USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2015-2016

Cumulative Results

Locations	80
Collected	4,495
Tested	4,444

Influenza A	**746**
A(H1N1)pdm09	637
A(H1N1)pdm09 & B	1
A(H1N1)pdm09 & Coronavirus	1
A(H1N1)pdm09 & Parainfluenza	1
A(H3N2)	105
A(H3N2) & B	1

Influenza B*	**377**
B	376
B & Adenovirus	1

Other Respiratory Pathogens	**1,122**
Adenovirus	164
Bordetella pertussis	1
Chlamydophila pneumoniae	2
Coronavirus	88
Human Metapneumovirus	87
Mycoplasma pneumoniae	58
Parainfluenza	125
RSV	130
Rhinovirus/Enterovirus	323
Non-influenza Viral Coinfections	127
Non-influenza Bacterial Coinfections	17
-B. pertussis (3)	
-B. pertussis & M. pneumo (1)	
-C. pneumo (2)	
-C. pneumo & M. pneumo (1)	
-M. pneumo (10)	

Lab data are current as of 6 September 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
7 August - 3 September 2016 (Surveillance Weeks 32 - 35)

- During 7 August - 3 September 2016, a total of 39 specimens were collected and received from 25 locations. Results were finalized for 37 specimens from 25 locations. During Week 32, one influenza B virus was identified. The percent positive for Week 32 was 14.3% while Weeks 33, 34, and 35 were 0%. The influenza percent positive for the season is currently 25%.

- In preparation for the 2016-2017 influenza surveillance season, we are holding five Defense Collaboration Service (DCS) training sessions for our sentinel sites. Training information:

  https://conference.apps.mil/webconf/884b6962688d4a371c7f182dd8396fa9

  - Tuesday, 20 Sep 16 / 0800-0900 EST / 937-255-0118 / DSN: 785-0118
  - Tuesday, 20 Sep 16 / 1500-1600 EST / 937-255-0118 / DSN: 785-0118
  - Wednesday, 21 Sep 16 / 0800-0900 EST / 937-255-0109 / DSN: 785-0109
  - Wednesday, 21 Sep 16 / 1500-1600 EST / 937-255-0109 / DSN: 785-0109
  - Wednesday, 21 Sep 16 / 1700-1800 EST / 937-255-0109 / DSN: 785-0109

- This report contains the monthly supplemental EUCOM report for surveillance through 3 September 2016. See page 13 for more details.

- This report contains the 11th molecular sequence analysis report and includes 165 specimens collected between 8 January 2016 and 17 May 2016. See page 8 for further details.

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1. Results by region and location for specimens collected during Weeks 32-35

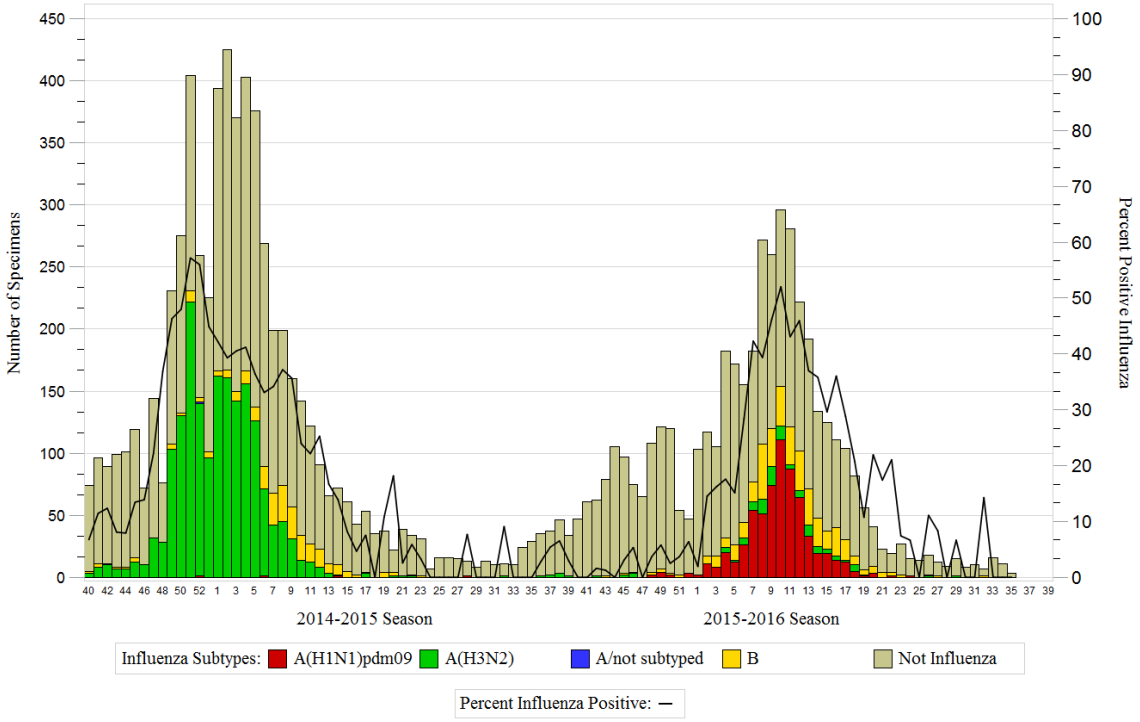
Region*		B	hMNV	*M. pneumoniae*	Parainfluenza	Rhinovirus/ Enterovirus	No Pathogen	Total
PACOM	Eielson AFB, AK	-	-	-	-	-	1	1
	Yokota AB, Japan	-	-	1	-	1	-	2
Region 2	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	1	1	2
	USMA - West Point, NY	-	-	-	1	2	-	3
Region 3	JB Langley-Eustis, VA	-	-	-	-	-	1	1
Region 4	CGS Mobile, AL	-	-	-	-	1	-	1
	Eglin AFB, FL	-	-	-	-	-	1	1
	Keesler AFB, MS	-	-	-	-	-	1	1
	Robins AFB, GA	-	-	-	-	-	1	1
	Shaw AFB, SC	-	-	-	-	1	-	1
Region 5	Scott AFB, IL	-	1	-	-	-	-	1
	Wright-Patterson AFB, OH	-	-	-	-	-	1	1
Region 6	Altus AFB, OK	-	-	-	-	1	-	1
	Cannon AFB, NM	-	-	-	-	1	-	1
	Sheppard AFB, TX	-	-	-	-	1	1	2
	Tinker AFB, OK	-	-	-	-	2	-	2
	Vance AFB, OK	-	-	-	-	1	-	1
Region 7	McConnell AFB, KS	-	-	-	-	-	1	1
	Offutt AFB, NE	-	-	-	-	1	1	2
Region 8	Hill AFB, UT	-	-	-	-	-	1	1
	Peterson AFB, CO	-	-	-	-	1	-	1
Region 9	Davis-Monthan AFB, AZ	-	-	-	-	1	1	2
	Nellis AFB, NV	1	-	-	-	1	-	2
	Travis AFB, CA	-	-	-	-	2	2	4
Region 10	Fairchild AFB, WA	-	-	-	-	1	-	1
Total		1	1	1	1	19	14	37

**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 35 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.

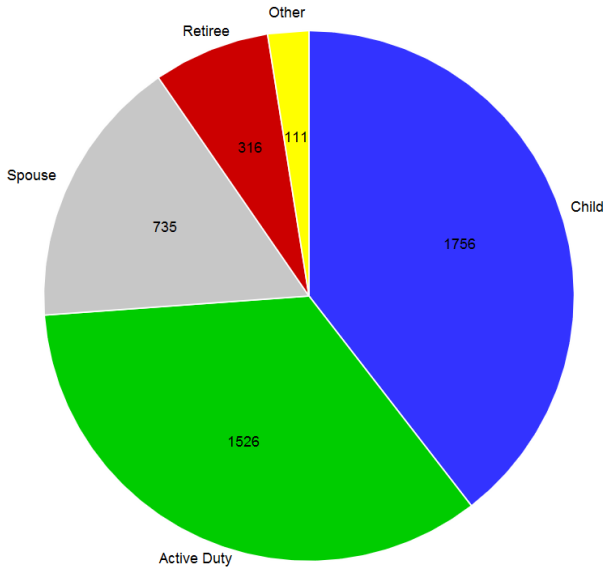
Table 2. ILI by age group for the 2015-2016 surveillance year through Week 35

Age Group	Frequency	Percent
0-5	1002	22.55
6-9	341	7.67
10-17	416	9.36
18-24	611	13.75
25-44	1429	32.16
45-64	523	11.77
65+	122	2.75

Demographic Summary

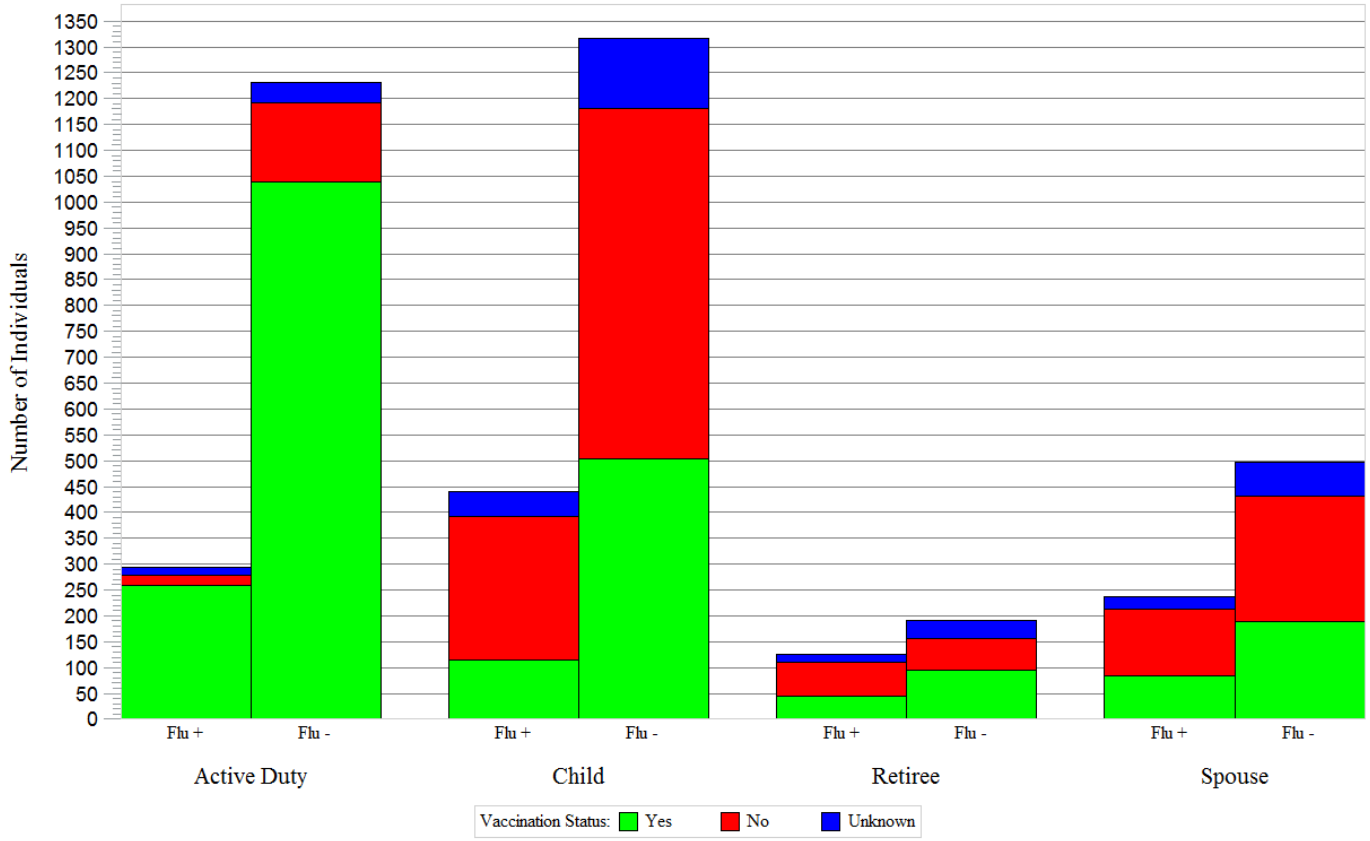
Of 4,444 ILI cases, 1,526 are service members (34.3%), 1,756 are children (39.5%), 735 are spouses (16.6%), and 427 (9.6%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=4,444) is 23 (range 0, 95).

Graph 2. ILI by beneficiary status for the 2015-2016 surveillance year through Week 35

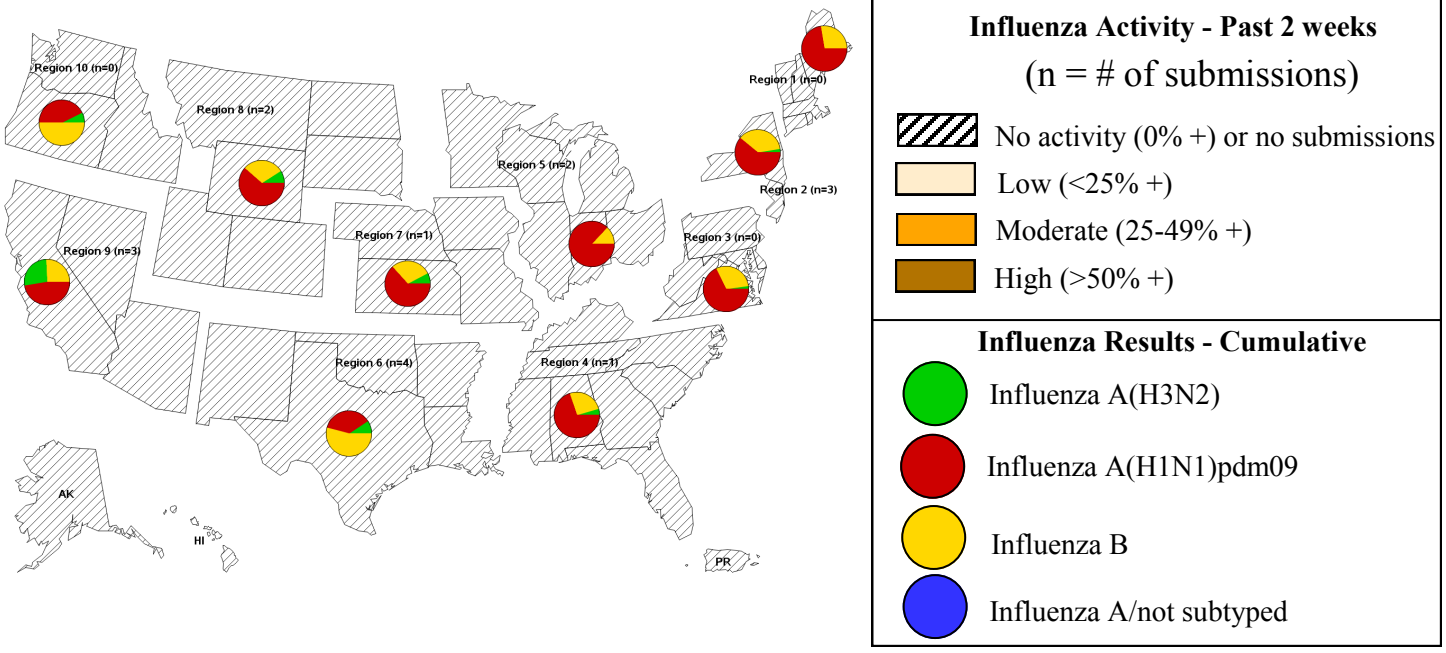


88ABW-2015-5508 and PA email guidance dated 10 November 2015.

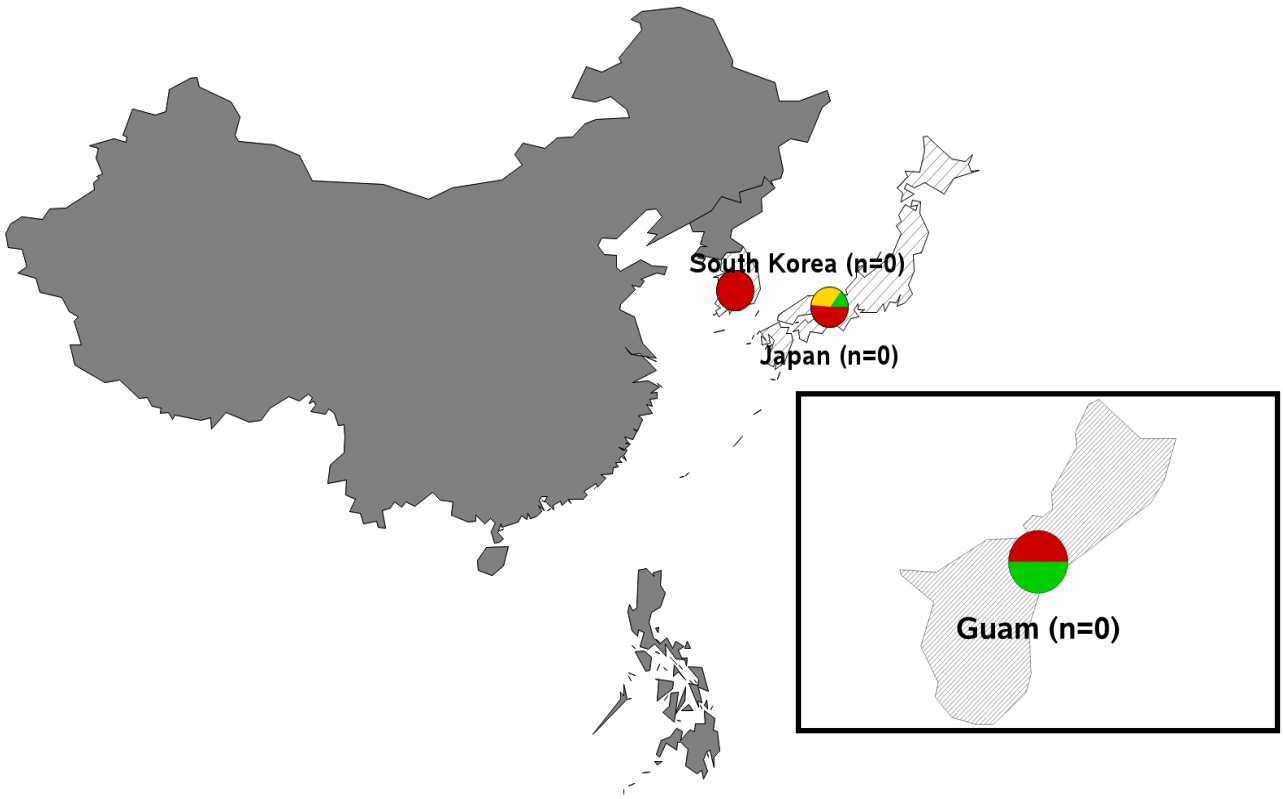
Graph 3. Vaccination status by beneficiary type for the 2015-2016 surveillance year through Week 35



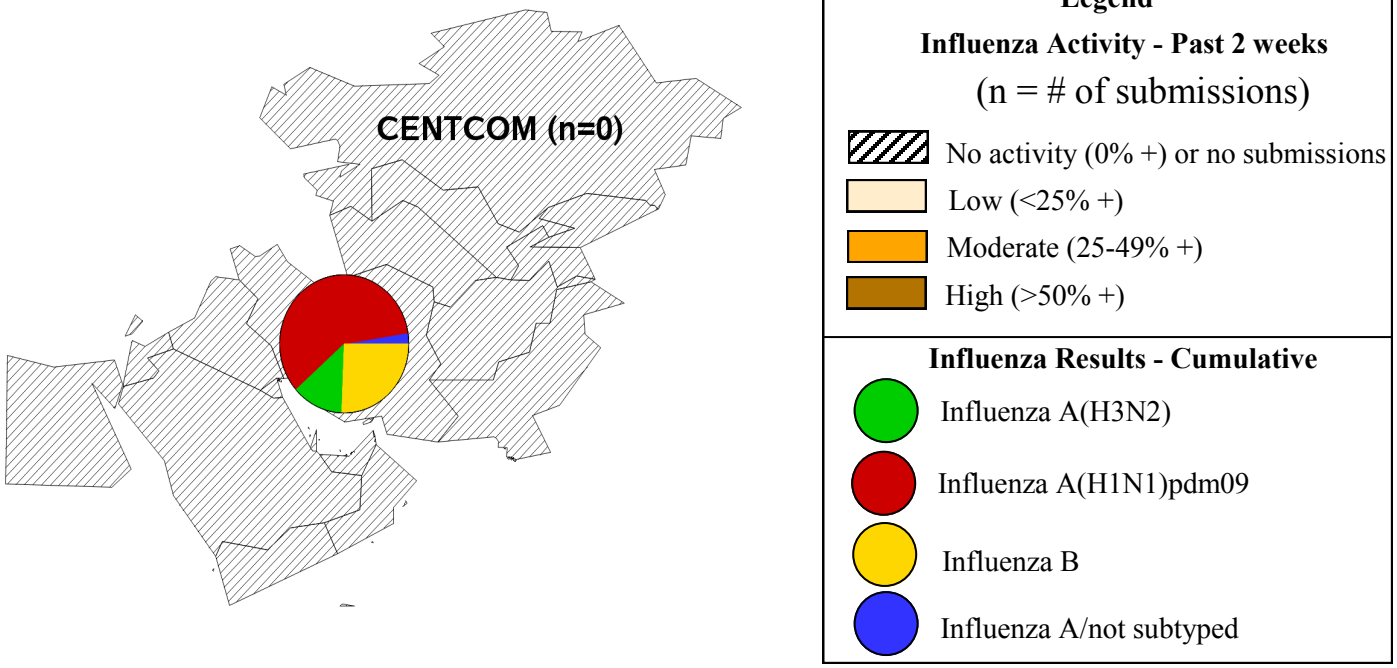
Map 1. Influenza subtypes and activity level by region for the 2015-2016 surveillance year through Week 35



Map 2. Influenza subtypes and activity level by country for the 2015-2016 surveillance year through Week 35 (Pacific)



Map 3. Influenza subtypes and activity level for CENTCOM for the 2015-2016 surveillance year through Week 35



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 35

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	-	-	7	12
	Country 2, Location A	8	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	14
PACOM	CFA Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	10	12
	Eielson AFB, AK	5	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	7	15
	JB Elmendorf-Richardson, AK	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	-	5	7
	JR Marianas - Andersen AFB, Guam	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	2	5
	JR Marianas - NH Guam, Guam	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Kadena AB, Japan	2	1	-	-	-	-	3	-	-	-	-	2	-	3	-	-	5	-	1	23	40
	Kunsan AB, South Korea	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Misawa AB, Japan	2	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	3	-	-	5	12
	Osan AB, South Korea	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	6
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1
	USCG Base Kodiak, AK	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	20	5	-	-	-	-	13	-	8	-	-	4	-	3	5	2	6	-	2	39	107
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	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	8	13
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	-	15	1	3	52	137
	USMA - West Point, NY	56	3	-	-	1	-	38	-	25	-	-	10	9	5	14	11	23	3	11	172	381
Region 3	Dover AFB, DE	24	-	-	-	-	-	8	-	3	-	1	-	2	1	1	2	3	-	1	84	130
	JB Anacostia-Bolling, DC	-	1	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	2	5
	JB Andrews, MD	7	-	-	-	-	-	3	-	2	-	-	-	2	1	-	2	-	-	-	12	29
	JB Langley-Eustis, VA	20	-	-	-	-	-	11	-	10	-	-	4	7	3	7	9	9	2	3	66	151
	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	-	-	-	-	-	-	-	2	-	-	2	8
	Columbus AFB, MS	6	-	-	-	-	-	-	-	2	-	-	2	1	-	-	2	4	-	-	26	43
	Eglin AFB, FL	10	1	-	-	-	-	3	-	6	-	-	1	1	1	5	7	8	-	1	71	115
	Ft Bragg, NC	9	-	-	-	-	-	12	-	4	-	-	4	1	1	-	3	2	1	2	41	80
	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	1	-	2	34	61
	JB Charleston (AF), SC	4	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Keesler AFB, MS	-	-	-	-	-	-	-	-	1	-	-	-	-	2	1	-	3	1	1	34	43
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-	1	1	5
	Maxwell AFB, AL	23	1	-	1	-	-	2	-	6	-	-	1	-	1	1	2	9	-	1	66	114
	Moody AFB, GA	13	1	-	-	-	-	11	-	8	-	-	2	1	2	7	6	18	-	6	39	114
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Camp Lejeune, NC	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	2	-	1	9	16
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	-	8	12
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Robins AFB, GA	6	-	-	-	-	-	1	-	-	-	-	-	-	2	1	1	2	-	-	18	31
	Seymour Johnson AFB, NC	12	-	-	-	-	-	1	-	2	-	-	2	-	-	1	-	4	1	1	13	37
	Shaw AFB, SC	2	1	-	-	-	-	2	-	-	-	-	5	-	4	-	-	6	1	1	14	36
	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 35

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	-	-	-	2	-	1	-	1	-	-	21	33
	Wright-Patterson AFB, OH	15	-	-	-	-	-	2	-	3	-	-	-	1	1	1	1	4	-	-	38	66
Region 6	Altus AFB, OK	7	-	-	-	-	-	4	-	4	-	-	3	5	-	6	10	13	-	5	74	131
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	5	6
	Cannon AFB, NM	13	4	1	-	-	-	12	-	3	-	-	2	4	-	2	2	8	-	12	45	108
	Laughlin AFB, TX	1	5	-	-	-	-	5	-	2	-	-	1	-	-	-	2	5	-	-	10	31
	Little Rock AFB, AR	5	1	-	-	-	-	1	-	-	-	-	1	1	-	-	-	4	-	1	27	41
	Sheppard AFB, TX	8	-	-	-	-	-	32	-	10	-	-	3	3	3	2	5	24	-	6	110	206
	Tinker AFB, OK	4	-	-	-	-	-	3	-	6	-	-	1	-	1	7	7	9	1	7	52	98
	USCG New Orleans, LA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	1	-	-	-	-	-	1	-	2	-	-	-	2	-	2	-	3	-	-	47	58
Region 7	Ft Leavenworth, KS	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	9	11
	McConnell AFB, KS	5	-	-	-	-	-	4	-	1	-	-	1	-	2	2	-	7	1	-	38	61
	Offutt AFB, NE	19	3	-	-	-	-	6	-	2	-	-	2	2	-	4	1	10	-	-	86	135
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	55	112
	Hill AFB, UT	38	6	-	-	-	-	33	-	3	-	-	2	3	1	-	2	14	1	1	123	227
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Minot AFB, ND	7	-	-	-	-	-	-	-	-	-	-	2	1	-	1	2	4	-	1	12	30
	Peterson AFB, CO	14	3	-	-	-	1	2	-	2	-	-	5	1	-	-	1	6	-	5	40	80
	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	-	-	-	-	3	-	1	18	39
	Edwards AFB, CA	1	-	-	-	-	-	1	-	-	-	-	1	-	-	-	1	1	-	-	8	13
	Luke AFB, AZ	30	24	-	-	-	-	21	-	3	-	-	-	9	1	1	9	6	-	10	54	168
	NH Twentynine Palms, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	19	2	-	-	-	-	5	-	7	-	-	3	-	-	10	4	9	-	8	88	155
	Travis AFB, CA	19	8	-	-	-	-	13	-	3	-	-	2	9	2	6	7	19	-	7	58	153
	USCG Island Alameda, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Vandenberg AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	11	14
Region 10	Fairchild AFB, WA	6	1	-	-	-	-	6	-	1	-	-	-	1	-	-	-	4	-	1	17	37
	JB Lewis-McChord, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Mt Home AFB, ID	1	1	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	10	14
	NH Bremerton, WA	44	7	-	-	-	-	57	-	5	-	-	2	2	2	13	6	16	1	12	82	249
Total		637	105	1	1	1	1	376	1	164	1	2	88	87	58	125	130	323	17	127	2199	4444

**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 11th USAFSAM influenza sequence surveillance report for the 2015-2016 influenza season and includes a total of 165 specimens collected between 8 January 2016 and 17 May 2016, with 76 specimens collected at USAFSAM and 89 specimen sequences provided by the Naval Health Research Center (NHRC) in San Diego, CA. Forty-two (25.4%) of the specimens were influenza A(H1N1)pdm09, including 25 from USAFSAM (59.5%) and 17 from NHRC (40.5%). Forty-four (26.7%) specimens were influenza A(H3N2), including 17 from USAFSAM (38.6%) and 27 from NHRC (61.4%). Forty-three (26.1%) specimens were influenza B/Victoria lineage, including 18 from USAFSAM (41.9%) and 25 from NHRC (58.1%). Thirty-six (21.8%) specimens were influenza B/Yamagata lineage, with 16 from USAFSAM (44.4%) and 20 from NHRC (55.6%).

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, Davis-Monthan AFB		1		
	Arizona, Luke AFB	1	3		2
	California, NHRC	12	21	11	19
	California, Travis AFB		2		
	Colorado, Peterson AFB	1			
	Delaware, Dover AFB	3			
	Florida, Hurlburt Field	1			
	Georgia, Moody AFB	1		1	1
	Georgia, NHRC			3	
	Illinois, NHRC	1		3	1
	Kentucky, Ft Campbell			1	
	Massachusetts, Hanscom AFB	2		2	1
	Mississippi, Columbus AFB	1			
	Missouri, NHRC	1	1	3	
	New Jersey, JB McGuire-Dix-Lakehurst	4			3
	New Jersey, NHRC	1		4	
	New Mexico, Cannon AFB		2		2
	New York, USMA – West Point	1		5	
	North Carolina, Ft Bragg			2	
	Ohio, Wright-Patterson AFB	2			2
	South Carolina, JB Charleston (AF)			1	
	South Carolina, NHRC	2	5		
	South Dakota, Ellsworth AFB	1	1		
	Texas, NHRC			1	
	Texas, SAMMC			1	
	Texas, Sheppard AFB			2	
	Utah, Hill AFB	1	3		1
	Virginia, JB Langley-Eustis	2		2	1
	Washington, Fairchild AFB		1		
	Washington, NH Bremerton	2	2	1	2
OCONUS	**Alaska, Eielson AFB**				**1**
	Germany, Spangdahlem AB		1		
	Italy, Aviano AB		1		
TOTAL		42	44	43	36

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

Influenza A(H1N1)pdm09

- Among the influenza A specimens, 48.8% 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 1].

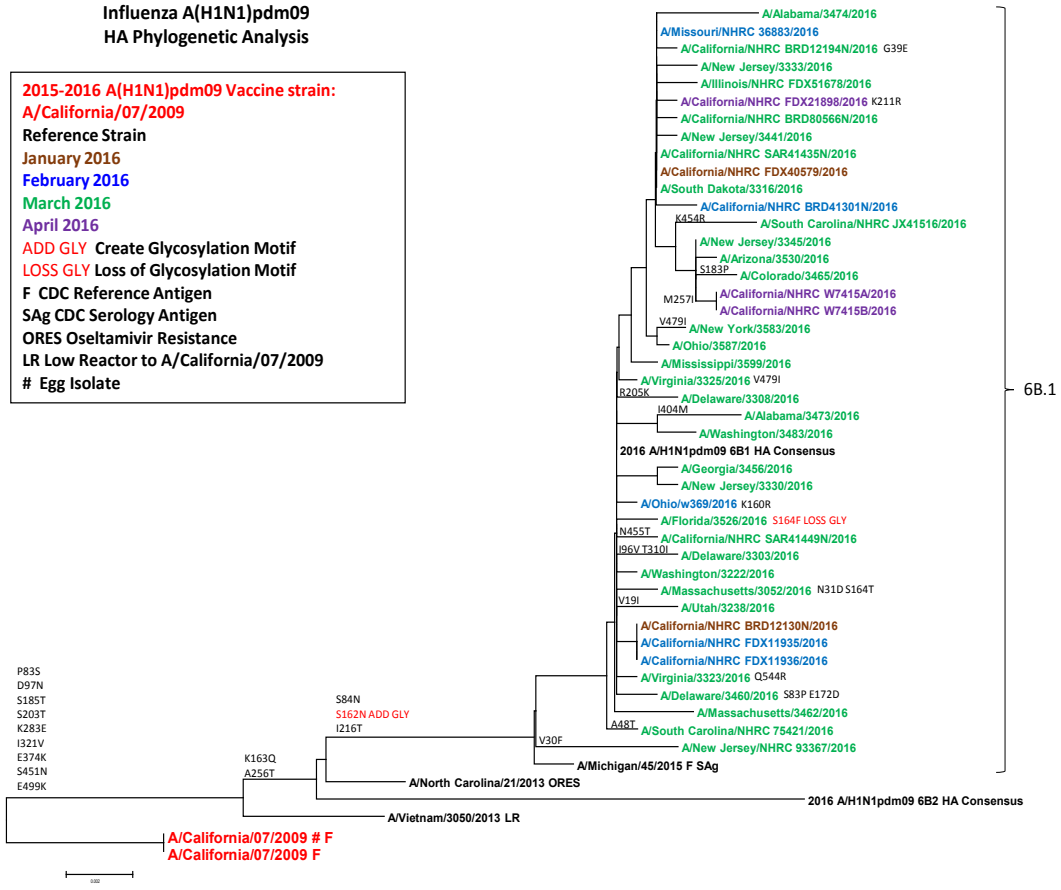
- The A(H1N1)pdm09 specimens characterized for this report exhibited an overall protein homology of 96.5-96.9% compared to the 2015-2016 influenza vaccine component, A/California/07/2009-like virus.

- All of the A(H1N1)pdm09 sequences for this report contain mutations consistent with one of the circulating subgroups, referred to as group 6B, and all classified as the newly determined 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 specimens characterized in this report, one mutation, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif and one mutation, S164F (serine to phenylalanine) was observed that could cause the loss of a glycosylation motif.

- Of the 33 mutations present in the A(H1N1)pdm09 specimens, 10 occurred at predicted antigenic sites (zero at site A, one at site B, two at site C, four at site D, and three at site E) and two occurred at the receptor binding site.[2,5]

Figure 1
Influenza A(H1N1)pdm09
HA Phylogenetic Analysis



Influenza A(H3N2)

- Among the influenza A specimens, 51.2% were 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].

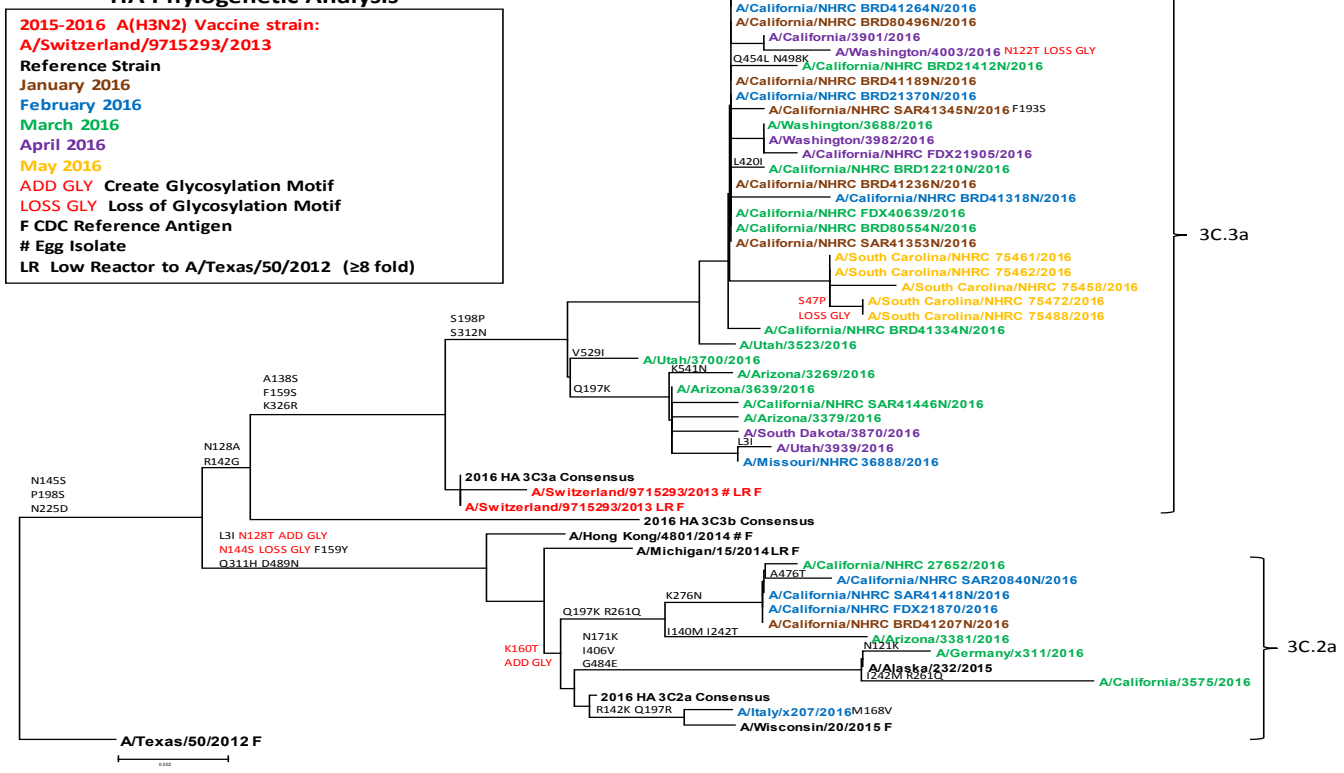
- The A(H3N2) specimens characterized for this report exhibited an overall protein homology of 96.4-98.9% compared to the 2015-2016 influenza vaccine component, A/Switzerland/9715293/2013-like virus and 97.1-98.7% compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014.

- All of the influenza A(H3N2) specimens sequenced for this report were in clade 3C. Nine (20.5%) of the influenza A(H3N2) sequences classified as subclade 3C.2a and 35 (79.5%) classified as subclade 3C.3a.

- Among the influenza A(H3N2) specimens characterized in this report, three mutations: S47P (serine to proline), N122T (asparagine to threonine), and N144S (asparagine to serine) 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 33 mutations present in the A(H3N2) specimens, 11 occurred at predicted antigenic sites (six at site A, three at site B, one at site C, zero at site D, and one at site E) and two occurred at the receptor binding site.[2,5]

Figure 2
Influenza A(H3N2)
HA Phylogenetic Analysis



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

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 vaccine strain B/Massachusetts/02/2012-like virus for B/Yamagata specimens [Figure 4].

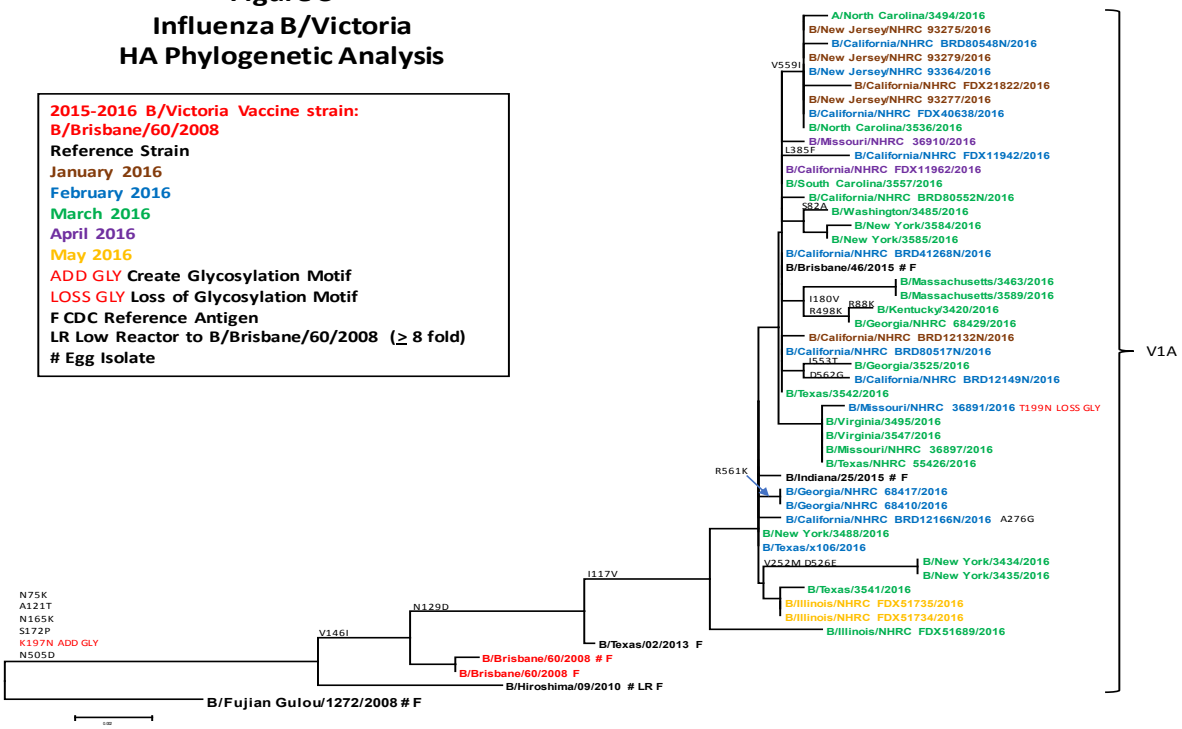
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.[1] Forty-three (54.4%) of the 79 influenza B viruses characterized in this report fall into the Victoria lineage, while the other 36 (45.6%) 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.

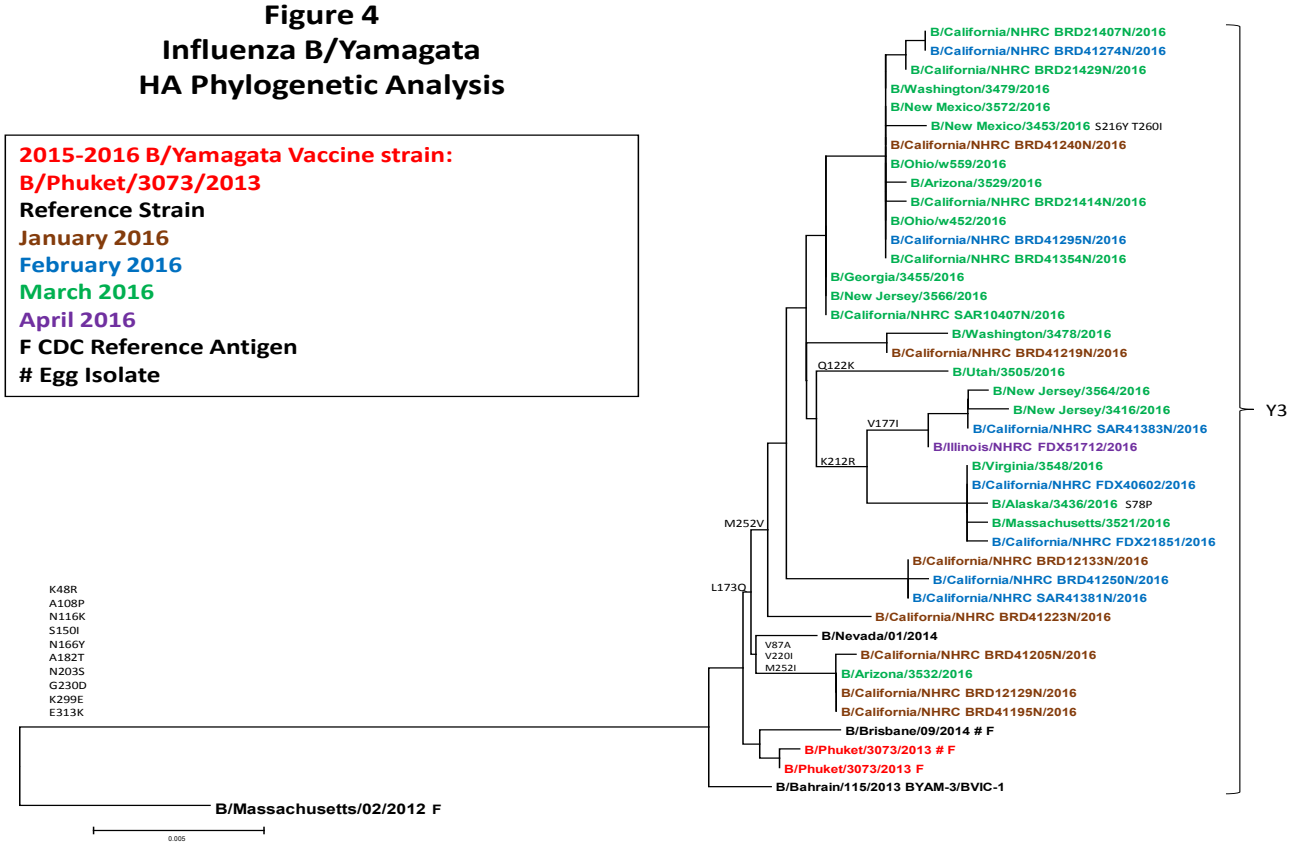
- In the Victoria lineage, one mutation, K197N (lysine to asparagine) was observed that adds a glycosylation motif, while another mutation, T199N (threonine to asparagine), causes the loss of this same glycosylation motif for one specimen.

Figure 3
Influenza B/Victoria
HA Phylogenetic Analysis



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

Figure 4
Influenza B/Yamagata
HA Phylogenetic Analysis



References:

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

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3. Cherry JL, Lipman DJ, Nikolskaya A, Wolf YI. Evolutionary Dynamics of N-Glycosylation Sites of Influenza Virus Hemagglutinin. *PLoS Curr Influenza*. 2009 August 18: RRN1001.

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5. Wolf YI, Viboud C, Holmes EC, Koonin EV, Lipman DJ. Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol Direct*. 2006; 1: 34. Published online 2006 October 26. doi: 10.1186/1745-6150-1-34.

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Monthly EUCOM Respiratory Surveillance Supplemental Report Through 3 September 2016

In cooperation and agreement with U.S. Army Public Health Command Region-Europe (PHCR-E), the DoD Global, Laboratory-based, Influenza Surveillance Program has analyzed data from surveillance sites that submit specimens to Landstuhl Regional Medical Center (LRMC), Germany. LRMC's laboratory is the forward laboratory for military sites in Europe. Lab results are preliminary and may change as more results are received.

Table 4. Results by region and location for specimens collected and finalized during Weeks 32-35

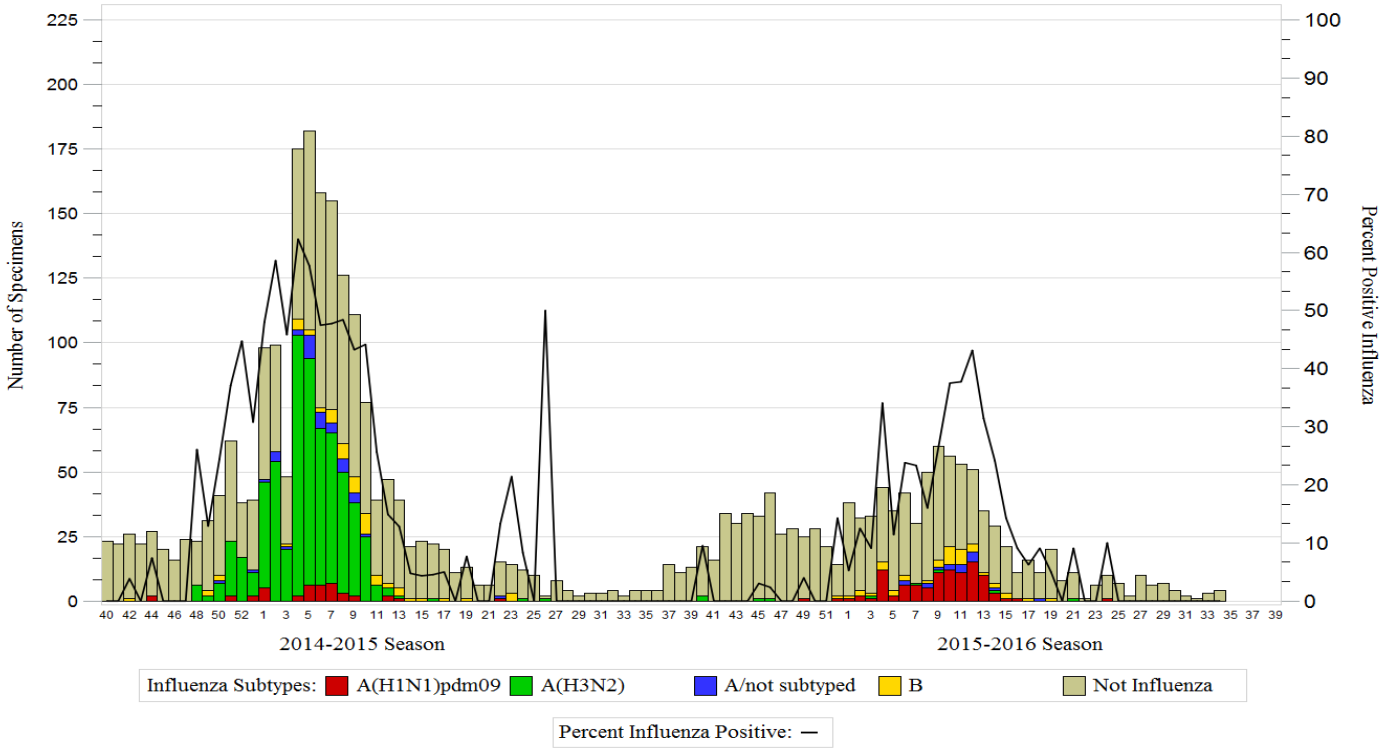
Region		Adenovirus	Parainfluenza	No Pathogen	Total
EUCOM	Landstuhl RMC, Germany	-	-	1	1
	RAF Lakenheath, England	-	-	2	2
	Ramstein AB, Germany	1	-	1	2
	USAG Stuttgart, Germany	-	-	2	2
	Vilseck AHC, Germany	-	1	-	1
Total		1	1	6	8

Table 5. Cumulative results by region and location for specimens collected during the 2015-2016 surveillance year

Region		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A/not subtyped & Adeno	A/not subtyped & hMNV	A/not subtyped & Para	A/not subtyped & RSV	A/not subtyped & Rhino/Entero	A(H1N1)pdm09 & B	A(H1N1)pdm09 & hMNV	A(H1N1)pdm09 & Para & Rhino/Entero	A(H1N1)pdm09 & RSV	A(H1N1)pdm09 & Rhino/Entero	A(H3N2) & Rhino/Entero	A/not subtyped & B	B	B & hMNV	B & Rhino/Entero	Adenovirus	hMNV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & RSV	Adeno & RSV & Rhino/Entero	Adeno & Rhino/Entero	hMNV & Para	hMNV & Rhino/Entero	Para & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
AFRICOM	Camp Lemonnier, Djibouti	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	2
Deployed	Country 2, Location A	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	2	7
	Country 6, Location A	14	2	1	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	2	2	1	32	-	-	-	-	-	-	68	125
EUCOM	Aviano AB, Italy	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	8
	Incirlik AB, Turkey	-	1	1	-	-	-	1	-	-	-	-	-	1	1	-	-	-	-	-	5	1	7	7	-	-	-	-	-	-	9	34
	Landstuhl RMC, Germany	17	-	1	-	2	-	-	-	-	-	-	-	2	1	1	7	-	-	3	6	7	19	40	-	-	1	-	1	3	3	136	250
	NAVSTA Rota, Spain	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	1	1	3	1	4	-	-	-	-	-	-	-	12	26
	NSA Naples, Italy	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2	1	1	4	-	-	-	-	-	-	-	13	23
	RAF Lakenheath, England	26	2	1	1	-	1	-	1	-	3	-	1	1	-	-	6	1	-	8	15	10	24	59	1	-	-	-	2	3	19	116	301
	Ramstein AB, Germany	3	-	2	-	-	-	-	-	-	-	-	-	-	-	-	4	-	-	2	2	2	3	13	-	-	-	-	-	-	1	27	59
	Spangdahlem AB, Germany	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	1	-	-	-	-	1	-	-	6	11
	USAG Stuttgart, Germany	13	-	1	-	-	-	-	-	-	-	1	-	-	-	1	2	-	-	2	6	3	5	18	-	-	-	-	1	-	-	43	96
	USAG Vicenza, Italy	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	1	5	-	-	-	-	-	-	-	10	19
	Vilseck AHC, Germany	12	-	1	-	-	-	1	-	1	-	-	-	2	-	1	8	-	-	1	5	7	13	27	1	1	2	1	3	4	2	51	144
Total		91	7	9	1	2	1	2	1	1	3	1	1	6	2	3	36	2	1	18	46	36	75	212	2	1	3	1	8	10	25	498	1105

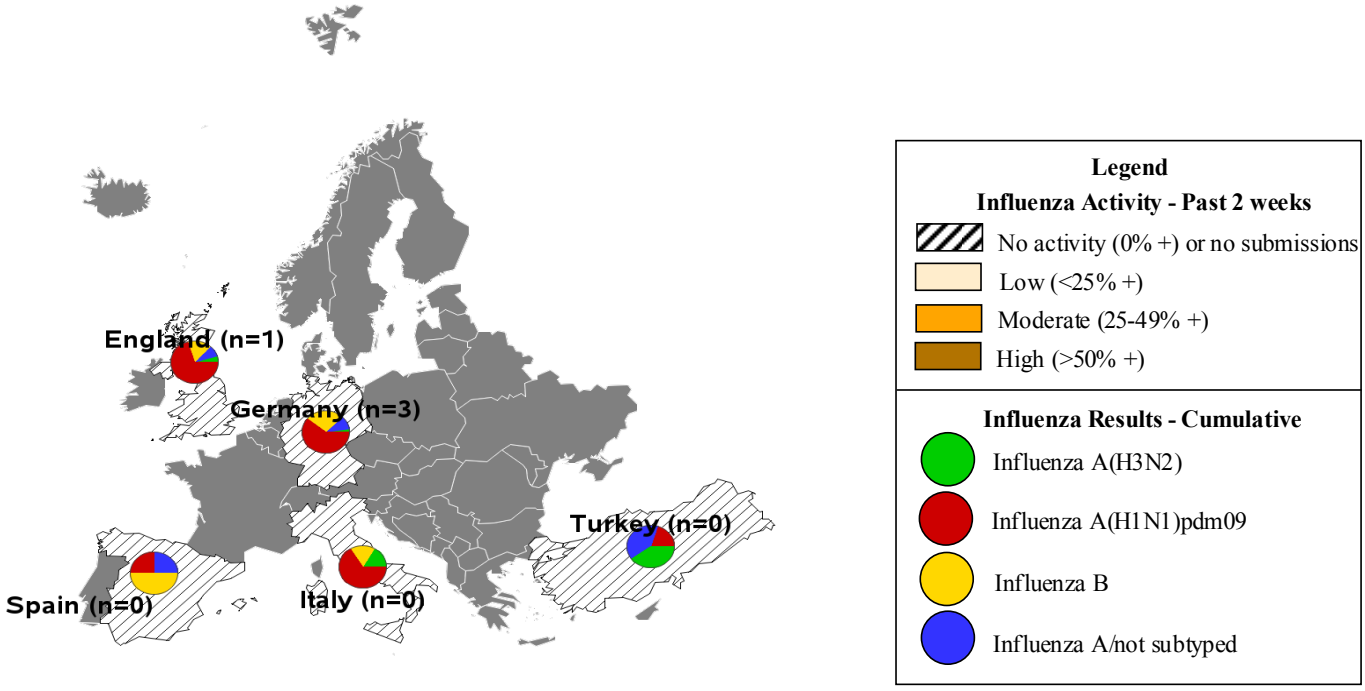
88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Graph 4. Percent influenza positive by week: 2014-2015 surveillance year and through Week 35 of the 2015-2016 surveillance year (EUCOM)



Note: Dual influenza co-infections have been excluded from the graph.

Map 4. Influenza subtypes and activity level by country for the 2015-2016 surveillance year through Week 35 (EUCOM)



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.

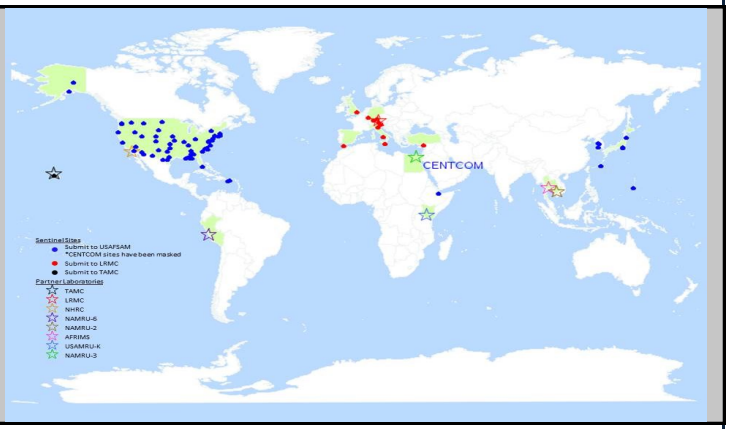
Available on our website (listed below) is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and a dashboard containing respiratory data for our sentinel sites.

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.