USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2015-2016

Cumulative Results

Locations	78
Collected	3,556
Tested	3,440

Influenza A	**634**
A(H1N1)pdm09	551
A(H1N1)pdm09 & B	1
A(H1N1)pdm09 & Parainfluenza	1
A(H3N2)	80
A(H3N2) & B	1

Influenza B*	**260**
B	259
B & Adenovirus	1

Other Respiratory Pathogens	**812**
Adenovirus	125
Bordetella pertussis	1
Chlamydophila pneumoniae	1
Coronavirus	77
Human Metapneumovirus	72
Mycoplasma pneumoniae	51
Parainfluenza	81
RSV	125
Rhino/Enterovirus	169
Non-influenza Viral Coinfections	94
Non-influenza Bacterial Coinfections	16
-*B. pertussis* (3)	
-*B. pertussis & M. pneumo (1)*	
-*C. pneumo* (3)	
-*C. pneumo & M. pneumo (1)*	
-*M. pneumo (8)*	

Lab data are current as of 4 April 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
20 March - 2 April 2016 (Surveillance Weeks 12 & 13)

- During 20 March - 2 April 2016, a total of 353 specimens were collected and received from 49 locations. Results were finalized for 274 specimens from 47 locations. During Week 12, 64 influenza A(H1N1)pdm09, six A(H3N2), and 32 influenza B viruses were identified. Twenty-one influenza A(H1N1)pdm09, seven A(H3N2), and 17 influenza B viruses were identified during Week 13.

- During Week 12 (20 - 26 March 2016), influenza activity decreased slightly, but remained elevated in the United States. **Viral Surveillance:** The most frequently identified influenza virus type reported by public health laboratories during Week 12 was influenza A, with influenza A(H1N1)pdm09 viruses predominating. The percentage of respiratory specimens testing positive for influenza in clinical laboratories decreased. **Pneumonia and Influenza (P&I) Mortality:** The proportion of deaths attributed to P&I was below the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System and above the system-specific epidemic threshold in the 122 Cities Mortality Reporting System. **Influenza-Associated Pediatric Deaths:** Three influenza-associated pediatric deaths were reported. **Influenza-Associated Hospitalizations:** A cumulative rate for the season of 21.4 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 2.9%, which is above the national baseline of 2.1%. **Geographic Spread of Influenza:** The geographic spread of influenza in Guam, Puerto Rico and 29 states was reported as widespread; 18 states reported regional activity; the District of Columbia and two states reported local activity; West Virginia state reported sporadic activity; and the U.S. Virgin Islands did not report. (CDC Fluview Summary, cited 6 April 2016).

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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 12 & 13

Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	Coronavirus	hMNV	*M. pneumoniae*	RSV	Rhinovirus/Enterovirus	Adeno & Corona & Rhino/Entero	Adeno & Rhino/Entero	hMNV & *M. pneumo* & Para	hMNV & RSV	hMNV & Rhino/Entero	Para & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
PACOM	CFA Okinawa, Japan	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	2
	Eielson AFB, AK	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Kadena AB, Japan	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	USCG Base Kodiak, AK	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	2	-	1	1	-	-	-	-	1	1	-	-	-	-	-	-	2	8
Region 1	Hanscom AFB, MA	2	-	3	-	-	-	1	-	-	-	-	-	-	-	-	-	1	7
	USCG Academy, CT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 2	JB McGuire-Dix-Lakehurst, NJ	9	-	5	-	1	1	-	-	1	-	-	-	-	-	-	-	12	29
	USMA - West Point, NY	6	-	9	1	-	-	-	2	1	-	-	-	-	-	-	-	9	28
Region 3	Dover AFB, DE	6	-	2	1	-	-	-	-	-	-	-	-	-	-	-	-	4	13
	JB Andrews, MD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	JB Langley-Eustis, VA	8	-	5	3	-	1	1	-	1	-	-	1	-	-	1	-	8	29
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 4	CGS Mobile, AL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Columbus AFB, MS	2	-	-	-	-	1	-	-	1	-	-	-	-	-	-	-	1	5
	Eglin AFB, FL	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Bragg, NC	2	-	3	-	-	-	-	-	-	-	1	-	-	-	-	-	-	6
	Hurlburt Field, FL	1	-	-	1	-	-	1	-	-	-	-	-	-	-	-	-	4	7
	JB Charleston (AF), SC	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Keesler AFB, MS	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1
	Maxwell AFB, AL	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Moody AFB, GA	1	-	2	-	-	-	-	-	-	-	1	-	-	-	-	-	-	4
	NH Camp Lejeune, NC	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Seymour Johnson AFB, NC	4	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	5
Region 5	Scott AFB, IL	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Wright-Patterson AFB, OH	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 6	Altus AFB, OK	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Cannon AFB, NM	-	2	2	-	-	-	-	-	-	-	-	-	1	2	-	1	-	8
	Little Rock AFB, AR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	7
	Sheppard AFB, TX	1	-	2	-	-	1	-	-	1	-	-	-	-	-	-	-	4	9
	USCG New Orleans, LA	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
Region 7	McConnell AFB, KS	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Offutt AFB, NE	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	6
Region 8	Ellsworth AFB, SD	3	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	8
	FE Warren AFB, WY	4	-	-	1	-	-	-	1	1	-	-	-	-	-	-	-	-	7
	Hill AFB, UT	6	3	2	-	-	-	-	-	-	-	-	-	-	-	-	-	3	14
	Minot AFB, ND	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1
	Peterson AFB, CO	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	6
	USAF Academy, CO	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
Region 9	CGS Humboldt Bay, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	3	3	3	-	-	1	1	1	-	-	-	-	-	-	-	-	2	14
	Nellis AFB, NV	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Travis AFB, CA	2	2	1	-	-	-	-	-	1	-	-	-	-	-	-	-	2	8
Region 10	Fairchild AFB, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Mt Home AFB, ID	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	NH Bremerton, WA	3	1	5	-	-	-	-	-	1	-	-	-	-	-	-	-	2	12
Total		85	13	49	10	1	5	5	5	12	1	2	1	1	2	1	2	79	274

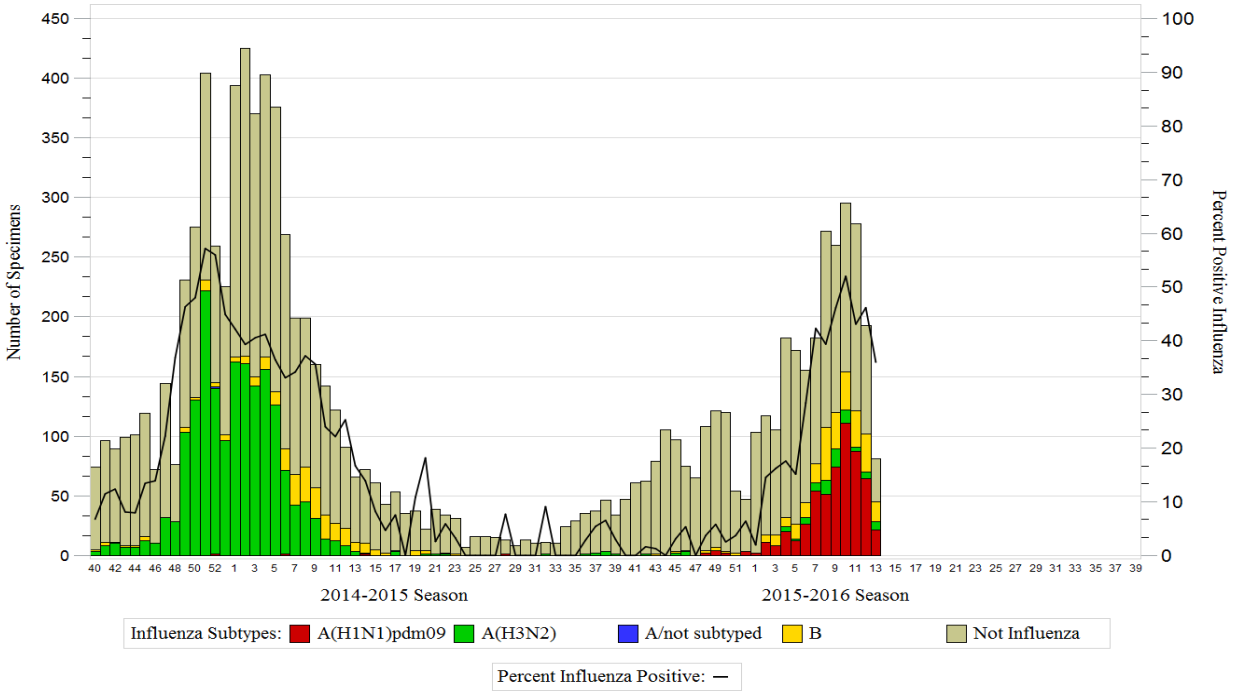
**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

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

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 13 of the 2015-2016 surveillance year



Note: Dual influenza co-infections 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.

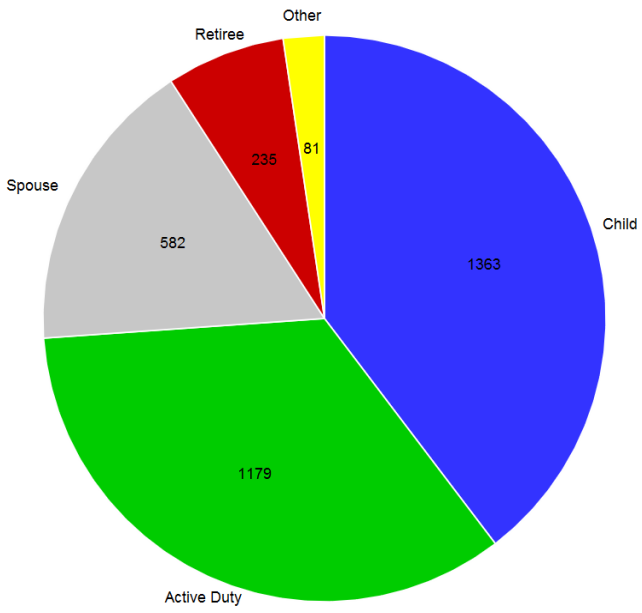
Table 2. ILI by age group for the 2015-2016 surveillance year through Week 13

Age Group	Frequency	Percent
0-5	783	22.76
6-9	268	7.79
10-17	315	9.16
18-24	465	13.52
25-44	1121	32.59
45-64	398	11.57
65+	90	2.62

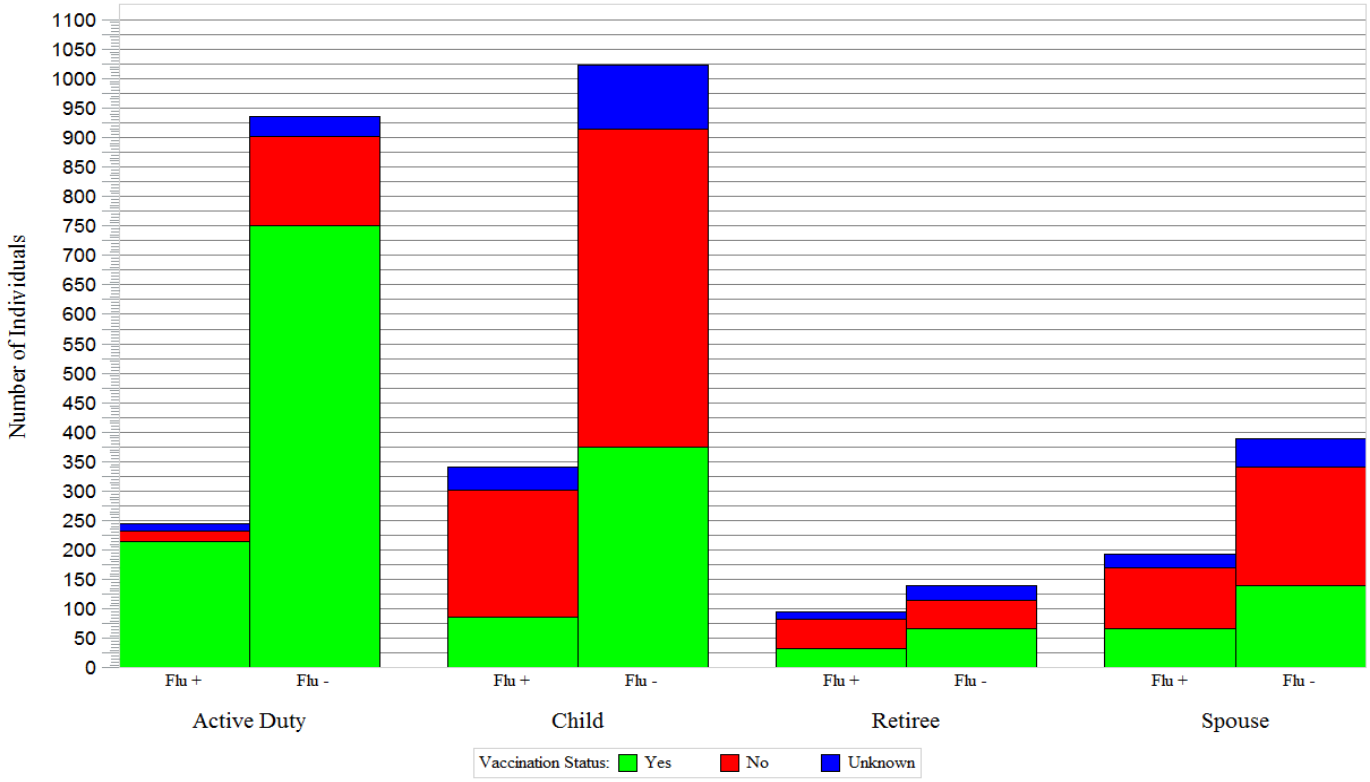
Demographic Summary

Of 3,440 ILI cases, 1,179 are service members (34.3%), 1,363 are children (39.6%), 582 are spouses (16.9%), and 316 (9.2%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=3,441) is 23 (range 0, 95).

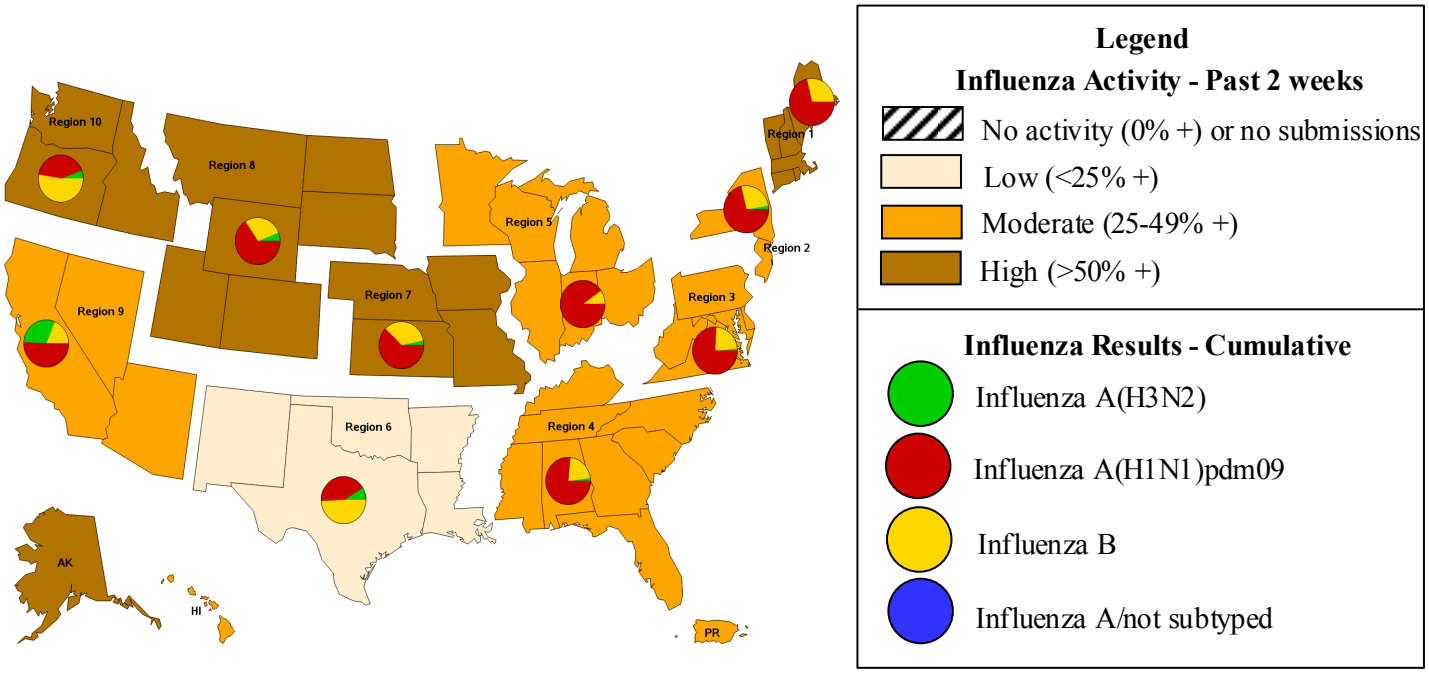
Graph 2. ILI by beneficiary status for the 2015-2016 surveillance year through Week 13



Graph 3. Vaccination status by beneficiary type for the 2015-2016 surveillance year through Week 13

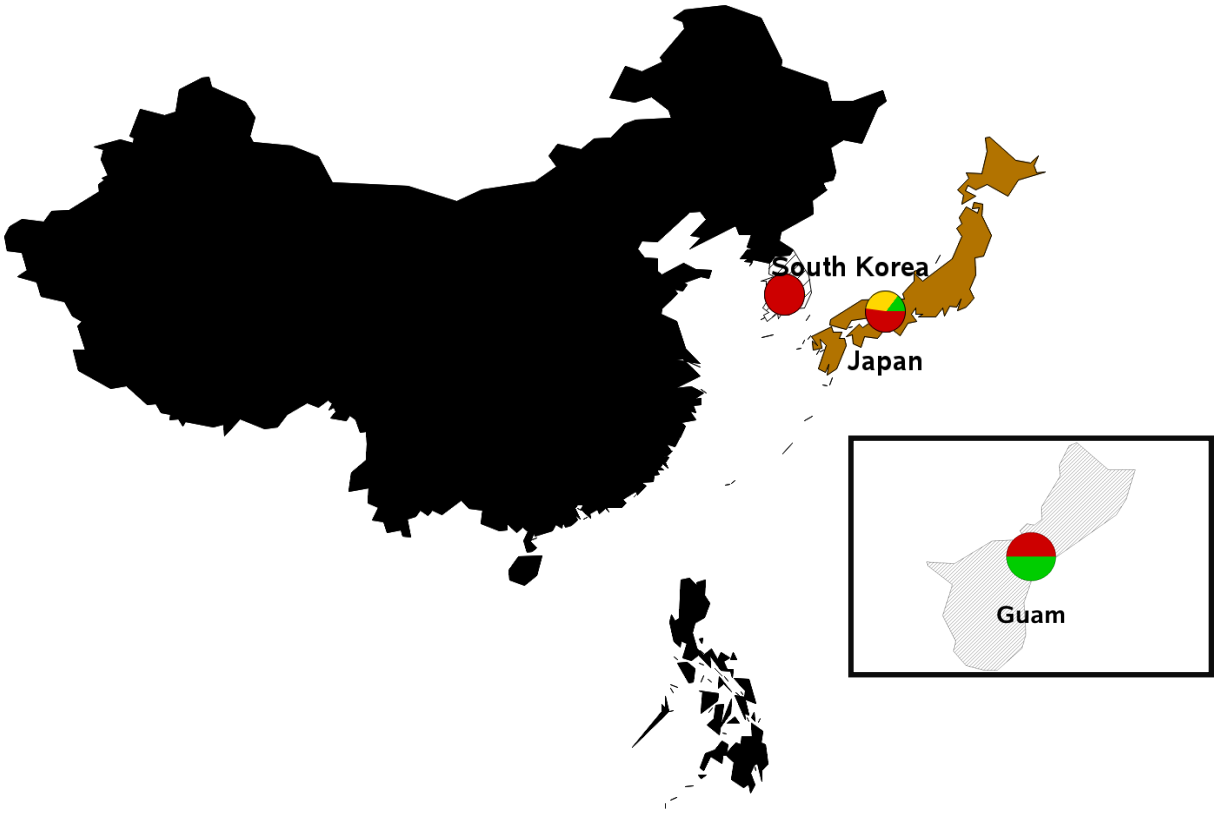


Map 1. Influenza subtypes and activity level by region for the 2015-2016 surveillance year through Week 13

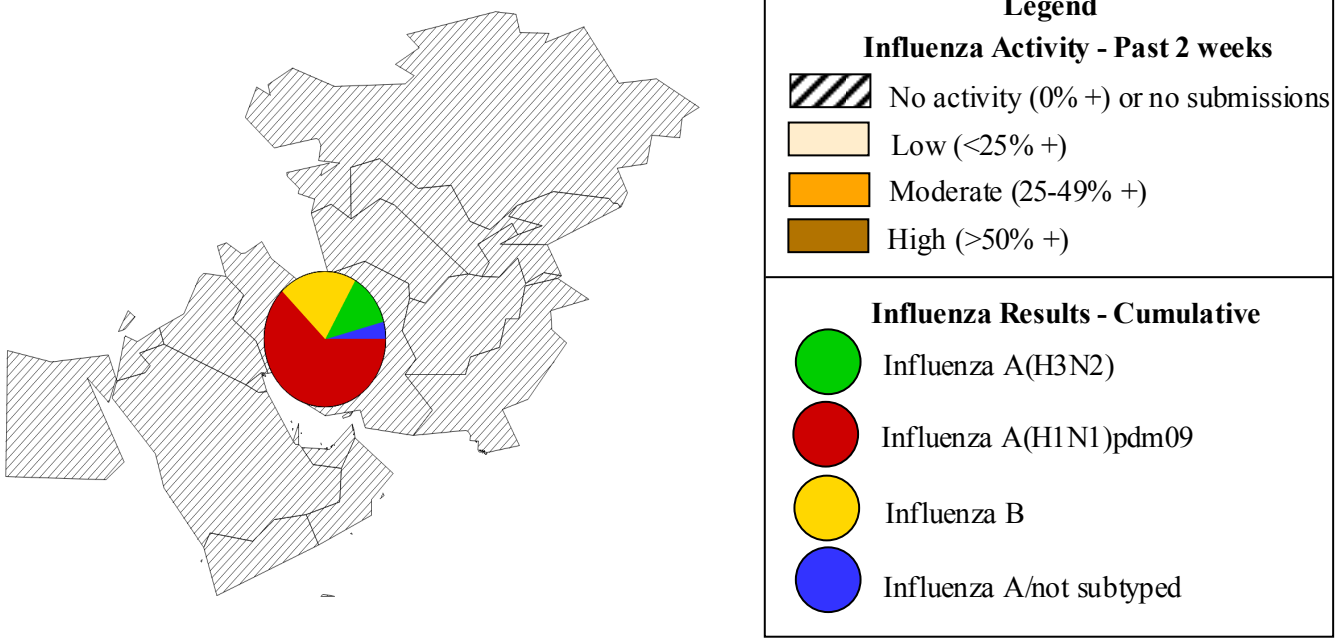


88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Map 2. Influenza subtypes and activity level by country for the 2015-2016 surveillance year through Week 13 (Pacific)*



Map 3. Influenza subtypes and activity level for CENTCOM for the 2015-2016 surveillance year through Week 13



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.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 13

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

Region*		A(H1N1)pdm09	A(H3N2)	A(H1N1)pdm09 & B	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 2, Location A	8	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	14
PACOM	CFA Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	9	11
	Eielson AFB, AK	2	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	5	9
	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	-	-	-	-	-	-	-	-	2	-	3	-	-	2	-	-	17	27
	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	17	4	-	-	-	12	-	6	-	-	4	-	2	3	2	2	-	2	24	78
Region 1	Hanscom AFB, MA	9	-	-	-	-	4	-	4	-	-	-	-	1	2	2	-	-	2	24	48
	NHCNE Newport, RI	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	1	-	-	11	14
	USCG Academy, CT	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
Region 2	Ft Drum, NY	6	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2	-	-	5	14
	JB McGuire-Dix-Lakehurst, NJ	29	-	-	-	-	8	1	2	-	-	1	3	3	-	-	7	1	3	33	91
	USMA - West Point, NY	51	3	-	1	-	22	-	15	-	-	8	7	4	3	11	7	3	4	141	280
Region 3	Dover AFB, DE	22	-	-	-	-	3	-	2	-	1	-	2	-	1	2	1	-	1	66	101
	JB Anacostia-Bolling, DC	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	2
	JB Andrews, MD	7	-	-	-	-	3	-	2	-	-	-	2	1	-	2	-	-	-	12	29
	JB Langley-Eustis, VA	15	-	-	-	-	6	-	8	-	-	4	4	2	4	8	5	2	2	37	97
	NCRM - Walter Reed NMMC, MD	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5
	NMC Portsmouth, VA	4	1	-	-	-	3	-	4	-	-	1	1	5	1	2	2	1	-	24	49
Region 4	CGS Mobile, AL	1	2	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1	5
	Columbus AFB, MS	4	-	-	-	-	-	-	1	-	-	1	1	-	-	1	3	-	-	17	28
	Eglin AFB, FL	6	-	-	-	-	1	-	6	-	-	-	1	1	4	7	5	-	1	55	87
	Ft Bragg, NC	7	-	-	-	-	8	-	3	-	-	3	1	1	-	3	2	1	1	36	66
	Ft Campbell, KY	24	1	-	-	-	9	-	1	-	-	4	2	-	2	1	4	-	-	43	91
	Hurlburt Field, FL	6	-	-	-	-	2	-	4	-	-	-	1	3	-	1	-	-	2	24	43
	JB Charleston (AF), SC	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	4
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	2	-	1	26	31
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-	-	1	4
	Maxwell AFB, AL	21	-	-	-	-	-	-	3	-	-	1	-	-	1	2	3	-	1	51	83
	Moody AFB, GA	13	-	-	-	-	7	-	7	-	-	2	1	2	2	5	9	-	6	28	82
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Camp Lejeune, NC	1	-	-	-	-	-	-	-	-	-	-	-	1	-	2	1	-	-	4	9
	NH Jacksonville, FL	-	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	-	7	11
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Robins AFB, GA	5	-	-	-	-	-	-	-	-	-	-	-	2	1	1	-	-	-	15	24
	Seymour Johnson AFB, NC	9	-	-	-	-	-	-	2	-	-	2	-	-	-	-	3	1	1	12	30
	Shaw AFB, SC	2	-	-	-	-	1	-	-	-	-	4	-	4	-	-	4	1	1	11	28
	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

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

Laboratory Results—Through Current Surveillance Week 13

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 & 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	13	-	-	-	-	1	-	2	-	-	-	1	1	1	1	3	-	-	20	43
Region 6	Altus AFB, OK	7	-	-	-	-	1	-	4	-	-	3	5	-	3	10	6	-	5	66	110
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	4	5
	Cannon AFB, NM	13	2	1	-	-	11	-	2	-	-	2	4	-	-	1	3	-	6	35	80
	Laughlin AFB, TX	-	5	-	-	-	2	-	1	-	-	1	-	-	-	2	-	-	-	7	18
	Little Rock AFB, AR	3	-	-	-	-	1	-	-	-	-	1	-	-	-	-	1	-	-	23	29
	Sheppard AFB, TX	5	-	-	-	-	21	-	7	-	-	3	3	3	1	5	10	-	3	81	142
	Tinker AFB, OK	4	-	-	-	-	2	-	6	-	-	1	-	1	5	7	5	1	6	47	85
	USCG New Orleans, LA	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	1	-	-	-	-	1	-	2	-	-	-	2	-	1	-	2	-	-	42	51
Region 7	Ft Leavenworth, KS	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	9	11
	McConnell AFB, KS	5	-	-	-	-	4	-	1	-	-	1	-	2	2	-	7	1	-	35	58
	Offutt AFB, NE	13	1	-	-	-	5	-	2	-	-	1	1	-	3	1	2	-	-	58	87
Region 8	Ellsworth AFB, SD	16	1	-	-	-	1	-	2	-	-	1	4	1	7	2	-	-	5	38	78
	FE Warren AFB, WY	18	1	-	-	-	5	-	1	1	-	3	2	1	3	7	3	-	2	45	92
	Hill AFB, UT	32	4	-	-	-	29	-	3	-	-	2	3	1	-	2	12	1	-	108	197
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Minot AFB, ND	7	-	-	-	-	-	-	-	-	-	2	1	-	1	1	2	-	1	12	27
	Peterson AFB, CO	13	2	-	-	1	1	-	2	-	-	4	-	-	-	1	4	-	4	33	65
	USAF Academy, CO	-	-	-	-	-	1	-	-	-	-	-	-	-	4	-	1	-	-	12	18
Region 9	Beale AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	CGS Humboldt Bay, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Davis-Monthan AFB, AZ	4	8	-	-	-	1	-	-	-	-	4	-	-	-	-	1	-	1	12	31
	Edwards AFB, CA	1	-	-	-	-	1	-	-	-	-	1	-	-	-	1	-	-	-	8	12
	Luke AFB, AZ	27	24	-	-	-	15	-	1	-	-	-	8	1	1	9	4	-	9	44	143
	NH Twentynine Palms, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	18	2	-	-	-	2	-	6	-	-	3	-	-	7	4	8	-	8	69	127
	Travis AFB, CA	17	7	-	-	-	7	-	3	-	-	2	9	1	5	7	11	-	6	42	117
	USCG Island Alameda, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Vandenberg AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	10	12
Region 10	Fairchild AFB, WA	4	-	-	-	-	3	-	-	-	-	-	1	-	-	-	-	-	-	10	18
	JB Lewis-McChord, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Mt Home AFB, ID	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	7	9
	NH Bremerton, WA	35	5	-	-	-	48	-	3	-	-	2	1	2	10	6	10	1	10	59	192
Total		551	80	1	1	1	259	1	125	1	1	77	72	51	81	125	169	16	94	1734	3440

**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

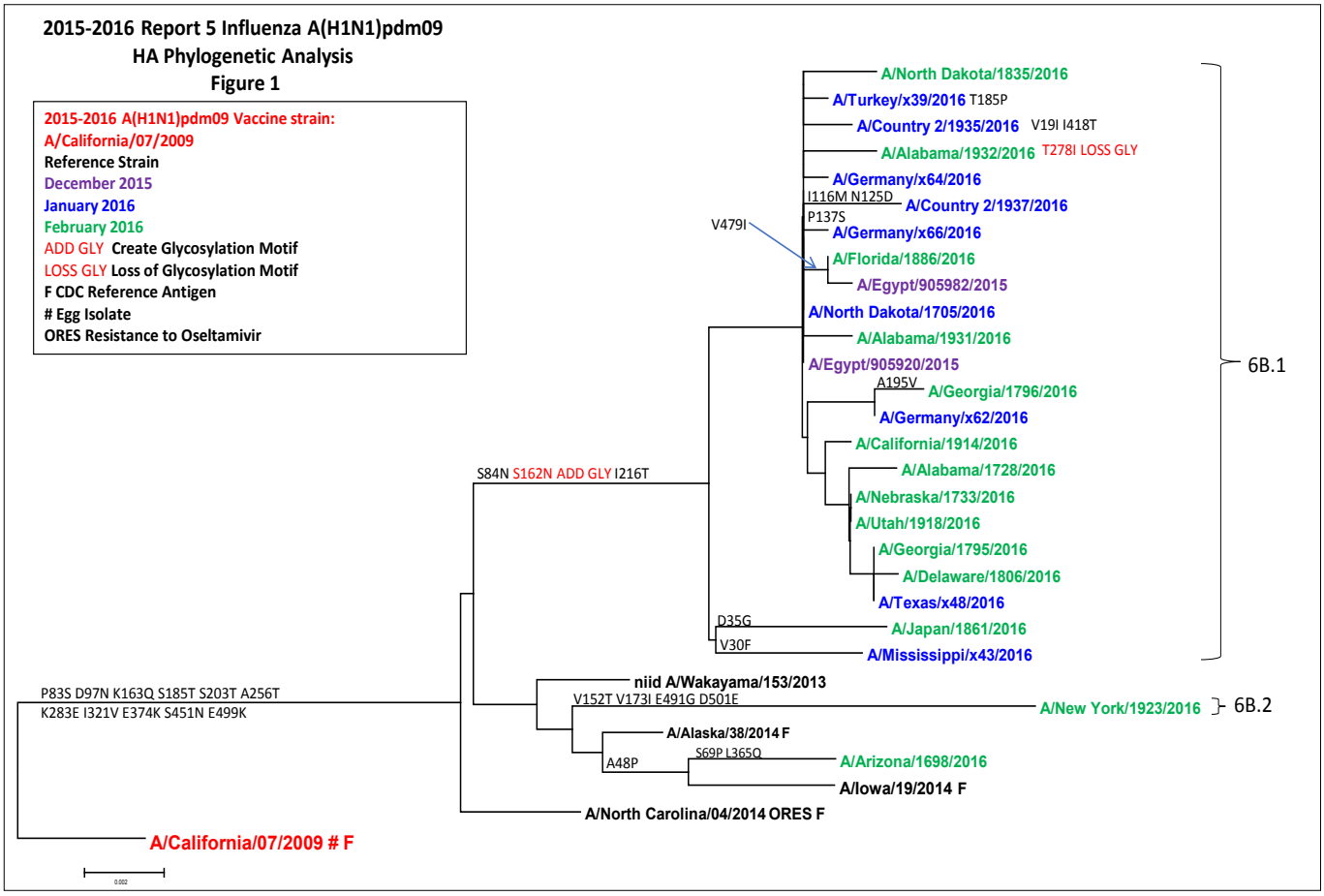
This is the fifth USAFSAM sequencing report for the 2015-2016 influenza season and includes 49 sequences from specimens collected between 1 December 2015 and 15 February 2016. Forty-one influenza positive specimens were collected from 23 sentinel sites and subsequently sequenced and analyzed at USAFSAM. Eight additional sequences were submitted to USAFSAM from NAMRU-3 in Egypt. Among the sequences analyzed for this report, 25 (51.0%) were influenza A(H1N1)pdm09, five (10.2%) were influenza A(H3N2), nine (18.4%) were influenza B/Victoria, and 10 (20.4%) 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	3			
	Arizona, Davis-Monthan AFB		1		
	Arizona, Luke AFB	1			
	California, Edwards AFB	1			
	California, Travis AFB		1		
	Delaware, Dover AFB	1			
	Florida, Hurlburt Field	1			
	Georgia, Robins AFB	2			
	Idaho, Mountain Home AFB				1
	Maryland, JB Andrews			1	
	Mississippi, Keesler AFB	1			
	Nebraska, Offutt AFB	1			
	New Mexico, Cannon AFB				1
	New York, USMA – West Point	1			
	North Dakota, Minot AFB	2			
	Texas, Laughlin AFB		2		
	Texas, SAMMC	1			1
	Utah, Hill AFB	1			1
	Washington, NH Bremerton				4
OCONUS	**Country 2,** Location A	2			
	Egypt, NAMRU-3	2		4	2
	Germany, Landstuhl RMC	3	1		
	Japan, Yokota AB	1		4	
	Turkey, Incirlik AB	1			
TOTAL		**25**	**5**	**9**	**10**

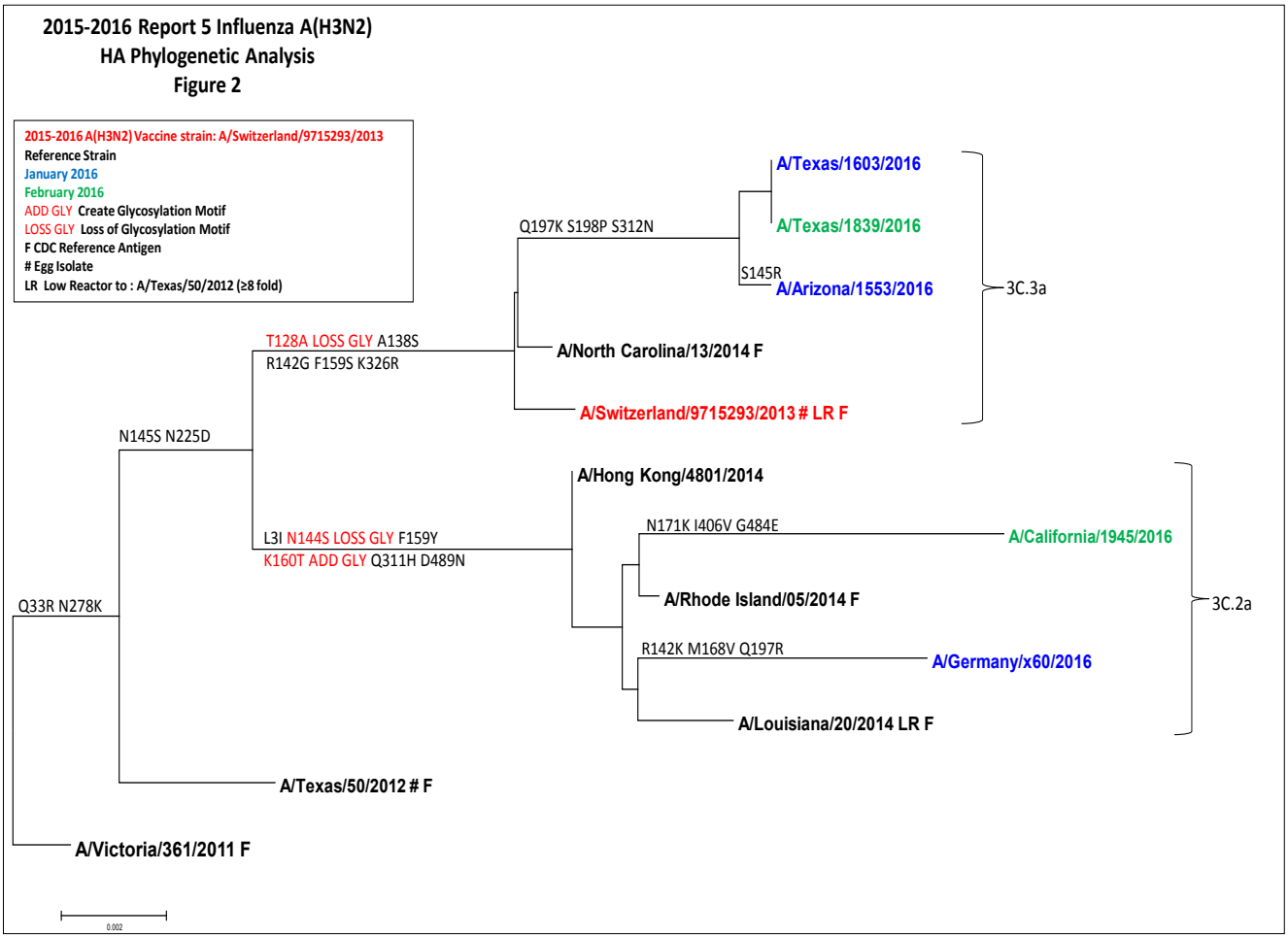
Influenza A(H1N1)pdm09

- 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 96.4-96.9% 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 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, T278I (threonine to isoleucine), was observed that could cause the loss of a glycosylation motif, while another mutation, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif.
- Of the 31 mutations present in the A(H1N1)pdm09 specimens, 12 occurred at predicted antigenic sites and three at the receptor binding site.[2,5]



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/Victoria/361/2011-like virus [Figure 2].
- The A(H3N2) specimens characterized for this report exhibited an overall protein homology of 96.9-98.7% compared to the 2015-2016 influenza vaccine component, A/Switzerland/9715293/2013-like virus.
- Two of the influenza A(H3N2) sequences classified as clade 3C.2a, while the remaining three sequences classified as clade 3C.3a.
- Among the influenza A(H3N2) specimens characterized in this report, two mutations; T128A (threonine to alanine), and N144S (asparagine to serine), were observed that could cause the loss of a glycosylation motif. One mutation, K160T (lysine to threonine), was observed that could cause the gain of a glycosylation motif.
- Of the 21 mutations present in the A(H3N2) specimens, seven occurred at predicted antigenic sites and two at the receptor binding site.[2,5]

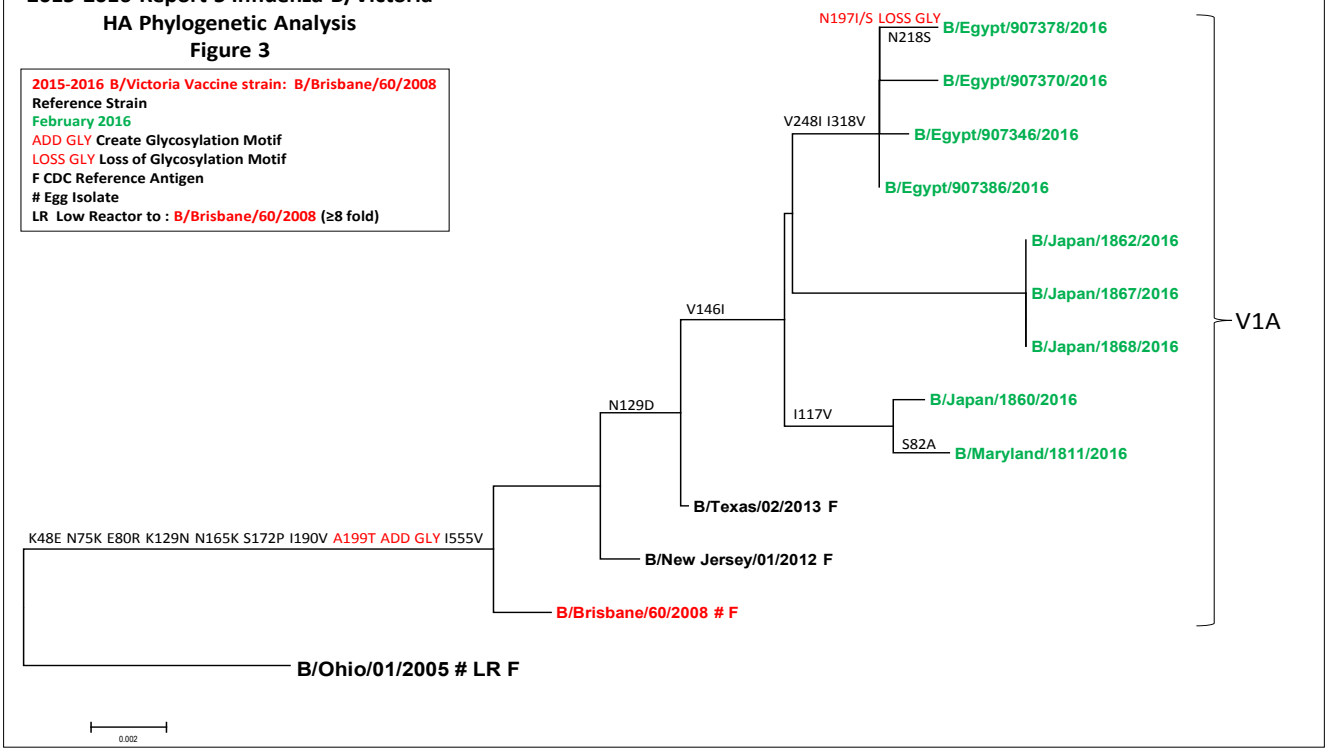


Influenza B

- The influenza B isolates are characterized in lineage specific; neighbor-joining phylogenetic trees with reference strains and are rooted from previous vaccines; B/Ohio/01/2005-like virus for B/Victoria specimens [Figure 3] and B/Florida/04/2006-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] Nine of the 19 influenza B viruses characterized in this report fall into the Victoria lineage, while the other 10 fall into the Yamagata lineage.
- The influenza B/Victoria specimens characterized for this report exhibited a protein homology of 98.9-99.5% 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 98.9-99.1% 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 1A, while all of the influenza B/Yamagata specimens classify into Clade 3.
- Among the influenza B/Victoria specimens one mutation, A199T (alanine to threonine), was observed that would cause the gain of a glycosylation motif. There was an ambiguous mutation in the Victoria specimens, N197I/S (asparagine to isoleucine or serine), which would cause the loss of a glycosylation motif regardless of the ambiguity. For the influenza B/Yamagata specimens, the mutation D197N (aspartic acid to asparagine) was observed that would lead to the gain of a glycosylation motif.

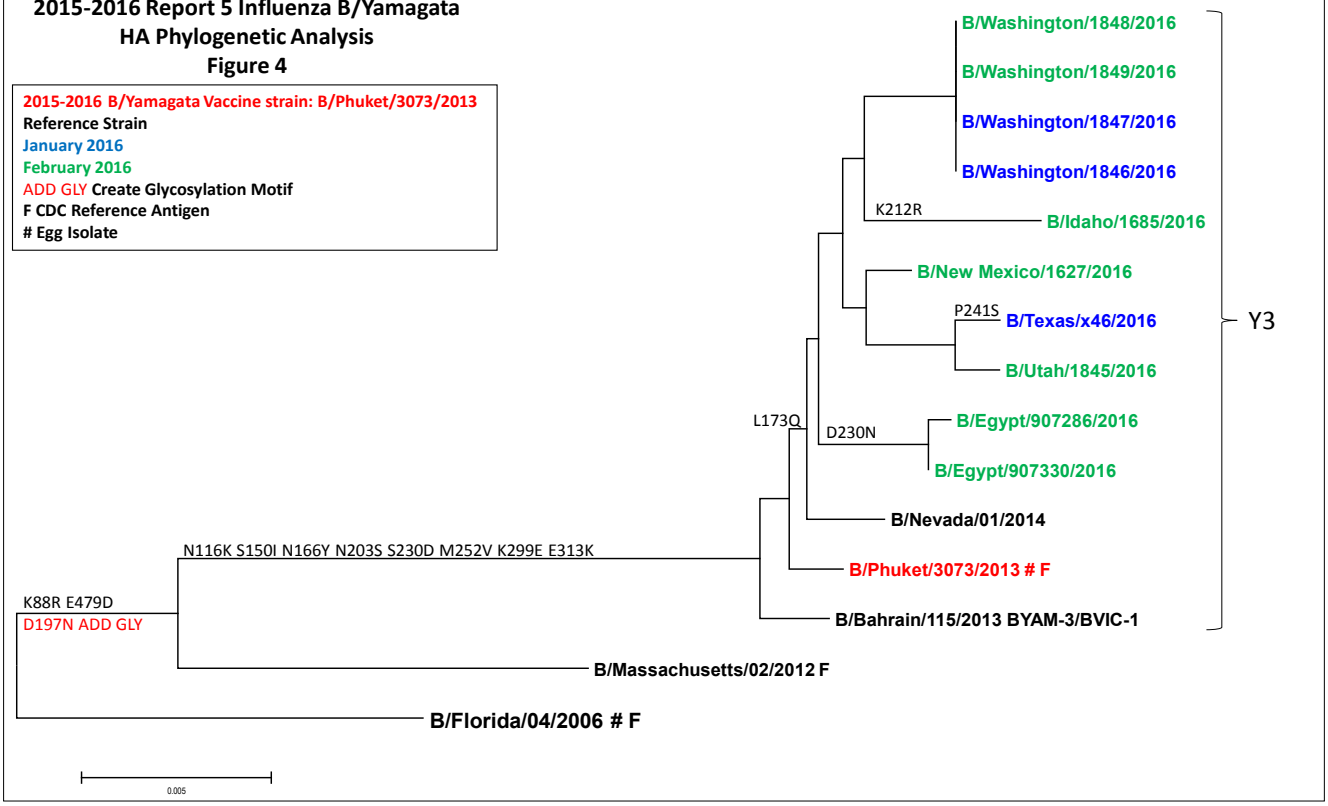
2015-2016 Report 5 Influenza B/Victoria HA Phylogenetic Analysis
Figure 3

2015-2016 B/Victoria Vaccine strain: B/Brisbane/60/2008
Reference Strain
February 2016
ADD GLY Create Glycosylation Motif
LOSS GLY Loss of Glycosylation Motif
F CDC Reference Antigen
Egg Isolate
LR Low Reactor to : B/Brisbane/60/2008 (≥8 fold)



2015-2016 Report 5 Influenza B/Yamagata HA Phylogenetic Analysis
Figure 4

2015-2016 B/Yamagata Vaccine strain: B/Phuket/3073/2013
Reference Strain
January 2016
February 2016
ADD GLY Create Glycosylation Motif
F CDC Reference Antigen
Egg Isolate



Molecular Sequence Analysis Report

USAFSAM Epidemiology Laboratory Service

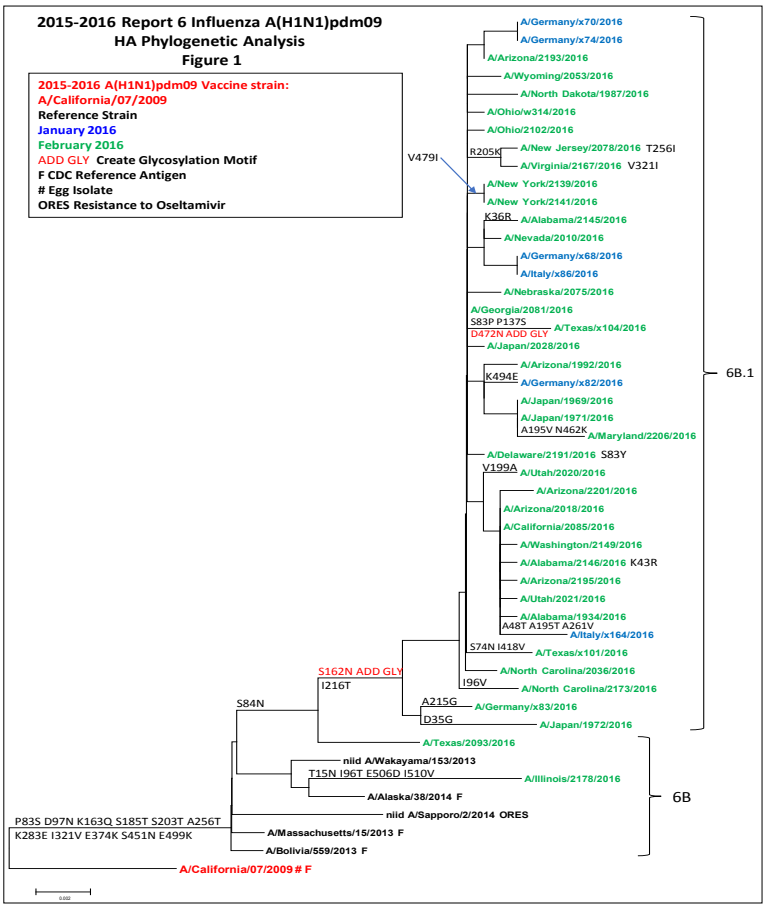
This is the sixth USAFSAM sequence and surveillance report for the 2015-2016 influenza season. It includes 79 specimens collected between 13 January 2016 and 22 February 2016. Among the sequences analyzed for this report, 42 (53.2%) were influenza A(H1N1)pdm09, 10 (12.7%) were influenza A(H3N2), 11 (13.9%) were influenza B/Victoria, and 16 (20.2%) 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	3			
	Arizona, Davis-Monthan AFB	1	1		
	Arizona, Luke AFB	4	4		1
	California, Travis AFB	1		1	1
	Delaware, Dover AFB	1			
	Georgia, Robins AFB	1			
	Illinois, Scott AFB	1			1
	Kentucky, Ft Campbell				1
	Maryland, JB Andrews	1			
	Nebraska, Offutt AFB	1			
	Nevada, Nellis AFB	1			
	New Jersey, JB McGuire-Dix-Lakehurst	1			
	New Mexico, Cannon AFB				1
	New York, USMA – West Point	2	1		
	North Carolina, Seymour Johnson AFB	1			
	North Carolina, Ft Bragg	1			
	North Dakota, Minot AFB	1			
	Ohio, Wright-Patterson AFB	2	1		
	Texas, Laughlin AFB			1	
	Texas, SAMMC	2	2	1	3
	Texas, Sheppard AFB	1		1	
	Utah, Hill AFB	2			3
	Virginia, NMC Portsmouth	1			
	Washington, Fairchild AFB	1			
	Washington, NH Bremerton				5
	Wyoming, FE Warren AFB	1			
OCONUS	**Country 2,** Location A		1	3	
	Germany, Landstuhl RMC	5		2	
	Germany, Spangdahlem AB			1	
	Italy, Aviano AB	2			
	Japan, Misawa AB	1			
	Japan, Yokota AB	3		1	
TOTAL		42	10	11	16

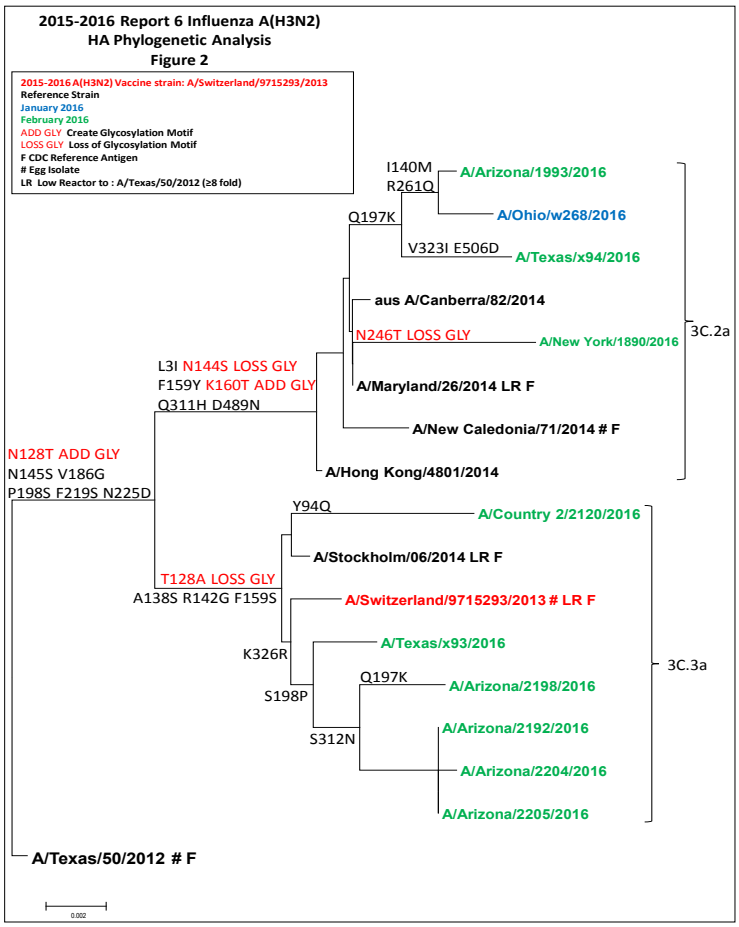
Influenza A(H1N1)pdm09

- 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 96.4-97.3% 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 subgroup, 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). Forty of the influenza A(H1N1)pdm09 specimens sequenced for this report were in subgroup 6B.1, while the remaining two classified as group 6B only.
- 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, two mutations, S162N (serine to asparagine) and D472N (aspartic acid to asparagine), were observed that could cause a gain of a glycosylation motif.
- Of the 34 mutations present in the A(H1N1)pdm09 specimens, 14 occurred at predicted antigenic sites and one at the receptor binding site.[2,5]



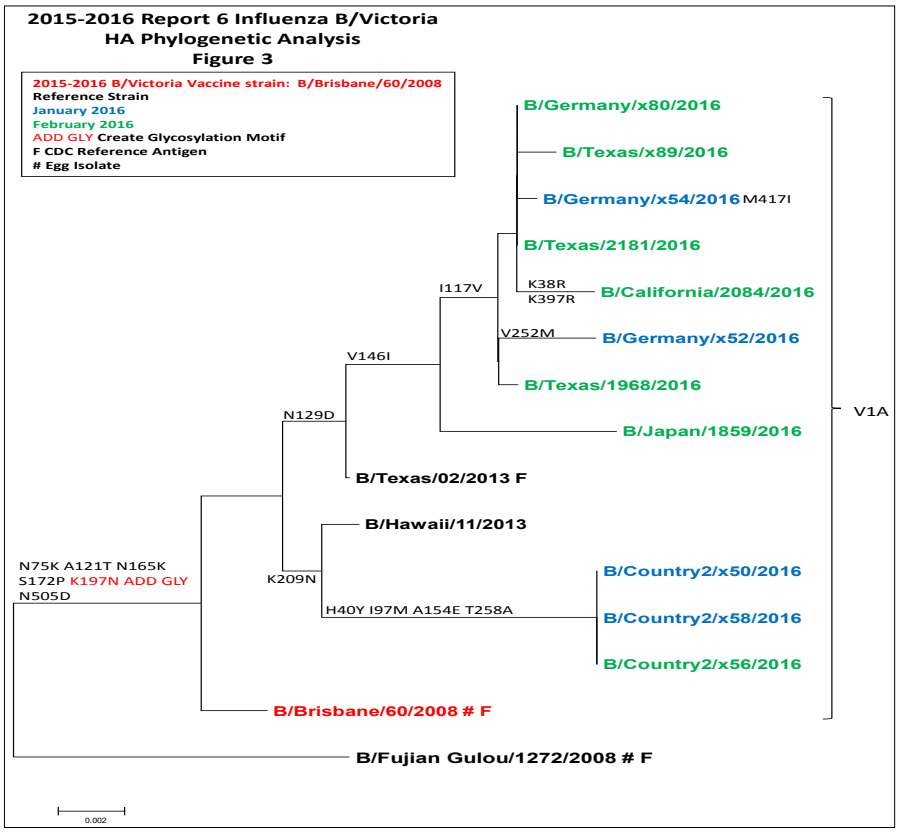
Influenza A(H3N2)

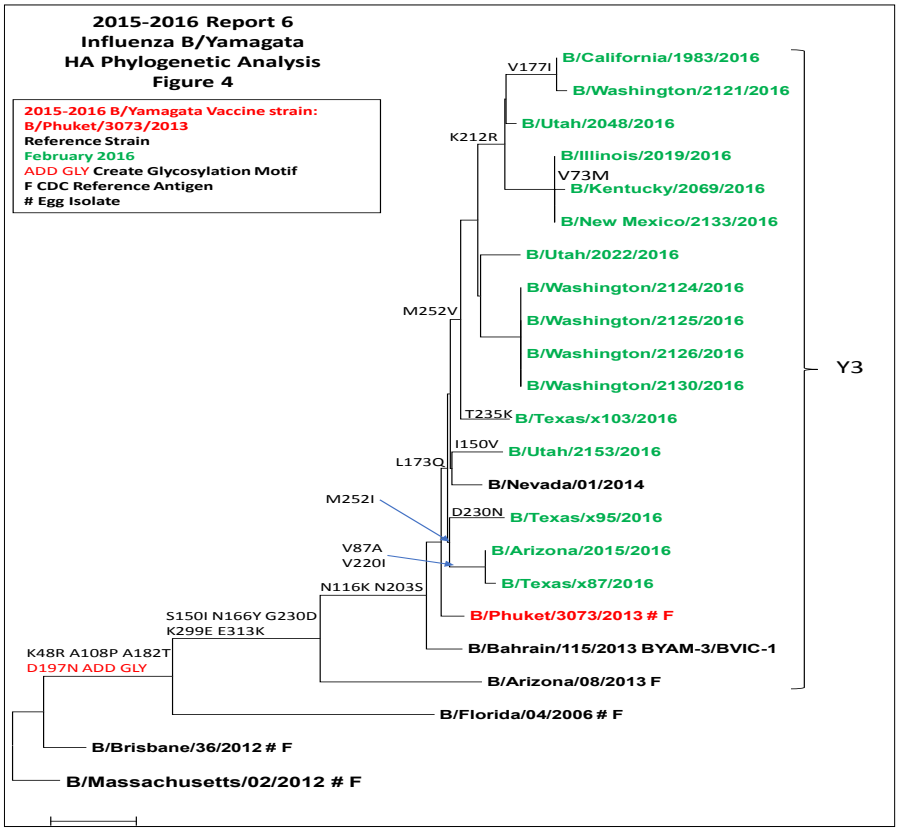
- The influenza A(H3N2) sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from a previous vaccine strain, A/Texas/50/2012-like virus [Figure 2]. Previous reports had the influenza A(H3N2) phylogenetic trees rooted from A/Victoria/361/2011-like virus, therefore some of the mutations may appear differently in this and subsequent reports.
- The A(H3N2) specimens characterized for this report exhibited an overall protein homology of 96.9-99.1% 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. Four of the influenza A(H3N2) sequences classified as subclade 3C.2a, while the remaining six sequences classified as subclade 3C.3a.
- Among the influenza A(H3N2) specimens characterized in this report, three mutations; T128A (threonine to alanine), and N144S (asparagine to serine), 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 23 mutations present in the A(H3N2) specimens, 12 occurred at predicted antigenic sites and three at the receptor binding site.[2,5]



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]. Previous reports had the influenza B/Victoria and B/Yamagata phylogenetic trees rooted from B/Ohio/1/2005 and B/Florida/04/2006-like virus, respectively, therefore some mutations may appear differently in this and subsequent reports.
- 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] Eleven (40.7%) of the 27 influenza B viruses characterized in this report fall into the Victoria lineage, while the other 16 (59.3%) fall into the Yamagata lineage.
- The influenza B/Victoria specimens characterized for this report exhibited a protein homology of 98.6-99.5% 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
- Among the influenza B/Victoria specimens one mutation, K197N (lysine to asparagine), was observed that would cause the gain of a glycosylation motif. For the influenza B/Yamagata specimens, the mutation D197N (aspartic acid to asparagine) was observed that would lead to the gain of a glycosylation motif.


2015-2016 Report 6 Influenza B/Victoria
HA Phylogenetic Analysis
Figure 3
2015-2016 B/Victoria Vaccine strain: B/Brisbane/60/2008
Reference Strain
January 2016
February 2016
ADD GLY Create Glycosylation Motif
F CDC Reference Antigen
Egg Isolate
B/Germany/x80/2016
B/Texas/x89/2016
B/Germany/x54/2016
M417I
B/Texas/2181/2016
I117V
K38R
K397R
B/California/2084/2016
V252M
B/Germany/x52/2016
V146I
B/Texas/1968/2016
N129D
B/Japan/1859/2016
V1A
B/Texas/02/2013 F
B/Hawaii/11/2013
N75K A121T N165K
S172P K197N ADD GLY
N505D
K209N
B/Country2/x50/2016
H40Y I97M A154E T258A
B/Country2/x58/2016
B/Country2/x56/2016
B/Brisbane/60/2008 # F
B/Fujian Gulou/1272/2008 # F
0.002


2015-2016 Report 6
Influenza B/Yamagata
HA Phylogenetic Analysis
Figure 4
2015-2016 B/Yamagata Vaccine strain:
B/Phuket/3073/2013
Reference Strain
February 2016
ADD GLY Create Glycosylation Motif
F CDC Reference Antigen
Egg Isolate
V177I
B/California/1983/2016
B/Washington/2121/2016
B/Utah/2048/2016
K212R
B/Illinois/2019/2016
V73M
B/Kentucky/2069/2016
B/New Mexico/2133/2016
B/Utah/2022/2016
B/Washington/2124/2016
M252V
B/Washington/2125/2016
B/Washington/2126/2016
B/Washington/2130/2016
Y3
T235K
B/Texas/x103/2016
I150V
B/Utah/2153/2016
L173Q
B/Nevada/01/2014
M252I
D230N
B/Texas/x95/2016
V87A
V220I
B/Arizona/2015/2016
B/Texas/x87/2016
N116K N203S
B/Phuket/3073/2013 # F
S150I N166Y G230D
K299E E313K
B/Bahrain/115/2013 BYAM-3/BVIC-1
K48R A108P A182T
D197N ADD GLY
B/Arizona/08/2013 F
B/Florida/04/2006 # F
B/Brisbane/36/2012 # F
B/Massachusetts/02/2012 # F

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.

2. Kongchanagul A., Suptawiwat, O., Kanrai, P., Uiprasertkul, M., Puthavathana, P., and Auewarakul P. (2008) Positive selection at the receptor-binding site of haemagglutinin H5 in viral sequences derived from human tissues. Journal of Gen. Vir. **89**, 1805-1810.

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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 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 4 April 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 10-13

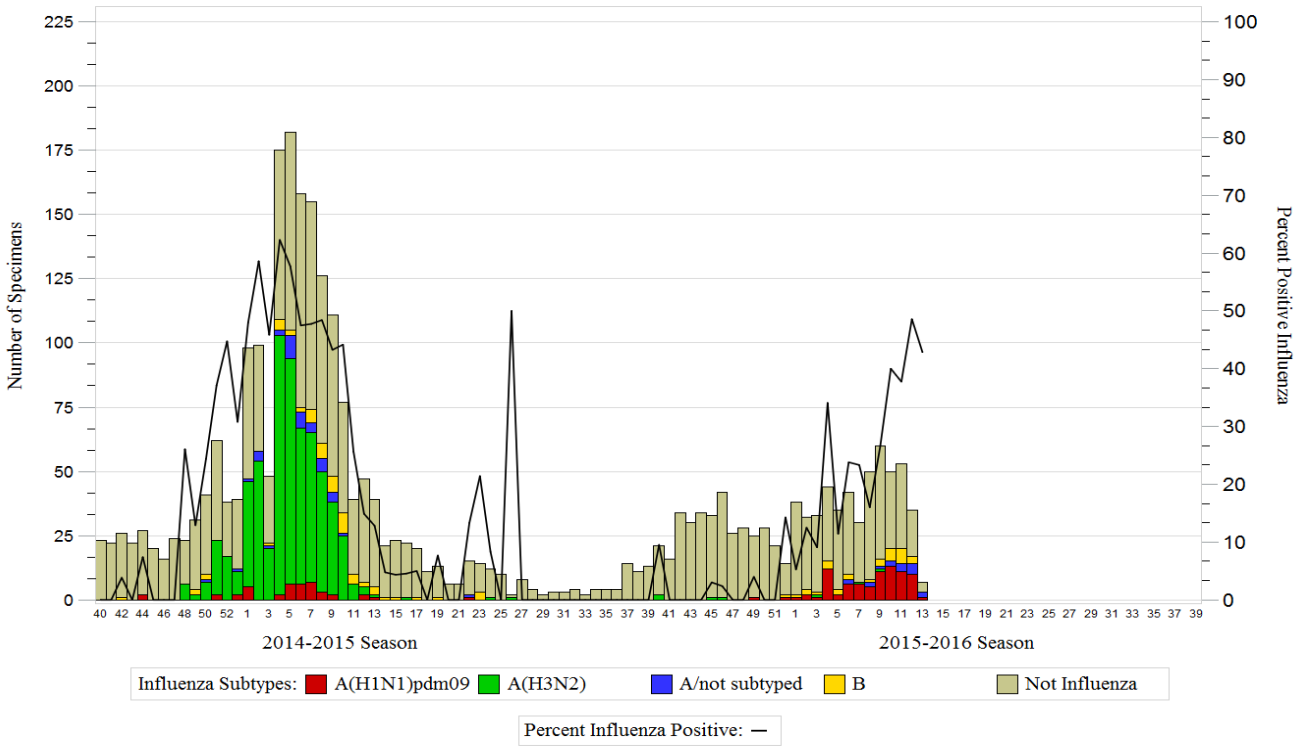
Region		A(H1N1)pdm09	A/not subtyped	A/not subtyped & hMNV	A/not subtyped & Para	A/not subtyped & RSV	A/not subtyped & Rhino/Entero	A(H1N1)pdm09 & B	A(H1N1)pdm09 & hMNV	A(H1N1)pdm09 & RSV	A(H1N1)pdm09 & Rhino/Entero	Influenza A & B	B	Adenovirus	hMNV	RSV	Rhinovirus/Enterovirus	Adeno & RSV	Adeno & RSV & Rhino/Entero	hMNV & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
Deployed	Country 6, Location A	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	5	9
EUCOM	Incirlik AB, Turkey	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Landstuhl RMC, Germany	11	2	2	-	-	-	-	-	-	-	-	2	-	2	7	3	-	-	-	1	17	47
	NAVSTA Rota, Spain	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NSA Naples, Italy	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	RAF Lakenheath, England	6	-	-	1	-	1	-	1	1	-	-	5	2	2	-	1	1	-	-	-	4	25
	Ramstein AB, Germany	-	1	-	-	-	-	-	-	-	-	-	1	-	-	1	1	-	-	-	-	2	6
	Spangdahlem AB, Germany	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	USAG Stuttgart, Germany	5	2	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-	-	-	1	10
	USAG Vicenza, Italy	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	2
	Vilseck AHC, Germany	8	1	-	-	1	-	1	-	-	1	1	4	1	-	3	4	-	1	1	-	14	41
Total		31	6	2	1	1	1	1	1	1	1	1	14	4	4	11	12	1	1	1	1	50	146

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 & 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 & RSV	A(H1N1)pdm09 & Rhino/Entero	A(H3N2) & Rhino/Entero	Influenza A & B	B	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
Deployed	Country 2, Location A	1	-	-	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	2	7
	Country 6, Location A	6	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	15	-	-	-	-	-	-	-	33	58
EUCOM	Aviano AB, Italy	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	7
	Incirlik AB, Turkey	-	1	1	-	-	1	-	-	-	-	1	1	-	-	-	-	5	1	7	7	-	-	-	-	-	-	-	9	34
	Landstuhl RMC, Germany	16	-	2	2	-	-	-	-	-	-	1	-	1	5	-	3	5	7	18	23	-	-	-	-	-	3	2	101	189
	NAVSTA Rota, Spain	-	-	1	-	-	-	-	-	-	-	-	-	-	1	-	1	1	3	1	4	-	-	-	-	-	-	-	10	22
	NSA Naples, Italy	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2	1	1	3	-	-	-	-	-	-	-	13	22
	RAF Lakenheath, England	24	2	1	-	1	-	1	-	3	1	1	-	-	6	-	5	11	9	23	52	1	-	-	-	1	3	19	95	259
	Ramstein AB, Germany	1	-	1	-	-	-	-	-	-	-	-	-	-	4	-	1	2	2	3	11	-	-	-	-	-	-	1	23	49
	Spangdahlem AB, Germany	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	1	-	-	-	-	1	-	-	6	11
	USAG Stuttgart, Germany	11	-	2	-	-	-	-	-	-	-	-	-	1	1	-	2	6	3	4	15	-	-	-	-	1	-	-	31	77
	USAG Vicenza, Italy	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	-	1	5	-	-	-	-	-	-	-	8	17
	Vilseck AHC, Germany	10	-	1	-	-	1	-	1	-	-	2	-	1	7	-	1	5	6	11	16	1	1	1	1	3	3	2	38	112
Total		73	6	10	2	1	2	1	1	3	1	5	1	3	29	1	14	39	33	70	152	2	1	1	1	6	9	24	373	864

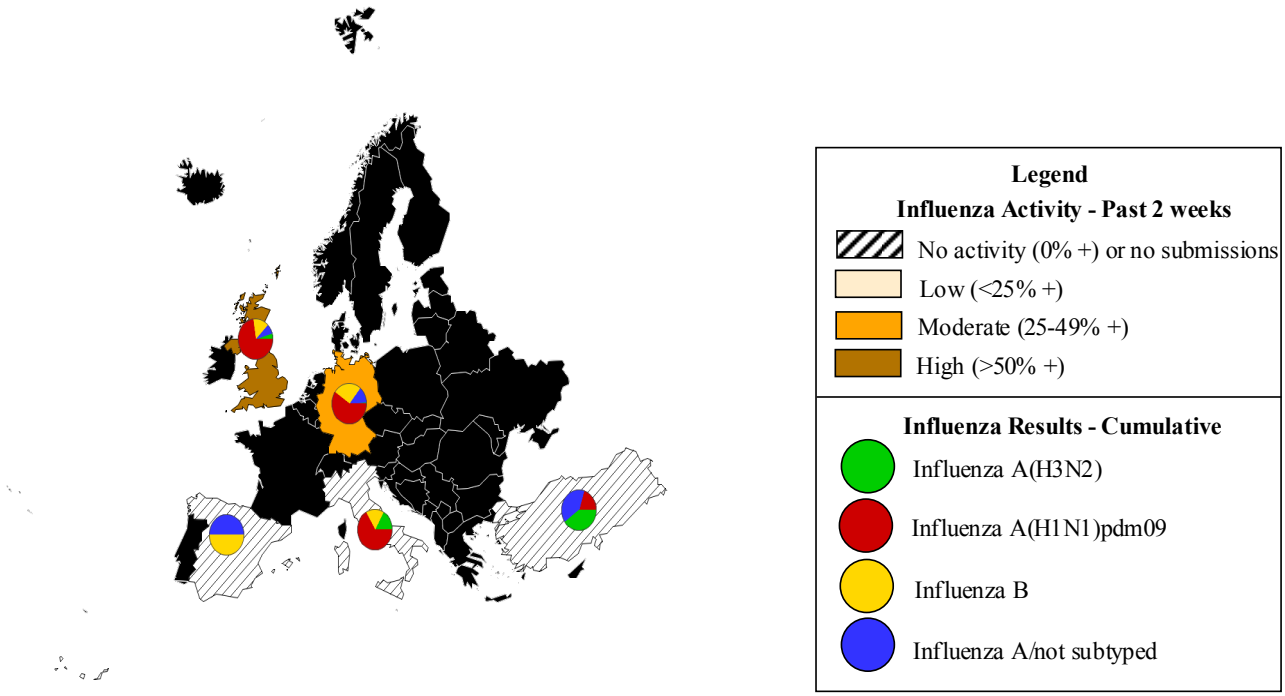
88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Graph 4. Percent influenza positive by week: 2014-2015 surveillance year and through Week 13 of the 2015-2016 surveillance year



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 13 (Europe)



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-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.

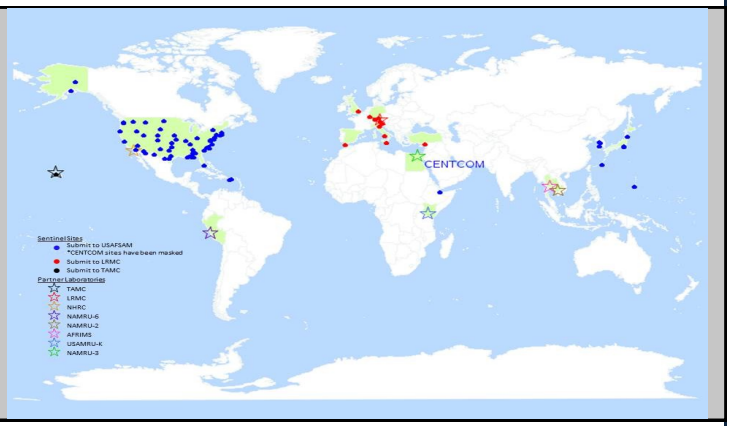
Since the 2006-2007 season, Landstuhl Regional Medical Center (LRMC) has served EUCOM as a USAFSAM contributing laboratory. The initiative seeks to provide more timely results and efficient transport of specimens.

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:

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.