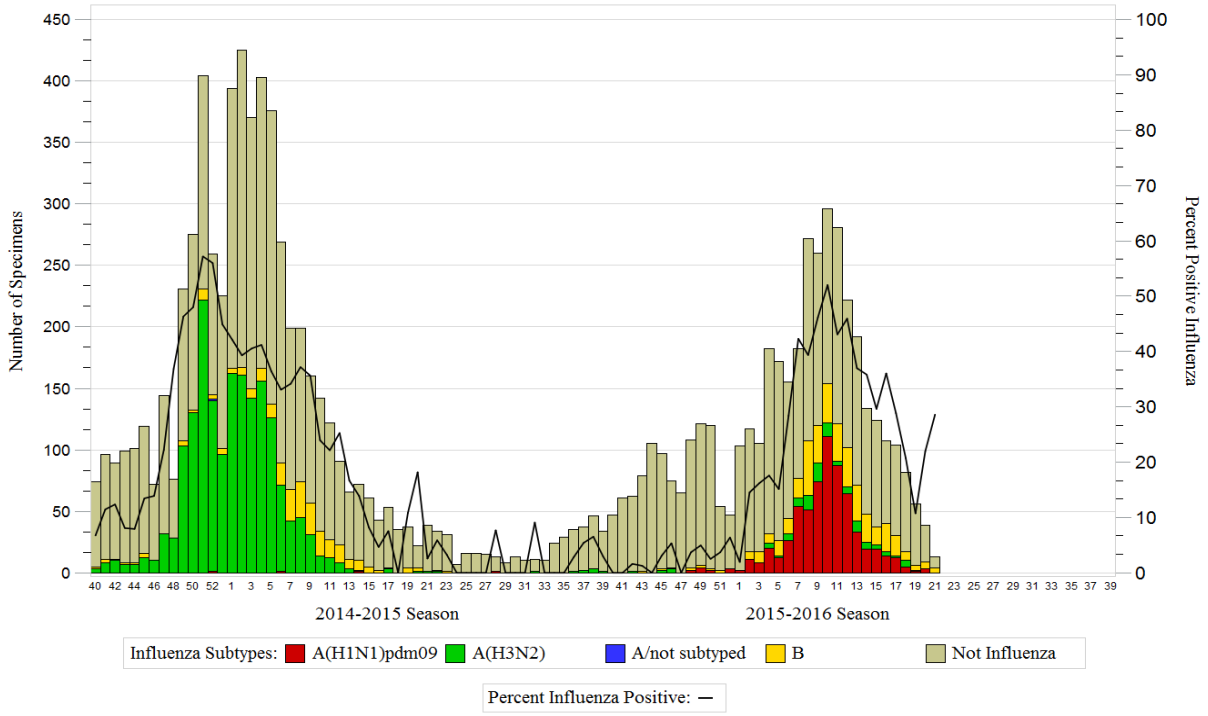
Region*		A(H1N1)pdm09	B	Adenovirus	hMNV	Parainfluenza	Rhinovirus/Enterovirus	No Pathogen	Total
PACOM	Kadena AB, Japan	-	1	-	-	-	-	-	1
Region 2	JB McGuire-Dix-Lakehurst, NJ	1	2	-	1	1	1	-	6
	USMA - West Point, NY	-	2	-	1	3	2	2	10
Region 3	NMC Portsmouth, VA	-	-	-	-	-	1	-	1
Region 4	Eglin AFB, FL	1	1	-	-	-	-	-	2
	Ft Bragg, NC	-	1	-	-	-	-	-	1
	Maxwell AFB, AL	-	-	-	-	-	2	-	2
	Moody AFB, GA	-	-	1	-	1	2	1	5
	Robins AFB, GA	-	-	-	-	-	-	1	1
	Shaw AFB, SC	-	-	-	-	-	1	-	1
Region 5	Wright-Patterson AFB, OH	-	-	-	-	-	-	1	1
Region 6	Altus AFB, OK	-	-	-	-	-	1	1	2
	Laughlin AFB, TX	-	-	-	-	-	1	-	1
	Little Rock AFB, AR	-	-	-	-	-	1	-	1
	Sheppard AFB, TX	-	-	-	-	-	1	1	2
Region 7	Offutt AFB, NE	-	-	-	-	-	1	2	3
Region 8	Ellsworth AFB, SD	-	-	-	-	-	1	-	1
	Hill AFB, UT	-	-	-	-	-	1	-	1
Region 9	Edwards AFB, CA	-	-	-	-	-	1	-	1
	Luke AFB, AZ	-	-	-	-	-	1	-	1
	Travis AFB, CA	-	3	-	-	-	-	-	3
Region 10	NH Bremerton, WA	1	-	-	-	2	-	2	5
Total		3	10	1	2	7	18	11	52

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2014-2015 surveillance year and through Week 21 of the 2015-2016 surveillance year

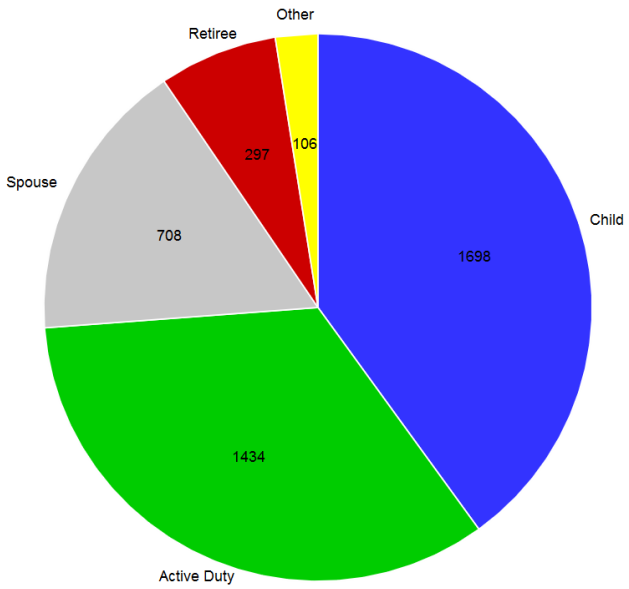


Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

Table 2. ILI by age group for the 2015-2016 surveillance year through Week 21

Age Group	Frequency	Percent
0-5	961	22.65
6-9	334	7.87
10-17	406	9.57
18-24	572	13.48
25-44	1363	32.12
45-64	493	11.62
65+	114	2.69

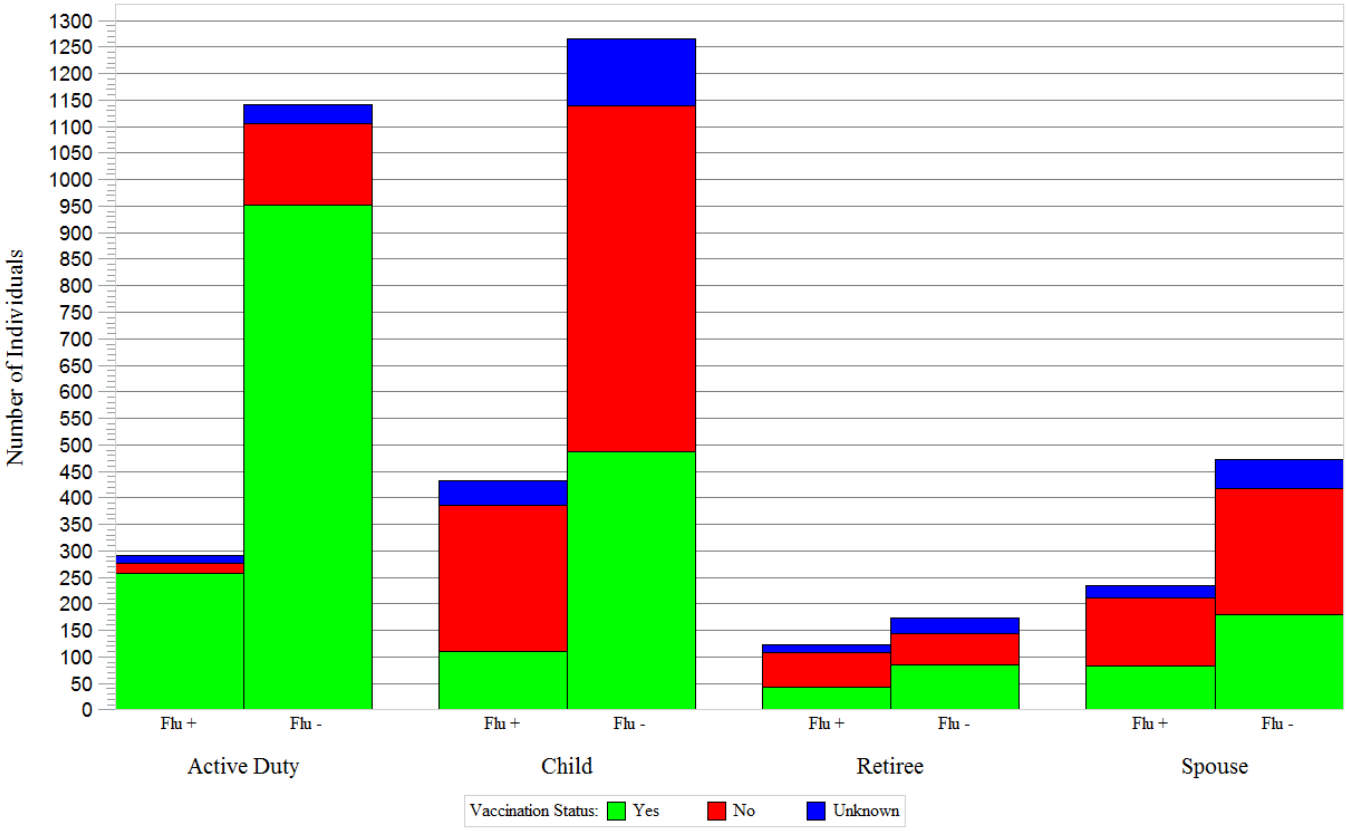
Graph 2. ILI by beneficiary status for the 2015-2016 surveillance year through Week 21



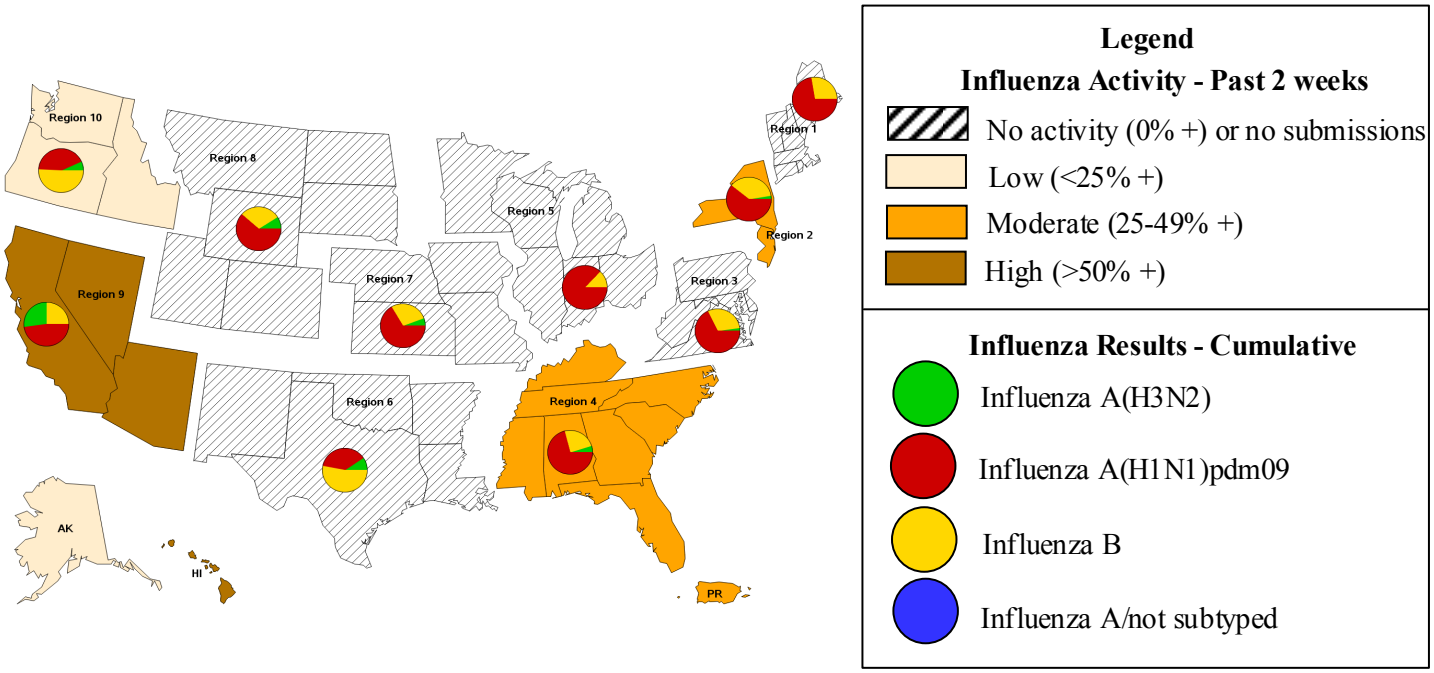
Demographic Summary

Of 4,243 ILI cases, 1,434 are service members (33.8%), 1,698 are children (40.0%), 708 are spouses (16.7%), and 403 (9.5%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=4,243) is 23 (range 0, 95).

Graph 3. Vaccination status by beneficiary type for the 2015-2016 surveillance year through Week 21

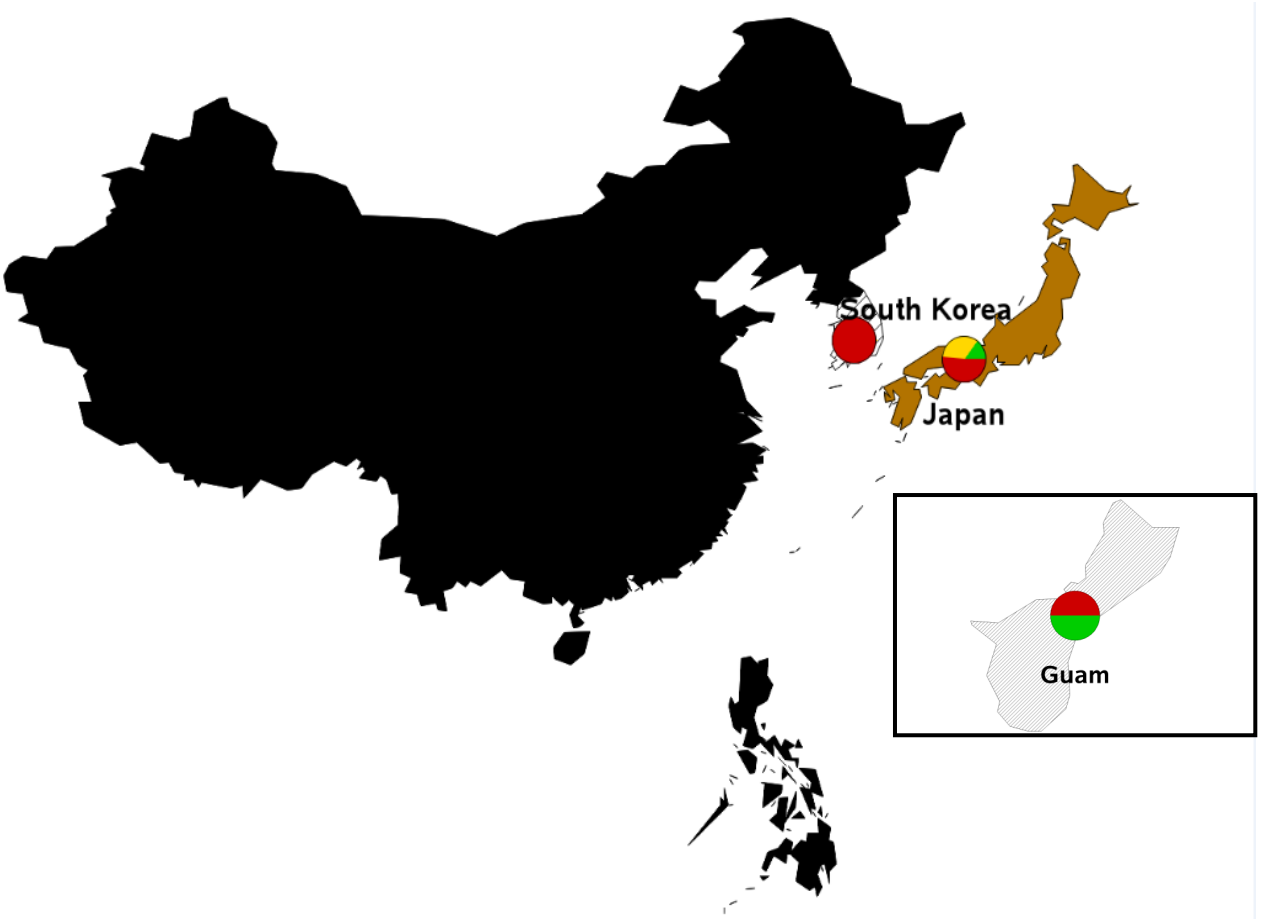


Map 1. Influenza subtypes and activity level by region for the 2015-2016 surveillance year through Week 21*

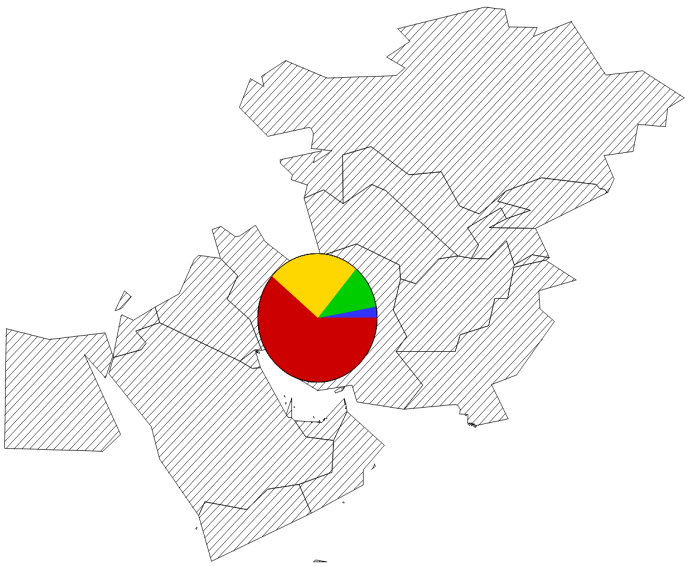


*Due to the receipt of a small number of specimens from Regions 1, 3, 5, 6, 7, 8, 9 and 10 activity level may be biased.

Map 2. Influenza subtypes and activity level by country for the 2015-2016 surveillance year through Week 21 (Pacific)*



Map 3. Influenza subtypes and activity level for CENTCOM for the 2015-2016 surveillance year through Week 21*



Legend

Influenza Activity - Past 2 weeks

- No activity (0% +) or no submissions
- Low (<25% +)
- Moderate (25-49% +)
- High (>50% +)

Influenza Results - Cumulative

- Influenza A(H3N2)
- Influenza A(H1N1)pdm09
- Influenza B
- Influenza A/not subtyped

Note - Specimens for CENTCOM were tested at USAFSAM or Landstuhl Regional Medical Center (LRMC).
*Due to the receipt of a small number of specimens from the region activity level may be biased.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 21

Table 3. Cumulative results by region and location for specimens collected during the 2015-2016 surveillance year

Region*		A(H1N1)pdm09	A(H3N2)	A(H1N1)pdm09 & B	A(H1N1)pdm09 & Corona	A(H1N1)pdm09 & Para	A(H3N2) & B	B	B & Adeno	Adenovirus	*B. pertussis*	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Bacterial Coinfection	Non-Influenza Viral Coinfection	No Pathogen	Total
Deployed	Country 1, Location B	-	1	-	-	-	-	-	-	-	-	-	1	1	-	-	-	2	-	-	2	7
	Country 2, Location A	8	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	14
PACOM	CFA Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	10	12
	Eielson AFB, AK	4	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	5	12
	JB Elmendorf-Richardson, AK	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	-	5	7
	JR Marianas - Andersen AFB, Guam	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	1	4
	JR Marianas - NH Guam, Guam	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Kadena AB, Japan	2	1	-	-	-	-	3	-	-	-	-	2	-	3	-	-	2	-	1	21	35
	Kunsan AB, South Korea	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Misawa AB, Japan	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3	-	-	5	11
	Osan AB, South Korea	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	6
	USCG Base Kodiak, AK	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	20	5	-	-	-	-	13	-	8	-	-	4	-	2	5	2	5	-	2	34	100
Region 1	Hanscom AFB, MA	9	-	-	-	-	-	5	-	4	-	-	-	-	1	2	2	-	-	2	26	51
	NHCNE Newport, RI	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	1	-	-	11	14
	USCG Academy, CT	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	11
Region 2	Ft Drum, NY	12	-	-	-	-	-	2	-	-	-	-	1	-	-	-	-	3	-	-	7	25
	JB McGuire-Dix-Lakehurst, NJ	31	1	-	-	-	-	20	1	3	-	-	1	4	3	2	-	13	1	3	49	132
	USMA - West Point, NY	55	3	-	-	1	-	37	-	24	-	-	10	9	5	11	11	18	3	9	170	366
Region 3	Dover AFB, DE	24	-	-	-	-	-	8	-	3	-	1	-	2	-	1	2	3	-	1	84	129
	JB Anacostia-Bolling, DC	-	1	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	4
	JB Andrews, MD	7	-	-	-	-	-	3	-	2	-	-	-	2	1	-	2	-	-	-	12	29
	JB Langley-Eustis, VA	20	-	-	-	-	-	11	-	10	-	-	4	7	3	7	8	9	2	3	64	148
	NCRM - Walter Reed NMMC, MD	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5
	NMC Portsmouth, VA	6	1	-	-	-	-	4	-	4	-	-	1	1	5	1	2	3	1	1	24	54
Region 4	CGS Mobile, AL	1	2	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	2	7
	Columbus AFB, MS	6	-	-	-	-	-	-	-	2	-	-	1	1	-	-	2	4	-	-	22	38
	Eglin AFB, FL	10	1	-	-	-	-	3	-	6	-	-	1	1	1	4	7	6	-	1	66	107
	Ft Bragg, NC	9	-	-	-	-	-	12	-	4	-	-	4	1	1	-	3	2	1	2	40	79
	Ft Campbell, KY	24	1	-	-	-	-	9	-	1	-	-	4	2	-	2	1	4	-	-	43	91
	Hurlburt Field, FL	7	1	-	-	-	-	2	-	5	-	1	-	2	4	-	1	1	-	2	33	59
	JB Charleston (AF), SC	4	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Keesler AFB, MS	-	-	-	-	-	-	-	-	1	-	-	-	-	2	-	-	2	-	1	32	38
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-	-	1	4
	Maxwell AFB, AL	23	1	-	1	-	-	2	-	6	-	-	1	-	1	1	2	8	-	1	62	109
	Moody AFB, GA	13	1	-	-	-	-	9	-	8	-	-	2	1	2	5	6	16	-	6	38	107
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Camp Lejeune, NC	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	2	-	-	9	15
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	-	8	12
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Robins AFB, GA	6	-	-	-	-	-	1	-	-	-	-	-	-	2	1	1	1	-	-	17	29
	Seymour Johnson AFB, NC	12	-	-	-	-	-	1	-	2	-	-	2	-	-	-	-	3	1	1	13	35
	Shaw AFB, SC	2	1	-	-	-	-	1	-	-	-	-	4	-	4	-	-	5	1	1	11	30
	Tyndall AFB, FL	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	3	6

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

(Cont'd on page 7)

Laboratory Results—Through Current Surveillance Week 21

Table 3. Cumulative results by region and location for specimens collected during the 2015-2016 surveillance year

(Cont'd from page 6)

Region*		A(H1N1)pdm09	A(H3N2)	A(H1N1)pdm09 & B	A(H1N1)pdm09 & Corona	A(H1N1)pdm09 & Para	A(H3N2) & B	B	B & Adeno	Adenovirus	*B. pertussis*	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Bacterial Coinfection	Non-Influenza Viral Coinfection	No Pathogen	Total
Region 5	Scott AFB, IL	5	-	-	-	-	-	1	-	2	-	-	-	1	-	1	-	1	-	-	20	31
	Wright-Patterson AFB, OH	15	-	-	-	-	-	2	-	3	-	-	-	1	1	1	1	4	-	-	31	59
Region 6	Altus AFB, OK	7	-	-	-	-	-	4	-	4	-	-	3	5	-	6	10	11	-	5	74	129
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	5	6
	Cannon AFB, NM	13	4	1	-	-	-	12	-	2	-	-	2	4	-	1	2	6	-	8	44	99
	Laughlin AFB, TX	1	5	-	-	-	-	2	-	2	-	-	1	-	-	-	2	3	-	-	9	25
	Little Rock AFB, AR	5	1	-	-	-	-	1	-	-	-	-	1	1	-	-	-	4	-	1	27	41
	Sheppard AFB, TX	8	-	-	-	-	-	32	-	10	-	-	3	3	3	2	5	21	-	6	101	194
	Tinker AFB, OK	4	-	-	-	-	-	3	-	6	-	-	1	-	1	7	7	7	1	7	51	95
	USCG New Orleans, LA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	1	-	-	-	-	-	1	-	2	-	-	-	2	-	1	-	2	-	-	46	55
Region 7	Ft Leavenworth, KS	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	9	11
	McConnell AFB, KS	5	-	-	-	-	-	4	-	1	-	-	1	-	2	2	-	7	1	-	36	59
	Offutt AFB, NE	19	2	-	-	-	-	5	-	2	-	-	2	2	-	3	1	6	-	-	79	121
Region 8	Ellsworth AFB, SD	16	2	-	-	-	-	2	-	3	-	-	1	4	1	7	2	1	-	5	44	88
	FE Warren AFB, WY	19	3	-	-	-	-	7	-	3	1	-	3	2	1	3	7	5	-	3	54	111
	Hill AFB, UT	38	6	-	-	-	-	33	-	3	-	-	2	3	1	-	2	13	1	1	121	224
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Minot AFB, ND	7	-	-	-	-	-	-	-	-	-	-	2	1	-	1	2	3	-	1	12	29
	Peterson AFB, CO	14	3	-	-	-	1	2	-	2	-	-	5	1	-	-	1	5	-	5	40	79
	USAF Academy, CO	-	-	-	-	-	-	1	-	-	-	-	-	-	-	4	-	1	-	-	12	18
Region 9	Beale AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	CGS Humboldt Bay, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Davis-Monthan AFB, AZ	4	8	-	-	-	-	1	-	-	-	-	4	-	-	-	-	1	-	1	17	36
	Edwards AFB, CA	1	-	-	-	-	-	1	-	-	-	-	1	-	-	-	1	1	-	-	8	13
	Luke AFB, AZ	30	24	-	-	-	-	21	-	3	-	-	-	9	1	1	9	6	-	10	53	167
	NH Twentynine Palms, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	19	2	-	-	-	-	4	-	6	-	-	3	-	-	7	4	8	-	8	85	146
	Travis AFB, CA	19	8	-	-	-	-	13	-	3	-	-	2	9	1	5	7	14	-	6	51	138
	USCG Island Alameda, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Vandenberg AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	11	14
Region 10	Fairchild AFB, WA	6	1	-	-	-	-	6	-	1	-	-	-	1	-	-	-	2	-	-	16	33
	JB Lewis-McChord, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Mt Home AFB, ID	1	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	8	11
	NH Bremerton, WA	44	7	-	-	-	-	57	-	5	-	-	2	2	2	12	6	15	1	12	80	245
Total		635	103	1	1	1	1	367	1	161	1	2	85	85	55	108	129	271	16	117	2103	4243

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

88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Molecular Sequence Analysis Report

USAFSAM Epidemiology Laboratory Service

This is the eighth USAFSAM influenza sequence surveillance report for the 2015-2016 influenza season and includes 93 specimens collected between 9 December 2015 and 8 March 2016. USAFSAM sentinel sites submitted specimens from which 87 of these sequences were determined, while the remaining six sequences were data obtained from the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Thailand. Among the sequences analyzed for this report, 55 (59.1%) were influenza A(H1N1)pdm09, 13 (14%) were influenza A(H3N2), eight (8.6%) were influenza B/Victoria, and 17(18.3%) were influenza B/Yamagata.

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 potentially contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

		A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata
CONUS	**Alabama,** Maxwell AFB	2			
	Arizona, Luke AFB	4	7		
	Delaware, Dover AFB	4			
	Georgia, Moody AFB	3			
	Illinois, Scott AFB	1			
	Kansas, McConnell AFB				1
	Kentucky, Ft Campbell	3	1	1	1
	Maryland, JB Andrews	3		1	
	Maryland, NCRM – Walter Reed NMMC	2			
	Massachusetts, Hanscom AFB	1			
	New Jersey, JB McGuire-Dix-Lakehurst	2			
	New Mexico, Cannon AFB				1
	New York, USMA – West Point	9			1
	North Carolina, Ft Bragg			1	
	Ohio, Wright-Patterson AFB	4			1
	Oklahoma, Altus AFB	1			
	Oklahoma, Tinker AFB	1			
	South Carolina, Shaw AFB	2			
	Texas, Laughlin AFB				1
	Utah, Hill AFB	4			7
	Virginia, JB Langley-Eustis	1			1
	Virginia, NMC Portsmouth	1			
	Washington, NH Bremerton	4		1	2
	Wyoming, FE Warren AFB	1			
OCONUS	**Alaska,** Eielson AFB	1			
	Alaska, JB Elmendorf-Richardson				1
	Germany, Vilseck AHC	1			
	Italy, USAG Vicenza		1		
	Japan, Kadena AB		1		
	Japan, Yokota AB		1		
	Thailand, AFRIMS		2	4	
TOTAL		**55**	**13**	**8**	**17**

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 1].

- The A(H1N1)pdm09 specimens characterized for this report exhibited an overall protein homology of 96.5-96.9% compared to the 2015-2016 influenza vaccine component, A/California/07/2009-like virus.

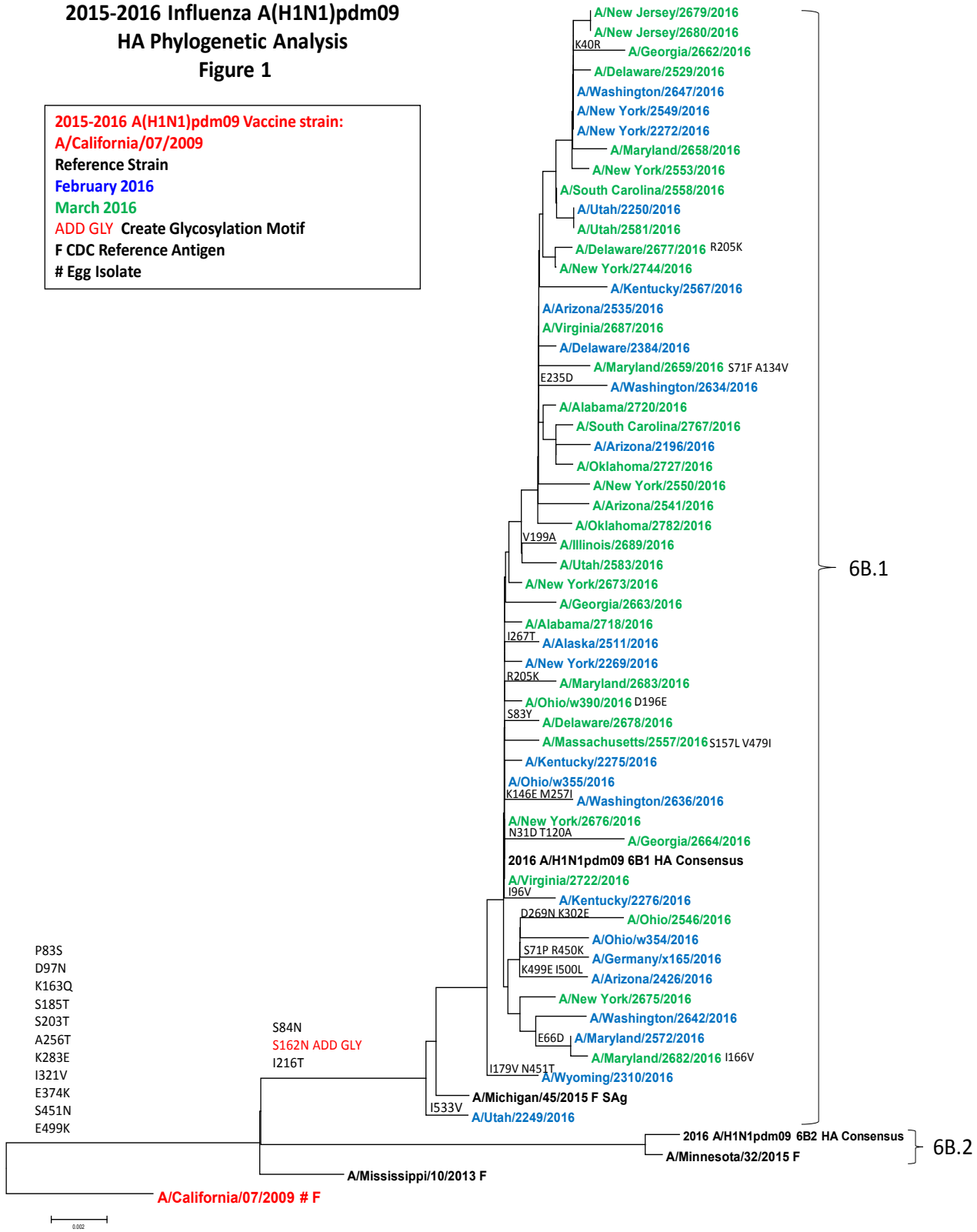
- All of the A(H1N1)pdm09 viruses sequenced for this report contain mutations consistent with one of the circulating subgroups, referred as group 6B. This clade has recently been divided into two subclades, 6B.1 (distinguished by the mutations S162N and I216T) and 6B.2 (distinguished by the mutations V152T, V173I, E491G, and D501E). All of the influenza A(H1N1)pdm09 specimens sequenced for this report were in subgroup 6B.1.

- 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 specimens characterized in this report, one mutation, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif.

- Of the 37 mutations present in the A(H1N1)pdm09 specimens, 13 occurred at predicted antigenic sites and two at the receptor binding site.[2,5]

2015-2016 Influenza A(H1N1)pdm09 HA Phylogenetic Analysis Figure 1

2015-2016 A(H1N1)pdm09 Vaccine strain:
A/California/07/2009
Reference Strain
February 2016
March 2016
ADD GLY Create Glycosylation Motif
F CDC Reference Antigen
Egg Isolate



Influenza A(H3N2)

- The influenza A(H3N2) sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from a previous vaccine strain, A/Texas/50/2012-like virus [Figure 2].

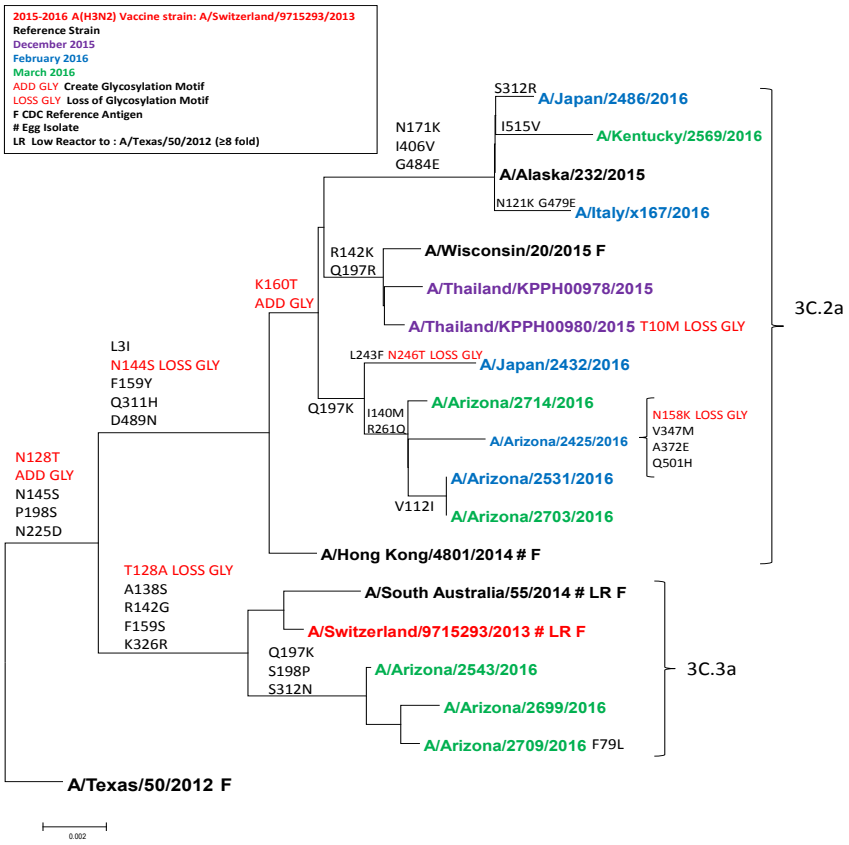
- The A(H3N2) specimens characterized for this report exhibited an overall protein homology of 96.4-98.7% compared to the 2015-2016 influenza vaccine component, A/Switzerland/9715293/2013-like virus.

- All of the influenza A(H3N2) specimens sequenced for this report were in clade 3C. Ten of the influenza A(H3N2) sequences classified as subclade 3C.2a and three classified as subclade 3C.3a.

- Among the influenza A(H3N2) specimens characterized in this report, five mutations: T10M (threonine to methionine), T128A (threonine to alanine), and N144S (asparagine to serine), and N158K (asparagine to lysine), and N246T (asparagine to threonine) 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 32 mutations present in the A(H3N2) specimens, 11 occurred at predicted antigenic sites and three at the receptor binding site.[2,5]

2015-2016 Influenza A(H3N2)
HA Phylogenetic Analysis
Figure 2



Influenza B

- The influenza B isolates are characterized in lineage specific; neighbor-joining phylogenetic trees with reference strains and are rooted from the reference strain B/Fujian Gulou/1272/2008 for B/Victoria specimens [Figure 3] and from the previous reference strain B/Massachusetts/02/2012-like virus for B/Yamagata specimens [Figure 4].

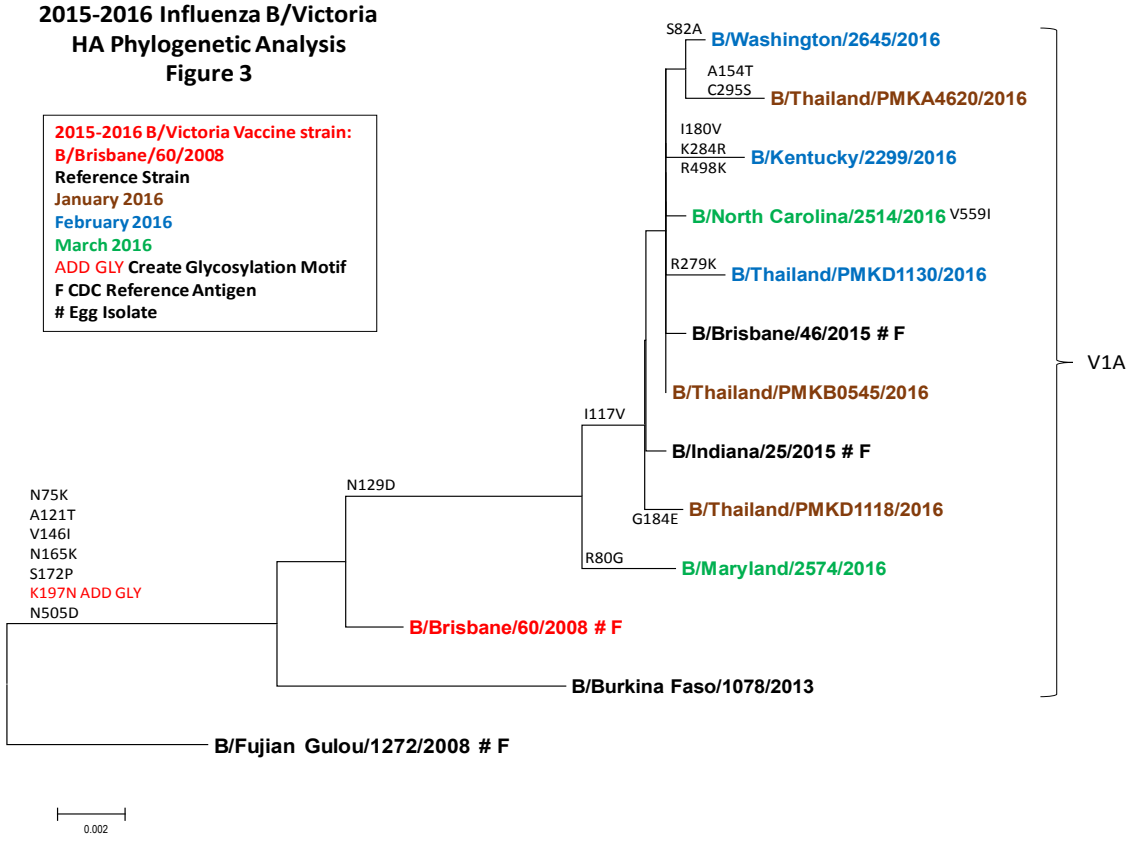
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.[1] Eight (32%) of the 25 influenza B viruses characterized in this report fall into the Victoria lineage, while the other 17 (68%) fall into the Yamagata lineage.

- The influenza B/Victoria specimens characterized for this report exhibited a protein homology of 98.8-99.3% when compared to the 2015-2016 B/Victoria vaccine component, B/Brisbane/60/2008-like virus, while the influenza B/Yamagata specimens exhibited a protein homology of 98.8-99.1% when compared to the 2015-2016 B/Yamagata vaccine strain, B/Phuket/3073/2013-like virus.

- All of the influenza B/Victoria specimens classify into clade V1A, while all of the influenza B/Yamagata specimens classify into clade Y3.

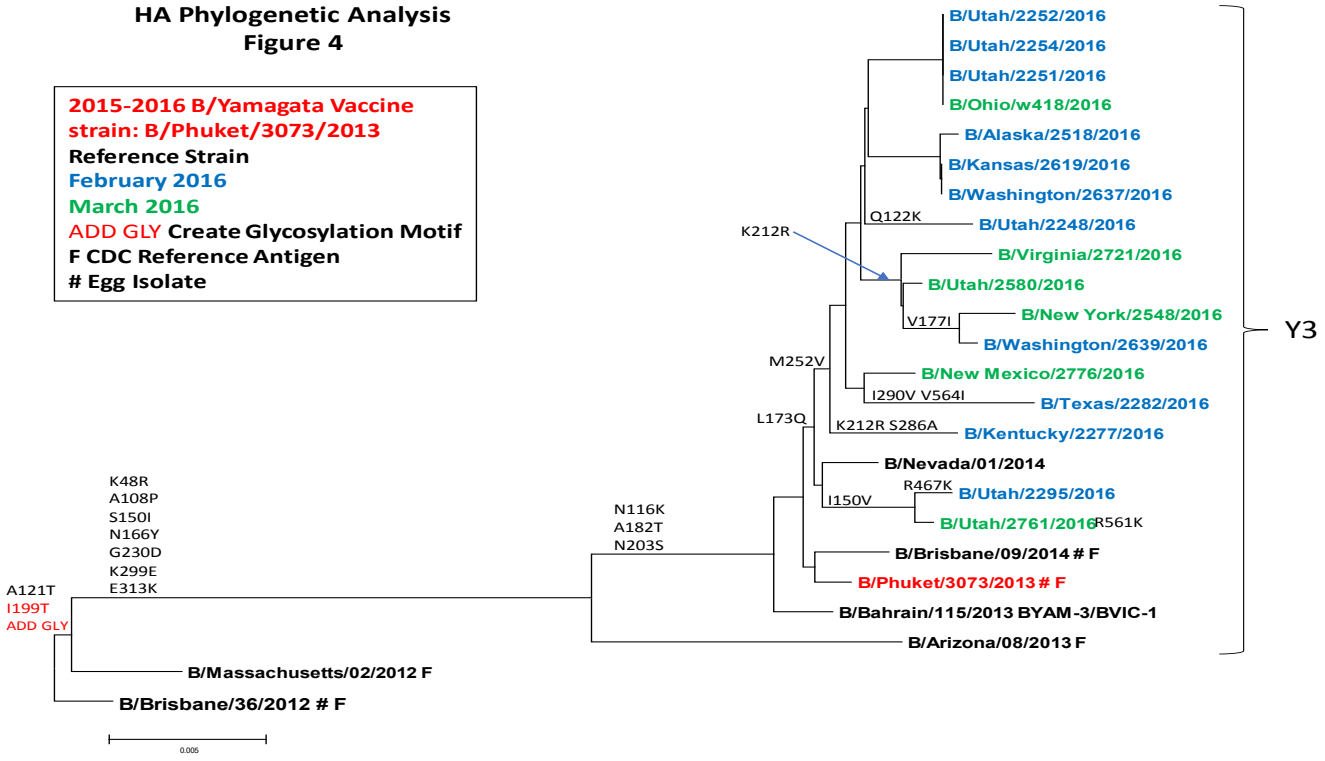
- Two mutations, one in each lineage, were capable of creating a glycosylation motif. For the influenza B/Victoria specimens, this was K197N (lysine to asparagine) and for the influenza B/Yamagata specimens, it was I199T (isoleucine to threonine).

2015-2016 Influenza B/Victoria HA Phylogenetic Analysis
Figure 3



88ABW-2015-5508 and PA email guidance dated 10 November 2015.

2015-2016 Influenza B/Yamagata HA Phylogenetic Analysis
Figure 4



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USAFSAM POCs for sequence data and analysis are:

[redacted]

USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the 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 at USAFSAM

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. 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 USAFSAM 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.

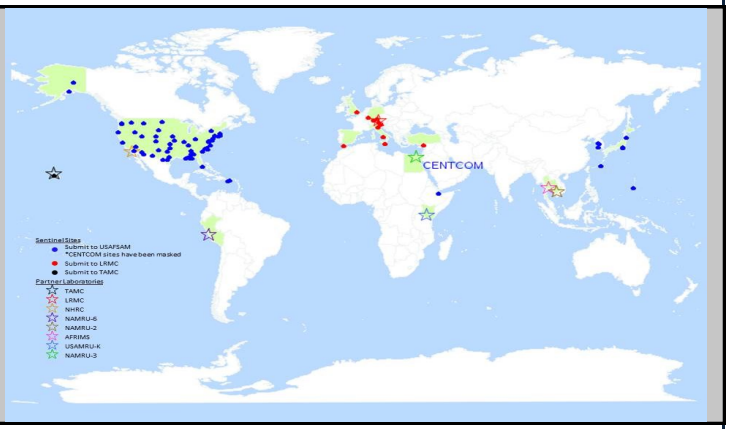
Available on our website (listed below) is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and a dashboard containing respiratory data for our sentinel sites.

Errata:

For Public Health Services
937-938-3196; DSN 798-3196

For Laboratory Services
937-938-4140; DSN 798-4140

USAFSAM.PHRFlu@us.af.mil



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.

88ABW-2015-5508 and PA email guidance dated 10 November 2015.