USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2015-2016

Cumulative Results

Locations	69
Collected	1,221
Tested	1,160

Influenza A	**23**
A(H1N1)pdm09	17
A(H3N2)	6
A/not subtyped	0

Influenza B*	**12**
B	12

Other Respiratory Pathogens	**373**
Adenovirus	63
Bordetella pertussis	1
Chlamydophila pneumoniae	0
Coronavirus	26
Human Metapneumovirus	8
Mycoplasma pneumoniae	29
Parainfluenza	68
RSV	37
Rhino/Enterovirus	96
Non-influenza Viral Coinfections	34
Non-influenza Bacterial Coinfections	11
-*C. pneumo* coinfections (2)	
-*C. pneumo & M. pneumo (1)*	
-*M. pneumo* coinfections (5)	
-*B. pertussis* coinfections *(3)*	

Lab data are current as of 19 January 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

3 - 16 January 2016 (Surveillance Weeks 1 & 2)

- During 3 - 16 January, a total of 167 specimens were collected and received from 46 locations. Results were finalized for 120 specimens from 42 locations. During Week 1, one influenza A(H1N1)pdm09 was identified. Six influenza A(H1N1)pdm09 and one influenza B viruses were identified during Week 2.
- During Week 1 (3 - 9 January 2016), influenza activity increased slightly in the United States. **Viral Surveillance:** The most frequently identified influenza virus type reported during Week 1 was influenza A, with influenza A (H1N1)pdm09 viruses predominating. **Pneumonia and Influenza (P&I) Mortality:** The proportion of deaths attributed to P&I was below their system-specific epidemic threshold. **Influenza-Associated Pediatric Deaths:** One influenza-associated pediatric death was reported. **Influenza-Associated Hospitalizations:** A cumulative rate for the season of 1.5 laboratory-confirmed influenza-associated hospitalizations per 100,000 population was reported. **Outpatient Illness Surveillance:** The proportion of outpatient visits for influenza-like illness (ILI) was 2.0%, which is below the national baseline of 2.1%. **Geographic Spread of Influenza:** The geographic spread of influenza in Guam, Puerto Rico, and nine states were reported as regional; 11 states reported local activity; the U.S. Virgin Islands and 28 states reported sporadic activity; and the District of Columbia and two states reported no influenza activity (CDC FluView Summary, Cited 21 January 2016).

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

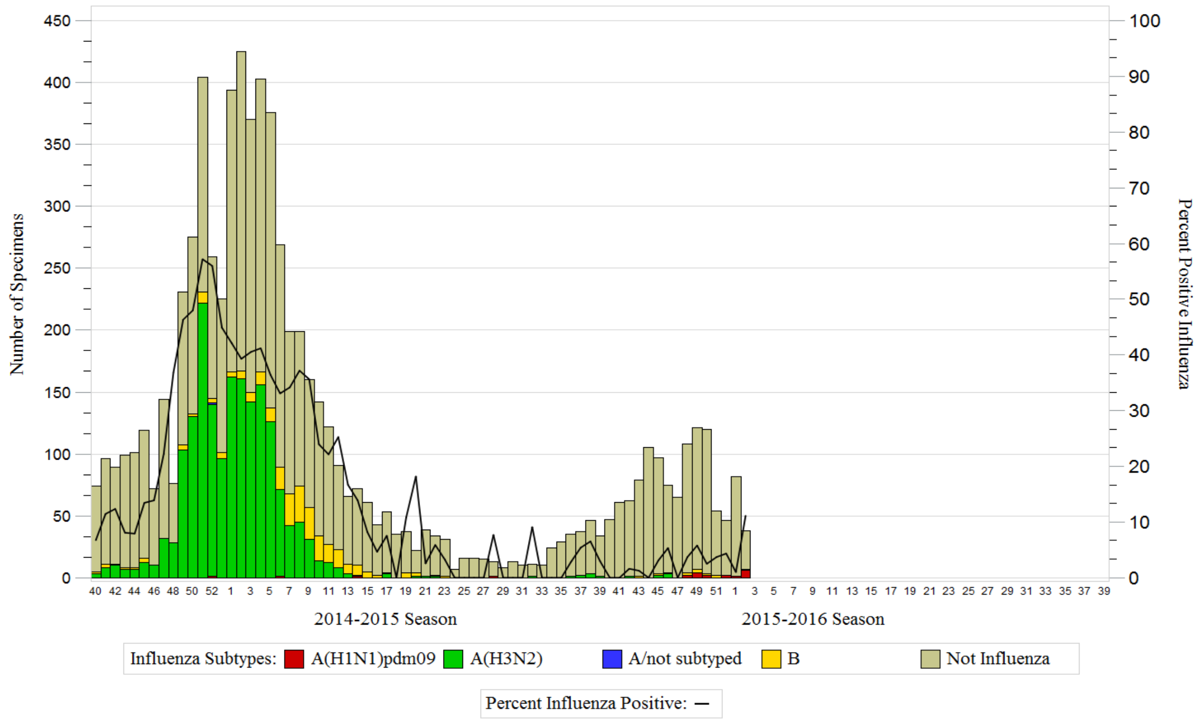
Region*		A(H1N1)pdm09	B	Adenovirus	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Rhino/Entero	Corona & RSV	hMNV & Rhino/Entero	No Pathogen	Total
Deployed	Country 2, Location A	1	-	-	-	-	-	-	-	-	-	-	-	-	1
PACOM	CFA Okinawa, Japan	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Kadena AB, Japan	-	-	-	-	-	1	-	-	-	-	-	-	-	1
	Yokota AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 1	Hanscom AFB, MA	-	-	1	-	-	-	-	-	-	-	-	-	1	2
	NHCNE Newport, RI	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 2	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	1	-	-	-	1	-	-	3	5
	USMA - West Point, NY	1	-	3	-	-	-	-	1	-	-	1	-	1	7
Region 3	Dover AFB, DE	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	JB Langley-Eustis, VA	-	-	2	-	-	-	-	2	-	-	-	-	-	4
	NMC Portsmouth, VA	-	-	3	-	-	-	-	-	-	-	-	-	-	3
Region 4	Columbus AFB, MS	-	-	1	-	-	-	-	-	-	-	-	-	1	2
	Eglin AFB, FL	1	-	-	-	-	-	-	-	1	-	-	-	2	4
	Ft Bragg, NC	-	-	1	-	1	-	-	-	-	-	-	-	4	6
	Ft Campbell, KY	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Hurlburt Field, FL	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	MacDill AFB, FL	-	-	-	-	-	-	1	-	-	-	-	-	-	1
	Maxwell AFB, AL	-	-	-	-	-	-	-	-	-	-	-	-	4	4
	Moody AFB, GA	-	-	1	-	1	-	-	1	-	-	-	1	1	5
	NH Camp Lejeune, NC	-	-	-	-	-	1	-	-	1	-	-	-	-	2
	Robins AFB, GA	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Seymour Johnson AFB, NC	-	-	-	1	-	-	-	-	-	-	-	-	1	2
	Shaw AFB, SC	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 5	Wright-Patterson AFB, OH	-	-	-	-	-	-	-	-	1	-	-	-	-	1
Region 6	Altus AFB, OK	-	-	1	-	-	-	-	-	1	-	-	-	3	5
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Cannon AFB, NM	-	-	-	-	-	-	-	-	1	-	-	-	-	1
	Little Rock AFB, AR	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Sheppard AFB, TX	1	-	-	1	-	-	-	-	-	-	-	-	1	3
	Tinker AFB, OK	-	-	-	-	-	-	-	1	-	-	-	1	4	6
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	2	2
Region 7	McConnell AFB, KS	-	-	-	-	-	-	-	-	2	-	-	-	2	4
	Offutt AFB, NE	1	-	-	-	-	-	-	-	-	-	-	-	3	4
Region 8	Ellsworth AFB, SD	-	-	-	-	1	-	1	-	-	-	-	-	1	3
	FE Warren AFB, WY	-	-	-	1	-	-	-	1	-	-	-	-	1	3
	Hill AFB, UT	1	-	-	-	1	-	-	1	-	-	-	-	1	4
	Peterson AFB, CO	-	-	-	-	-	-	-	-	-	1	-	-	5	6
Region 9	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Nellis AFB, NV	-	-	-	-	-	-	-	-	-	-	1	-	1	2
	Travis AFB, CA	1	1	-	-	2	-	-	-	1	-	-	-	4	9
Region 10	Mt Home AFB, ID	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Total		7	1	13	3	6	3	2	7	8	2	2	2	64	120

**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.

Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2014-2015 surveillance year and through Week 2 of the 2015-2016 surveillance year

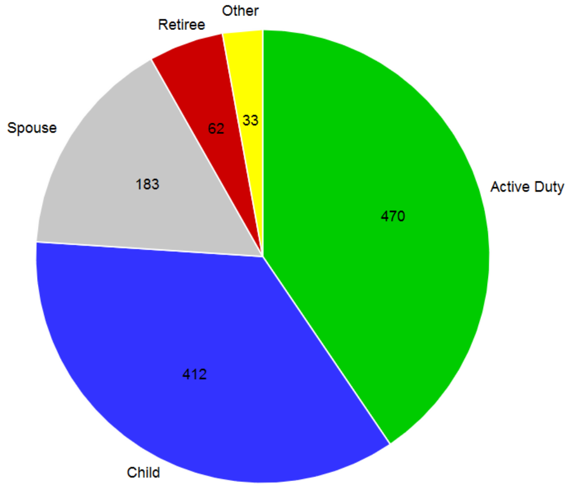


Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

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

Age Group	Frequency	Percent
0-5	265	22.84
6-9	58	5.00
10-17	91	7.84
18-24	210	18.10
25-44	398	34.31
45-64	106	9.14
65+	32	2.76

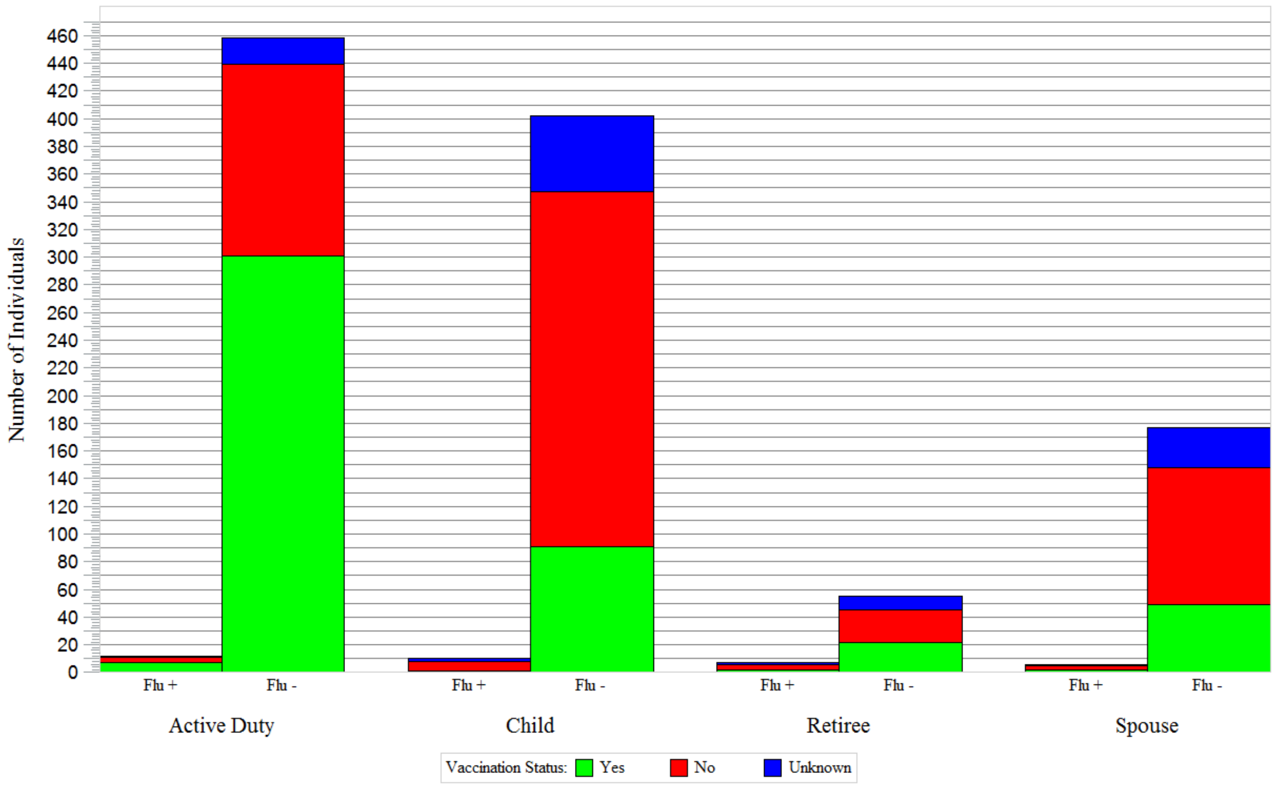
Graph 2. ILI by beneficiary status for the 2015-2016 surveillance year through Week 2



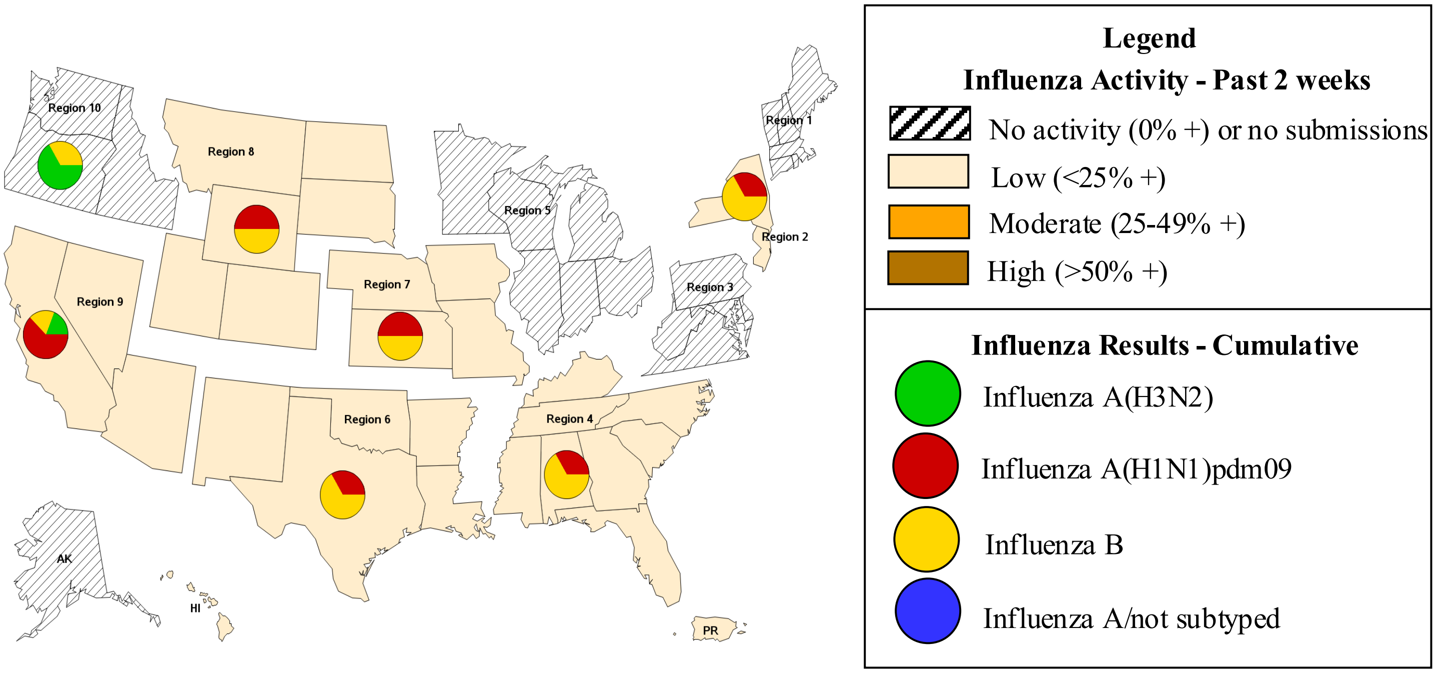
Demographic Summary

Of 1,160 ILI cases, 470 are service members (40.5%), 412 are children (35.5%), 183 are spouses (15.8%), and 95 (8.2%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=1,160) is 23 (range 0, 93).

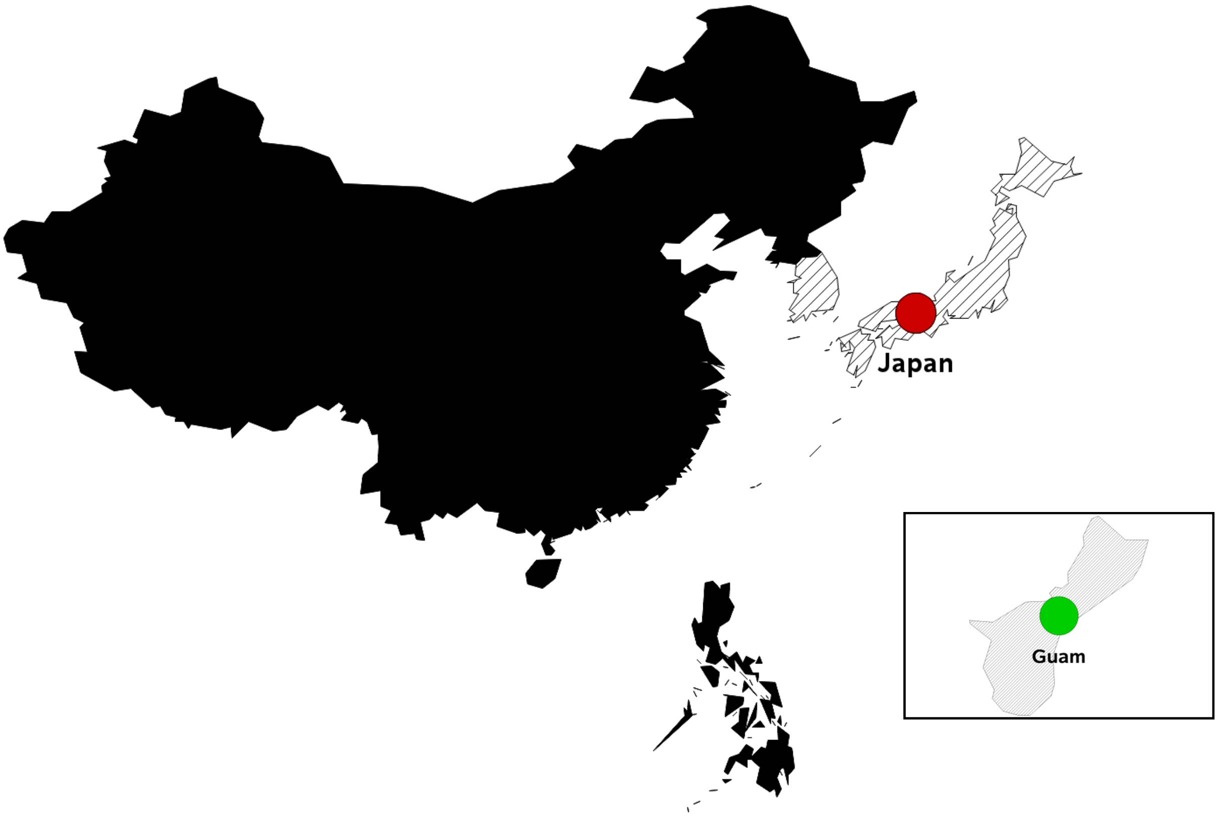
Graph 3. Vaccination status by beneficiary type for the 2015-2016 surveillance year through Week 2



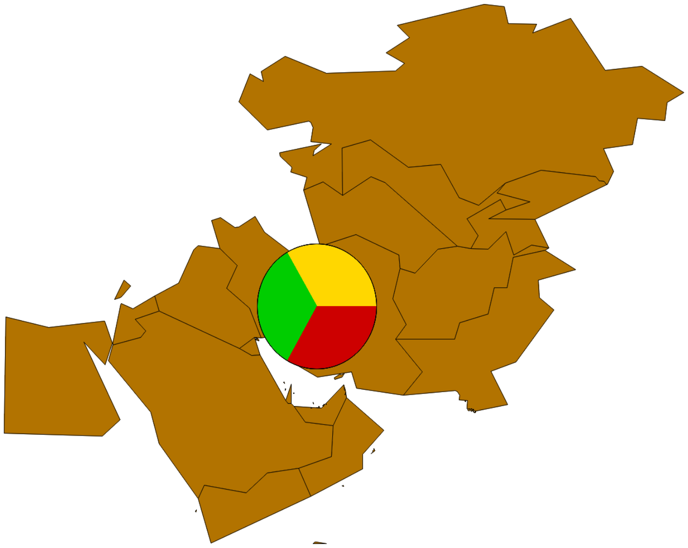
Map 1. Influenza subtypes and activity level by region for the 2015-2016 surveillance year through Week 2



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



Map 3. Influenza subtypes and activity level for CENTCOM for the 2015-2016 surveillance year through Week 2*



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 these areas that subsequently tested positive for influenza, flu activity level appears inflated.

Laboratory Results—Through Current Surveillance Week 2

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

Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	*B. pertussis*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	Non-Influenza Bacterial Coinfection	No Pathogen	Total
Deployed	**Country 2, Location A**	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
PACOM	**CFA Okinawa, Japan**	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Eielson AFB, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	4	5
	JB Elmendorf-Richardson, AK	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	JR Marianas - Andersen AFB, Guam	-	1	-	-	-	-	-	-	-	-	-	-	1	1	3
	Kadena AB, Japan	-	-	-	-	-	-	-	1	-	-	2	-	-	10	13
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	1	2	-	-	4	7
	Osan AB, South Korea	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Yokota AB, Japan	1	-	-	-	-	-	-	1	1	1	-	1	-	14	19
Region 1	**Hanscom AFB, MA**	-	-	-	2	-	-	-	-	2	-	-	-	-	11	15
	NHCNE Newport, RI	-	-	-	-	-	-	-	-	-	-	1	-	-	4	5
	USCG Academy, CT	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 2	**Ft Drum, NY**	-	-	-	-	-	-	-	-	-	-	2	-	-	3	5
	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	-	-	2	-	-	4	1	-	9	16
	USMA - West Point, NY	1	-	2	7	-	2	-	2	1	2	1	2	2	51	73
Region 3	**Dover AFB, DE**	-	-	-	-	-	-	-	-	-	-	-	-	-	6	6
	JB Anacostia-Bolling, DC	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	JB Andrews, MD	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1
	JB Langley-Eustis, VA	-	-	-	5	-	2	-	-	3	6	2	1	-	7	26
	NCRM - Walter Reed NMMC, MD	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NMC Portsmouth, VA	-	-	-	4	-	1	-	5	1	1	2	-	1	14	29
Region 4	**CGS Mobile, AL**	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Columbus AFB, MS	-	-	-	1	-	-	-	-	-	-	2	-	-	12	15
	Eglin AFB, FL	1	-	-	4	-	-	-	-	4	2	3	-	-	16	30
	Ft Bragg, NC	-	-	-	2	-	1	1	-	-	3	-	-	1	17	25
	Ft Campbell, KY	-	-	-	-	-	1	-	-	2	-	3	-	-	15	21
	Hurlburt Field, FL	-	-	-	-	-	-	-	-	-	-	-	2	-	7	9
	Keesler AFB, MS	-	-	-	-	-	-	-	1	-	-	2	-	-	20	23
	MacDill AFB, FL	-	-	-	-	-	-	-	-	2	1	-	-	-	1	4
	Maxwell AFB, AL	-	-	-	1	-	-	-	-	1	2	1	-	-	19	24
	Moody AFB, GA	-	-	2	5	-	1	1	2	2	3	7	2	-	13	38
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	1	-	1	1	-	-	3	6
	NH Jacksonville, FL	-	-	-	2	-	-	-	-	-	1	-	-	-	5	8
	Robins AFB, GA	-	-	-	-	-	-	-	1	1	1	-	-	-	7	10
	Seymour Johnson AFB, NC	-	-	-	1	-	1	-	-	-	-	2	1	1	7	13
	Shaw AFB, SC	-	-	-	-	-	1	-	2	-	-	4	1	1	7	16
	Tyndall AFB, FL	-	-	-	-	-	1	-	-	-	-	-	-	1	1	3
Region 5	**Scott AFB, IL**	-	-	-	2	-	-	-	-	1	-	1	-	-	15	19
	Wright-Patterson AFB, OH	-	-	-	1	-	-	-	-	-	-	3	-	-	3	7
Region 6	**Altus AFB, OK**	-	-	-	3	-	1	-	-	2	-	2	2	-	26	36
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Cannon AFB, NM	-	-	-	1	-	-	-	-	-	-	2	-	-	13	16
	Laughlin AFB, TX	-	-	-	-	-	1	-	-	-	-	-	-	-	2	3
	Little Rock AFB, AR	-	-	-	-	-	1	-	-	-	-	-	-	-	9	10
	Sheppard AFB, TX	1	-	2	3	-	1	1	3	1	-	5	2	-	41	60
	Tinker AFB, OK	-	-	-	1	-	-	-	1	5	2	3	5	1	22	40
	Vance AFB, OK	-	-	-	1	-	-	-	-	1	-	1	-	-	29	32
Region 7	**Ft Leavenworth, KS**	-	-	1	-	-	-	-	-	-	-	1	-	-	8	10
	McConnell AFB, KS	-	-	-	1	-	-	-	2	2	-	6	-	1	24	36
	Offutt AFB, NE	1	-	-	2	-	-	-	-	3	-	1	-	-	28	35
Region 8	**Ellsworth AFB, SD**	-	-	-	1	-	-	1	1	4	-	-	2	-	17	26
	FE Warren AFB, WY	-	-	-	-	1	1	-	-	3	1	2	-	-	16	24
	Hill AFB, UT	1	-	1	1	-	-	2	1	-	1	6	-	-	34	47
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Minot AFB, ND	-	-	-	-	-	-	-	-	1	-	1	-	-	2	4
	Peterson AFB, CO	-	-	-	1	-	3	-	-	-	-	1	1	-	15	21
	USAF Academy, CO	-	-	-	-	-	-	-	-	4	-	1	-	-	9	14
Region 9	**Davis-Monthan AFB, AZ**	-	-	-	-	-	1	-	-	-	-	-	-	-	7	8
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	5	5
	Luke AFB, AZ	-	-	-	-	-	-	-	-	-	-	-	-	-	7	7
	Nellis AFB, NV	9	2	2	6	-	3	-	-	7	3	5	4	-	38	79
	Travis AFB, CA	1	1	1	2	-	2	2	1	4	2	7	3	-	27	53
	USCG Island Alameda, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	6	6
Region 10	**Fairchild AFB, WA**	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	JB Lewis-McChord, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Mt Home AFB, ID	-	-	-	-	-	-	-	-	-	-	-	-	-	6	6
	NH Bremerton, WA	-	1	1	3	-	1	-	1	10	3	6	4	1	31	62
Total		17	6	12	63	1	26	8	29	68	37	96	34	11	752	1160

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

Molecular Sequence Analysis Report

USAFSAM Epidemiology Laboratory Service

This is the first report for the 2015-2016 season. Among the 11 specimens collected between 18 September to 2 December 2015 from six different sentinel sites and subsequently analyzed by USAFSAM, two (18%) were influenza A (H1N1)pdm09 viruses, eight (73%) were influenza A(H3N2) viruses, and one (9%) was an influenza B/Yamagata virus.

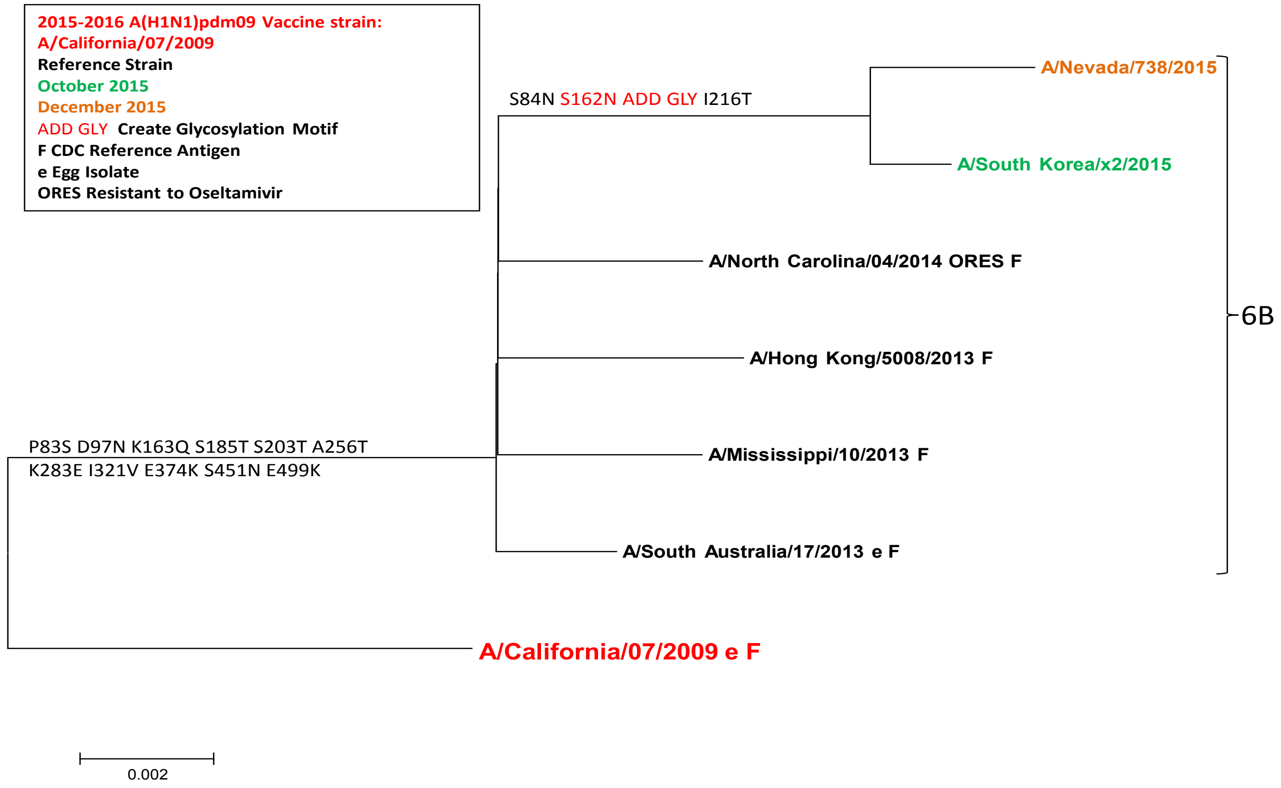
The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously 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/Yamagata
CONUS	**Alaska,** Eielson AFB		1	
	Kansas, McConnell AFB		1	
	Nevada, Nellis AFB	1		1
	Washington, NH Bremerton		5	
OCONUS	**Japan,** Yokota AB		1	
	South Korea, Brian Allgood ACH	1		
TOTAL		**2**	**8**	**1**

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 96.9% compared to the 2015-2016 influenza vaccine component, A/California/07/2009-like virus.
- Both of the A(H1N1)pdm09 viruses sequenced for this report contain mutations consistent with one of the circulating subgroup, referred as group 6B. Isolates of this group share two distinguishing mutations, K163Q (lysine to glutamine), and A256T (alanine to threonine).
- 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 14 mutations present in the A(H1N1)pdm09 specimens, five occurred at predicted antigenic sites and one at the receptor binding site.[2,5]

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



Influenza A(H3N2)

- The influenza A(H3N2) isolates are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the previous vaccine, A/Victoria/361/2011-like virus [Figure 2].

- The influenza A(H3N2) specimens characterized for this report exhibited an overall protein identity of 96.9-99.6% as compared to the influenza A(H3N2) component of the 2015-2016 vaccine formulation, A/Switzerland/9715293/2013-like virus.

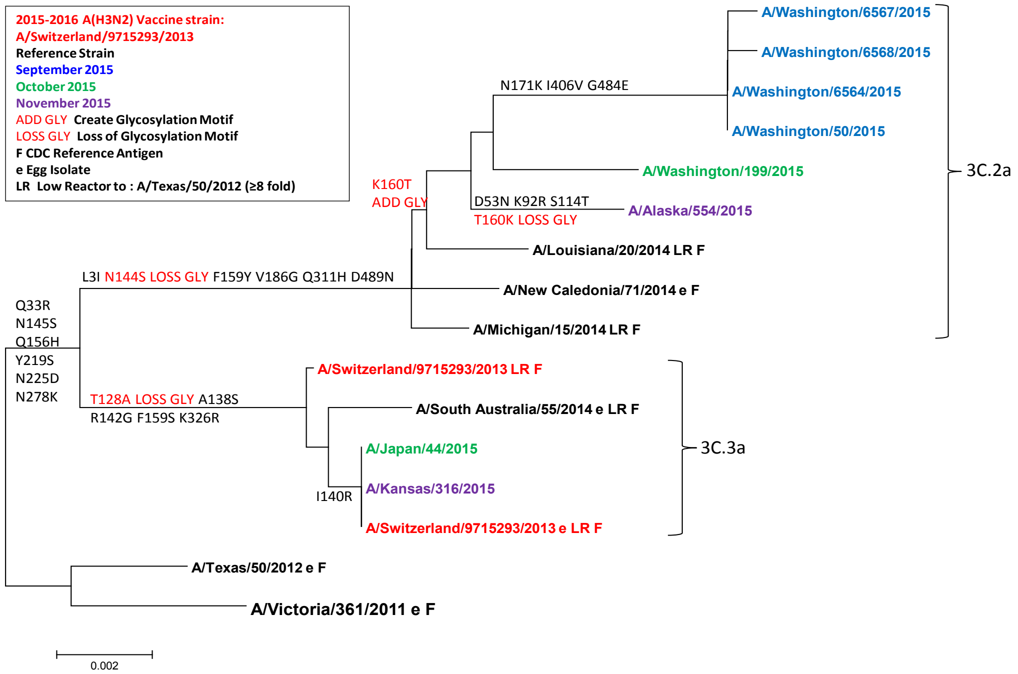
- One specimen, A/Kansas/316/2015, was tested as an original sample rather than a cultured isolate because the specimen returned a positive PCR result but yielded no viral growth, and the patient was vaccinated five days prior to specimen collection. The sequence for this specimen was a 99.9% nucleotide match and a 99.6% amino acid match to A/Switzerland/9715293/2013, and was therefore likely a collection of the influenza A(H3N2) LAIV component. One other specimen, A/Japan/44/2015, was also a 99.9% nucleotide and 99.6% amino acid match to A/Switzerland/9715293/2013, but a vaccination date for that patient is not available at this time.

- Based on the mutations observed, all of the influenza A(H3N2) viruses analyzed belong to clade 3C. Six of the specimens can be further classified as clade 3C.2a and two as clade 3C.3a.

- For the influenza A(H3N2) specimens characterized in this report, three mutations were observed that could cause a loss of a glycosylation motif: T128A (threonine to alanine), N144S (asparagine to serine), and T160K (threonine to lysine). One mutation, K160T (lysine to threonine), was observed that could cause a gain of a glycosylation motif.

- Of the 24 mutations present in the influenza A(H3N2) specimens, 11 occurred at predicted antigenic sites and three at the receptor binding site.[2,5]

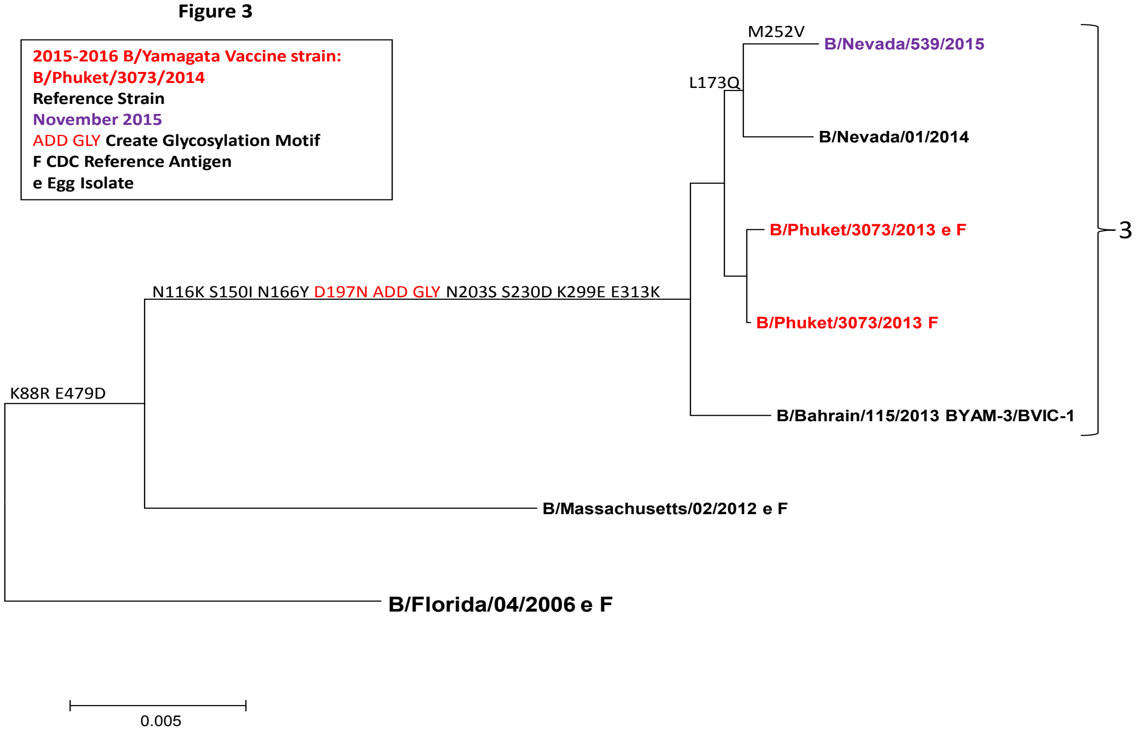
Recent 2015-2016 Influenza A(H3N2) HA Phylogenetic Analysis
Figure 2



Influenza B

- The influenza B isolate is characterized in a lineage specific, neighbor-joining phylogenetic tree with reference strains and is rooted from a previous vaccine, B/Florida/04/2006-like virus [Figure 3].
- 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]. The influenza B virus characterized in this report falls into the Yamagata lineage.
- The influenza B/Yamagata specimen characterized for this report exhibited a protein homology of 99.1% when compared to the 2015-2016 influenza B/Yamagata vaccine strain, B/Phuket/3073/2013-like virus.
- This influenza B/Yamagata specimen classifies into group 3 and contains one mutation, D197N (aspartic acid to asparagine), that could cause a gain of a glycosylation motif.

Recent 2015-2016 Influenza B/Yamagata HA
Phylogenetic Analysis
Figure 3



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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-6 (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 the Division of Global Emerging Infections Surveillance and Response System (GEIS) Operations, a Division of the Armed Forces Health Surveillance Center (AFHSC).

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 80 sentinel sites (including deployed locations) and many non-sentinel sites (please see map on the left). Unique sentinel sites include three DoD overseas medical research laboratories (AFRIMS, NAMRU-6, USAMRU-K) and the US Army Public Health Command Region South (PHCR-S). These sites collect specimens from local residents in surrounding countries that may not otherwise be covered in existing surveillance efforts.

Since the 2006-2007 season, Landstuhl Regional Medical Center (LRMC) has served EUCOM as a USAFSAM contributing laboratory. The initiative seeks to provide more timely results and efficient transport of specimens.

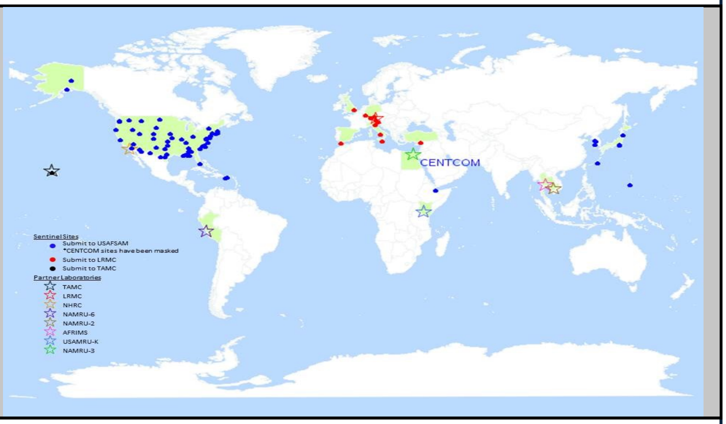
For an expanded view of this report, visit our website. Also available on the website is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and an overview of historical data. Please visit the AFHSC/GEIS website for an overview of influenza surveillance at all collaborating organizations.

Errata:

DoD Global, Laboratory-Based,
Influenza Surveillance Program
https://gumbo2.wpafb.af.mil/
epi-consult/influenza/index.cfm

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

For Laboratory Services
937-938-3163; DSN 798-3163



Collaborating Partners

In addition to all participating DoD military sentinel sites, several collaborating partners (described above) may be further understood by reviewing the partner's website.

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