USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2015-2016

Cumulative Results

Location
Collecte
Teste

Influenza A	**139**
A(H1N1)pdm09	118
A(H1N1)pdm09 & Parainfluenza	1
A(H3N2)	19
A(H3N2) & B	1
A/not subtyped	0
Influenza B*	**59**
Other Respiratory Pathogens	**586**
Adenovirus	92
Bordetella pertussis	1
Chlamydophila pneumoniae	1
Coronavirus	61
Human Metapneumovirus	32
Mycoplasma pneumoniae	41
Parainfluenza	74
RSV	81
Rhino/Enterovirus	124
Non-influenza Viral Coinfections	67
Non-influenza Bacterial Coinfections	12
-*C. pneumo* coinfections (2)	
-*C. pneumo* & *M. pneumo* (1)	
-*M. pneumo* coinfections (6)	
-*B. pertussis* coinfections (3)	

Lab data are current as of 22 February 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 - 20 February 2016 (Surveillance Weeks 6 & 7)

- During 7 - 20 February 2016, a total of 268 specimens were collected and received from 55 locations. Results were finalized for 193 specimens from 45 locations. During Week 6, 26 influenza A(H1N1)pdm09, five A(H3N2), and six influenza B viruses were identified. Twenty-nine influenza A(H1N1)pdm09, two A(H3N2), and seven influenza B viruses were identified during Week 7.

- During Week 6 (7 - 13 February 2016), influenza activity increased slightly in the United States. **Viral Surveillance:** The most frequently identified influenza virus type reported by public health laboratories during Week 6 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:** Two influenza-associated pediatric deaths were reported. **Influenza-Associated Hospitalizations:** A cumulative rate for the season of 4.1 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 3.1%, which is above the national baseline of 2.1%. **Geographic Spread of Influenza:** The geographic spread of influenza in Puerto Rico and 12 states was reported as widespread; 20 states reported regional activity; the District of Columbia, Guam, and 15 states reported local activity; and the U.S. Virgin Islands and three states reported sporadic activity (CDC Fluview Summary, cited 23 February 2016).

Table of Contents

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1. Results by region and location for specimens collected during Weeks 6 & 7

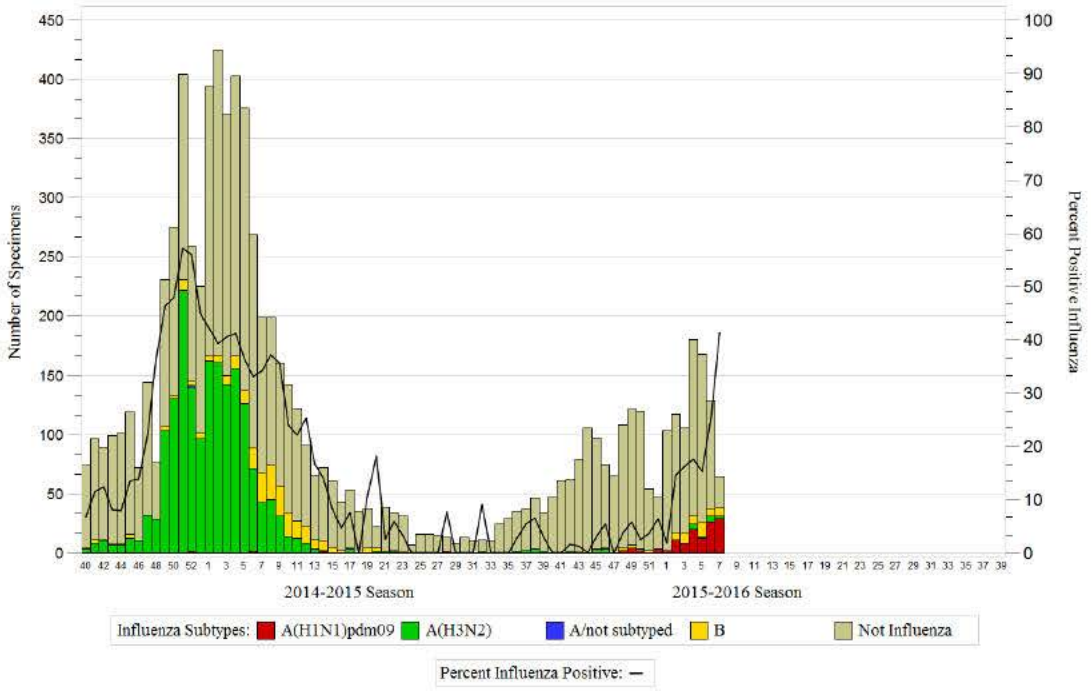
Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona & RSV	Adeno & RSV	Corona & hMNV	Corona & RSV	hMNV & RSV	hMNV & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
PACOM	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Misawa AB, Japan	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Osan AB, South Korea	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	3	-	2	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	6
Region 1	NHCNE Newport, RI	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	3	4
Region 2	JB McGuire-Dix-Lakehurst, NJ	2	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	3
	USMA - West Point, NY	3	1	-	-	-	1	-	-	-	3	-	-	-	-	-	-	-	-	9	17
Region 3	Dover AFB, DE	-	-	-	-	1	-	-	-	1	1	-	-	-	-	-	-	-	-	7	10
	JB Anacostia-Bolling, DC	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	JB Andrews, MD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	JB Langley-Eustis, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 4	Columbus AFB, MS	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Eglin AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	4	5	
	Ft Bragg, NC	1	-	-	1	-	1	-	-	-	-	1	-	-	-	-	-	-	-	2	6
	Ft Campbell, KY	2	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	8
	Hurlburt Field, FL	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	4
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Maxwell AFB, AL	4	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	6
	Moody AFB, GA	3	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	4
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	4
	Seymour Johnson AFB, NC	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Shaw AFB, SC	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1	2
	Tyndall AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 5	Scott AFB, IL	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Wright-Patterson AFB, OH	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5
Region 6	Altus AFB, OK	2	-	-	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	2	6
	Laughlin AFB, TX	-	-	1	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	3	6
	Little Rock AFB, AR	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
	Sheppard AFB, TX	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	3	5
	Tinker AFB, OK	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 7	McConnell AFB, KS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Offutt AFB, NE	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	3	6
Region 8	Ellsworth AFB, SD	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	FE Warren AFB, WY	2	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	4
	Hill AFB, UT	4	-	3	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	12
	Minot AFB, ND	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	2
	Peterson AFB, CO	1	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	5	8
Region 9	Davis-Monthan AFB, AZ	2	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Edwards AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	4	2	2	-	-	-	1	-	-	1	-	-	-	1	2	1	-	-	2	16
	Nellis AFB, NV	3	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	1	6
	Travis AFB, CA	2	1	2	-	-	-	1	-	-	2	-	-	-	-	1	-	-	1	2	12
Region 10	Fairchild AFB, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Bremerton, WA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Total		55	7	13	4	1	5	4	2	2	10	7	1	1	2	3	1	1	2	72	193

**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 7 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.

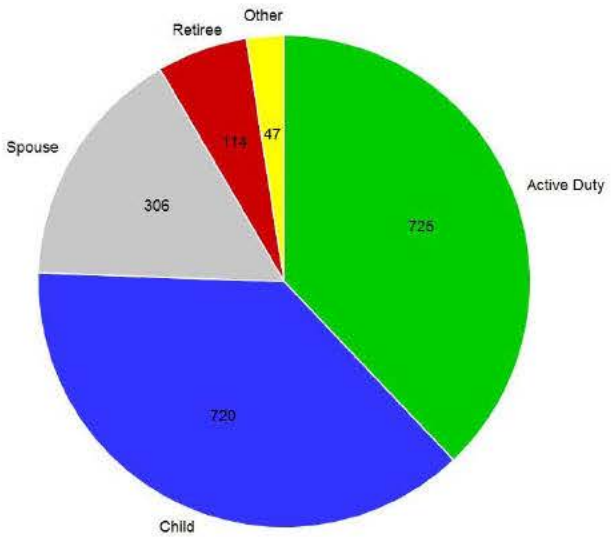
Table 2. ILI by age group for the 2015-2016 surveillance year through Week 7

Age Group	Frequency	Percent
0-5	457	23.90
6-9	114	5.96
10-17	152	7.95
18-24	303	15.85
25-44	637	33.32
45-64	199	10.41
65+	50	2.62

Demographic Summary

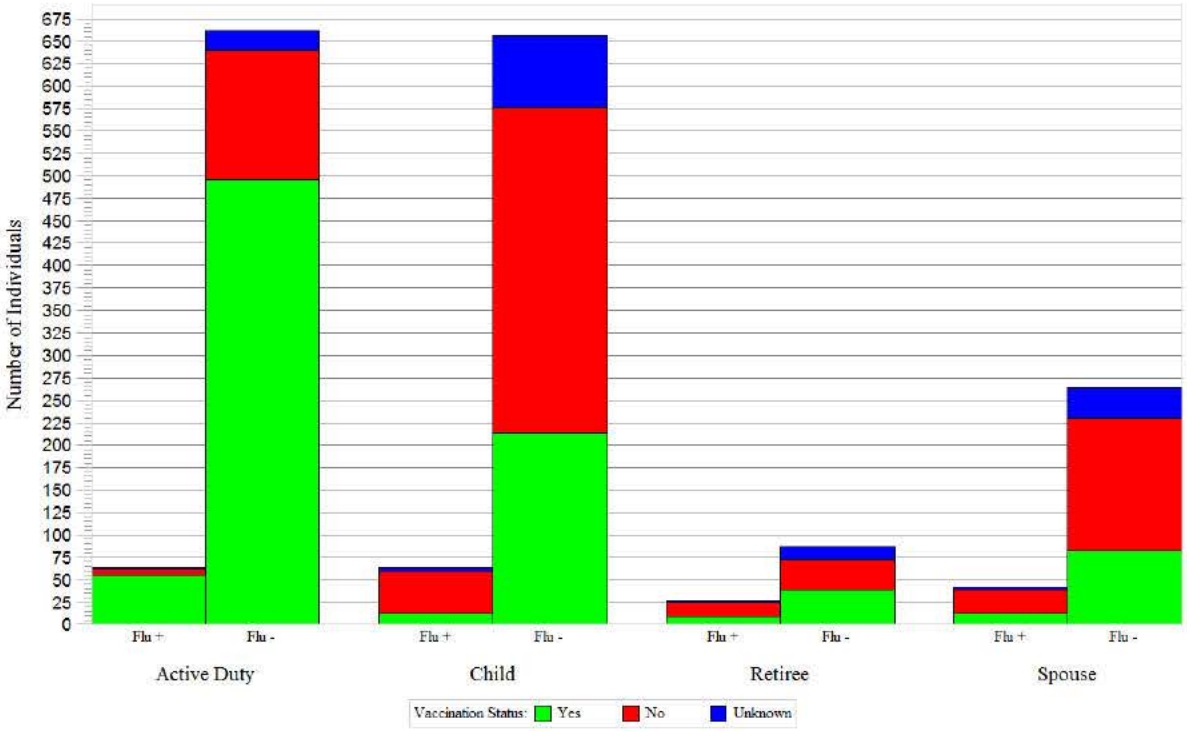
Of 1,912 ILI cases, 725 are service members (37.9%), 720 are children (37.7%), 306 are spouses (16.0%), and 161 (8.4%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=1,912) is 23 (range 0, 93).

Graph 2. ILI by beneficiary status for the 2015-2016

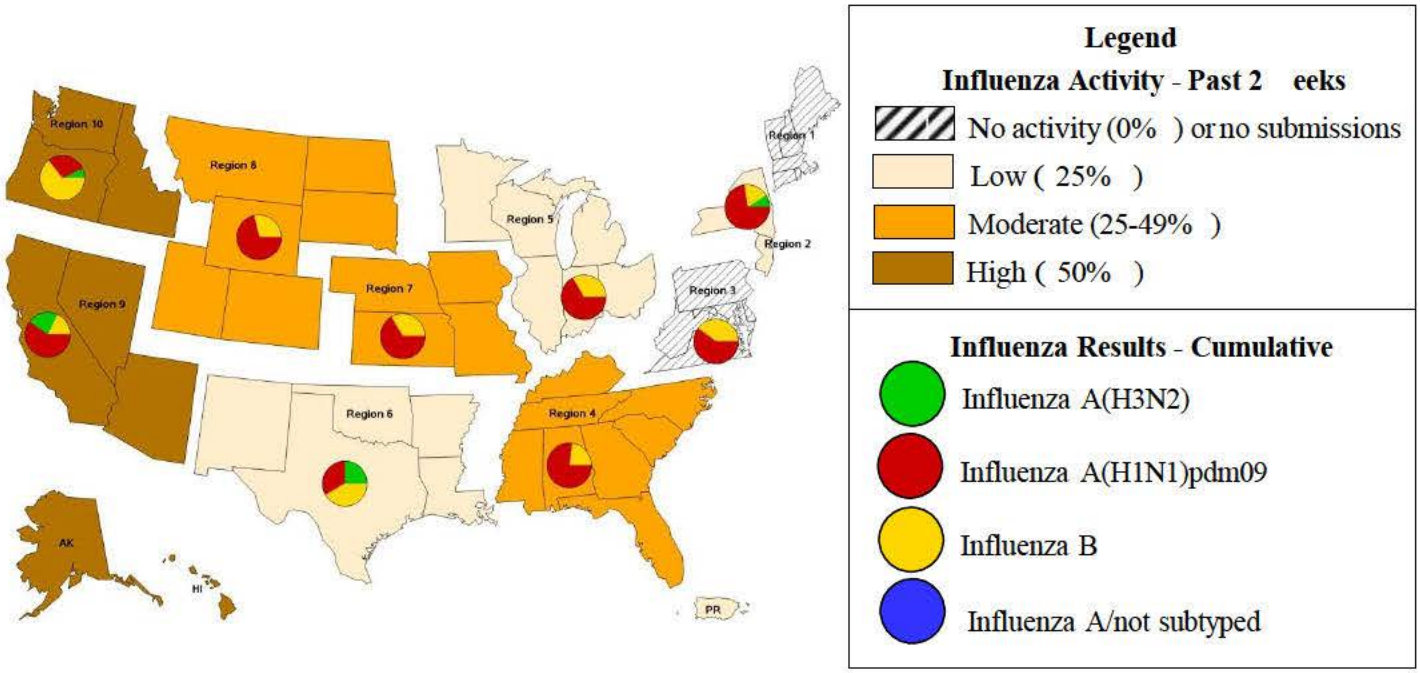


88ABW-2015-5508 and PA email guidance dated 10 November 2015.

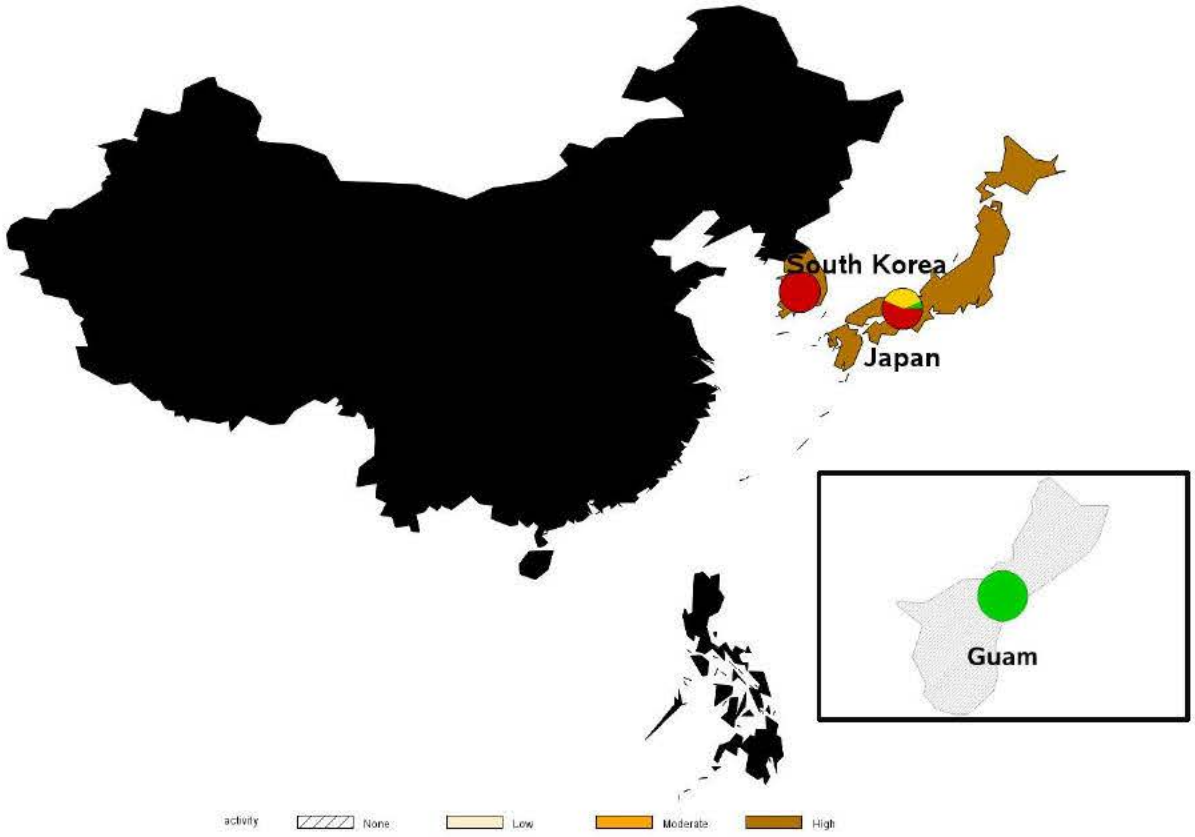
Graph 3. Vaccination status by beneficiary type for the 2015-2016 surveillance year through Week 7



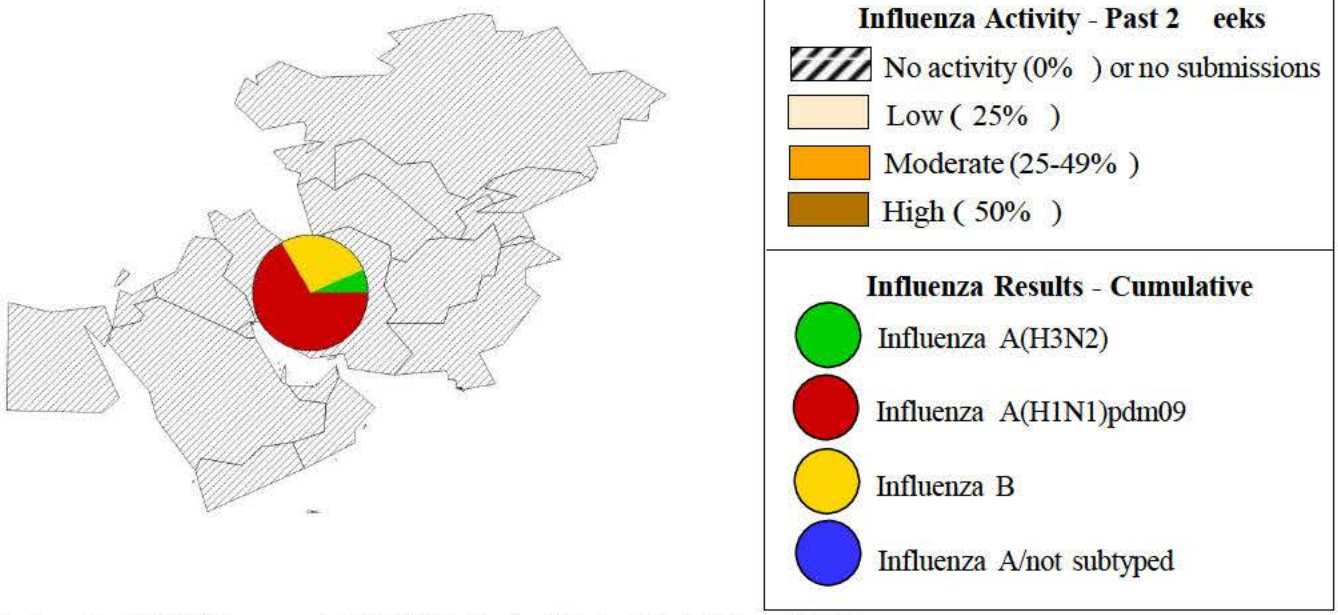
Map 1. Influenza subtypes and activity level by region for the 2015-2016 surveillance year through Week 7



Map 2. Influenza subtypes and activity level by country for the 2015-2016 surveillance year through Week 7 (Pacific)*



Map 3. Influenza subtypes and activity level for CENTCOM for the 2015-2016 surveillance year through Week 7



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.

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 7

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 & Para	Influenza A & B	B	Adenovirus	*B. pertussis*	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	Non-Influenza Bacterial Coinfection	No Pathogen	Total
Deployed	Country 2, Location A	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	11
PACOM	CFA Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
	Eielson AFB, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	JB Elmendorf-Richardson, AK	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	2	3
	JR Marianas - Andersen AFB, Guam	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	3
	Kadena AB, Japan	-	-	-	-	-	-	-	-	2	-	3	-	-	2	-	-	16	23
	Misawa AB, Japan	2	-	-	-	-	-	-	-	-	-	-	-	1	3	-	-	4	10
	Osan AB, South Korea	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	6
	Yokota AB, Japan	7	-	-	-	6	4	-	-	2	-	2	2	2	-	1	-	18	44
Region 1	Hanscom AFB, MA	-	-	-	-	-	4	-	-	-	-	-	2	-	-	2	-	16	24
	NHCNE Newport, RI	-	-	-	-	-	-	-	-	1	-	-	-	1	1	-	-	8	11
	USCG Academy, CT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 2	Ft Drum, NY	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	3	5
	JB McGuire-Dix-Lakehurst, NJ	2	-	-	-	-	1	-	-	-	-	3	-	-	5	3	-	14	28
	USMA - West Point, NY	5	1	1	-	2	12	-	-	7	5	3	3	7	3	3	2	78	132
Region 3	Dover AFB, DE	1	-	-	-	-	-	-	1	-	1	-	1	1	-	1	-	32	38
	JB Anacostia-Bolling, DC	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	2
	JB Andrews, MD	-	-	-	-	1	1	-	-	-	1	1	-	1	-	-	-	4	9
	JB Langley-Eustis, VA	1	-	-	-	-	5	-	-	4	2	-	3	8	4	1	-	12	40
	NCRM - Walter Reed NMMC, MD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NMC Portsmouth, VA	1	-	-	-	1	4	-	-	1	-	5	1	2	2	-	1	19	37
Region 4	CGS Mobile, AL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Columbus AFB, MS	1	-	-	-	-	1	-	-	1	-	-	-	1	2	-	-	15	21
	Eglin AFB, FL	2	-	-	-	-	6	-	-	-	1	-	4	6	5	1	-	43	68
	Ft Bragg, NC	1	-	-	-	-	3	-	-	3	1	1	-	3	1	-	1	24	38
	Ft Campbell, KY	2	-	-	-	2	1	-	-	1	2	-	2	-	3	-	-	24	37
	Hurlburt Field, FL	1	-	-	-	-	-	-	-	-	-	1	-	-	-	2	-	18	22
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	1	-	-	2	1	-	24	28
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-	-	1	4
	Maxwell AFB, AL	5	-	-	-	-	3	-	-	-	-	-	1	2	3	1	-	34	49
	Moody AFB, GA	3	-	-	-	4	7	-	-	1	1	2	2	5	9	5	-	18	57
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	1	-	1	1	-	-	4	7
	NH Jacksonville, FL	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	-	7	11
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	4	-	-	-	-	-	-	-	-	-	2	1	1	-	-	-	10	18
	Seymour Johnson AFB, NC	1	-	-	-	-	2	-	-	1	-	-	-	-	2	1	1	9	17
	Shaw AFB, SC	-	-	-	-	-	-	-	-	2	-	4	-	-	4	1	1	10	22
	Tyndall AFB, FL	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	2	4
Region 5	Scott AFB, IL	1	-	-	-	1	2	-	-	-	-	-	1	-	1	-	-	16	22
	Wright-Patterson AFB, OH	1	-	-	-	-	2	-	-	-	-	-	-	-	3	-	-	13	19
Region 6	Altus AFB, OK	2	-	-	-	-	3	-	-	3	2	-	2	3	3	3	-	40	61
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	3	4
	Cannon AFB, NM	-	-	-	-	1	1	-	-	2	-	-	-	-	2	-	-	16	22
	Laughlin AFB, TX	-	3	-	-	1	1	-	-	1	-	-	-	1	-	-	-	6	13
	Little Rock AFB, AR	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	11	13
	Sheppard AFB, TX	2	-	-	-	2	3	-	-	2	2	3	1	1	6	3	-	56	81
	Tinker AFB, OK	-	-	-	-	1	5	-	-	1	-	1	5	7	4	6	1	33	64
	Vance AFB, OK	-	-	-	-	-	1	-	-	-	-	-	1	-	1	-	-	37	40
Region 7	Ft Leavenworth, KS	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	9	11
	McConnell AFB, KS	-	-	-	-	-	1	-	-	1	-	2	2	-	7	-	1	30	44
	Offutt AFB, NE	4	-	-	-	1	2	-	-	1	-	-	3	-	1	-	-	35	47
Region 8	Ellsworth AFB, SD	4	-	-	-	-	1	-	-	1	1	1	5	-	-	4	-	23	40
	FE Warren AFB, WY	2	-	-	-	-	-	1	-	3	1	1	3	6	2	2	-	21	42
	Hill AFB, UT	8	-	-	-	8	1	-	-	1	3	1	-	1	9	-	1	61	94
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Minot AFB, ND	5	-	-	-	-	-	-	-	1	-	-	1	-	1	1	-	8	17
	Peterson AFB, CO	1	-	-	1	-	1	-	-	4	-	-	-	1	3	3	-	24	38
	USAF Academy, CO	-	-	-	-	-	-	-	-	-	-	-	4	-	1	-	-	10	15
Region 9	Davis-Monthan AFB, AZ	2	4	-	-	-	-	-	-	3	-	-	-	-	1	-	-	9	19
	Edwards AFB, CA	1	-	-	-	-	-	-	-	1	-	-	-	1	-	-	-	7	10
	Luke AFB, AZ	5	2	-	-	4	-	-	-	-	1	-	-	1	-	4	-	13	30
	NH Twentynine Palms, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	15	2	-	-	2	6	-	-	3	-	-	7	4	7	8	-	51	105
	Travis AFB, CA	6	3	-	-	3	2	-	-	2	8	1	5	5	8	5	-	36	84
	USCG Island Alameda, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9	9
Region 10	Fairchild AFB, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	4
	JB Lewis-McChord, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Mt Home AFB, ID	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	7	8
	NH Bremerton, WA	8	1	-	-	17	3	-	-	2	-	2	10	4	7	5	1	40	100
Total		118	19	1	1	9	92	1	1	61	32	41	74	81	124	67	12	1128	1912

**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

Third USAFSAM Epidemiology Laboratory Service

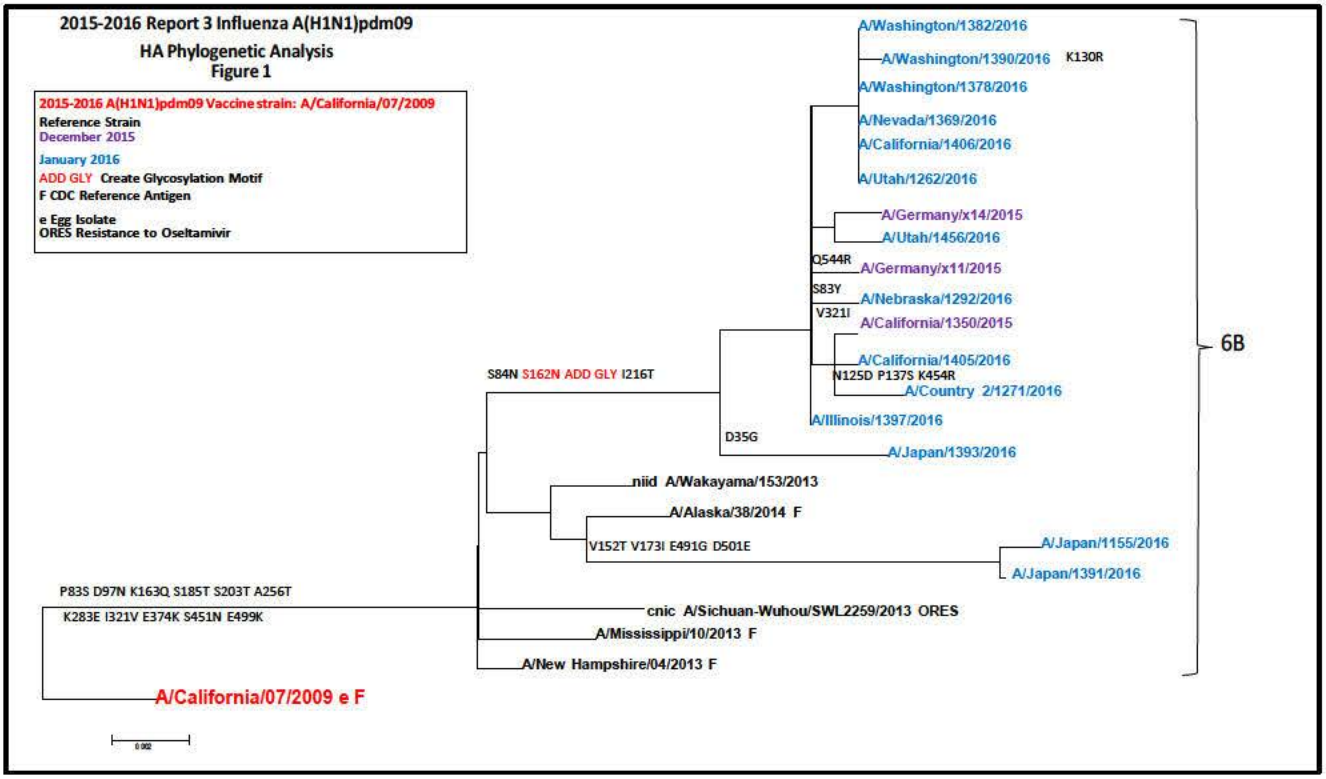
This is the third USAFSAM Sequencing report for the 2015-2016 influenza season. It contains sequence data for 26 specimens that were collected from 11 sentinel sites between 9 December 2015 and 22 January 2016 and subsequently analyzed by USAFSAM. Among these specimens, 17 (65%) were influenza A(H1N1)pdm09, three (12%) were influenza B/Victoria, and six (23%) 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	B/Victoria	B/Yamagata
CONUS	**California,** NH Twentynine Palms	1		
	California, Travis AFB	2	1	
	Georgia, Moody AFB		1	
	Illinois, Scott AFB	1		
	Nebraska, Offutt AFB	1		
	Nevada, Nellis AFB	1		
	Utah, Hill AFB	2		
	Washington, NH Bremerton	3	1	4
OCONUS	**Country 2,** Location A	1		
	Germany, Landstuhl RMC	2		2
	Japan, Yokota AB	3		
TOTAL		**17**	**3**	**6**

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 96.4-97.1% 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, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif.
- Of the 24 mutations present in the A(H1N1)pdm09 specimens, eight 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 2] and B/Florida/04/2006-like virus for B/Yamagata specimens [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] Three of the influenza B viruses characterized in this report fall into the Victoria lineage, while the other six fall into the Yamagata lineage.

- The influenza B/Victoria specimens characterized for this report exhibited a protein homology of 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 98.9-99.1% when compared to the 2015-2016 B/Yamagata vaccine strain, B/Phuket/3073/2013-like virus.

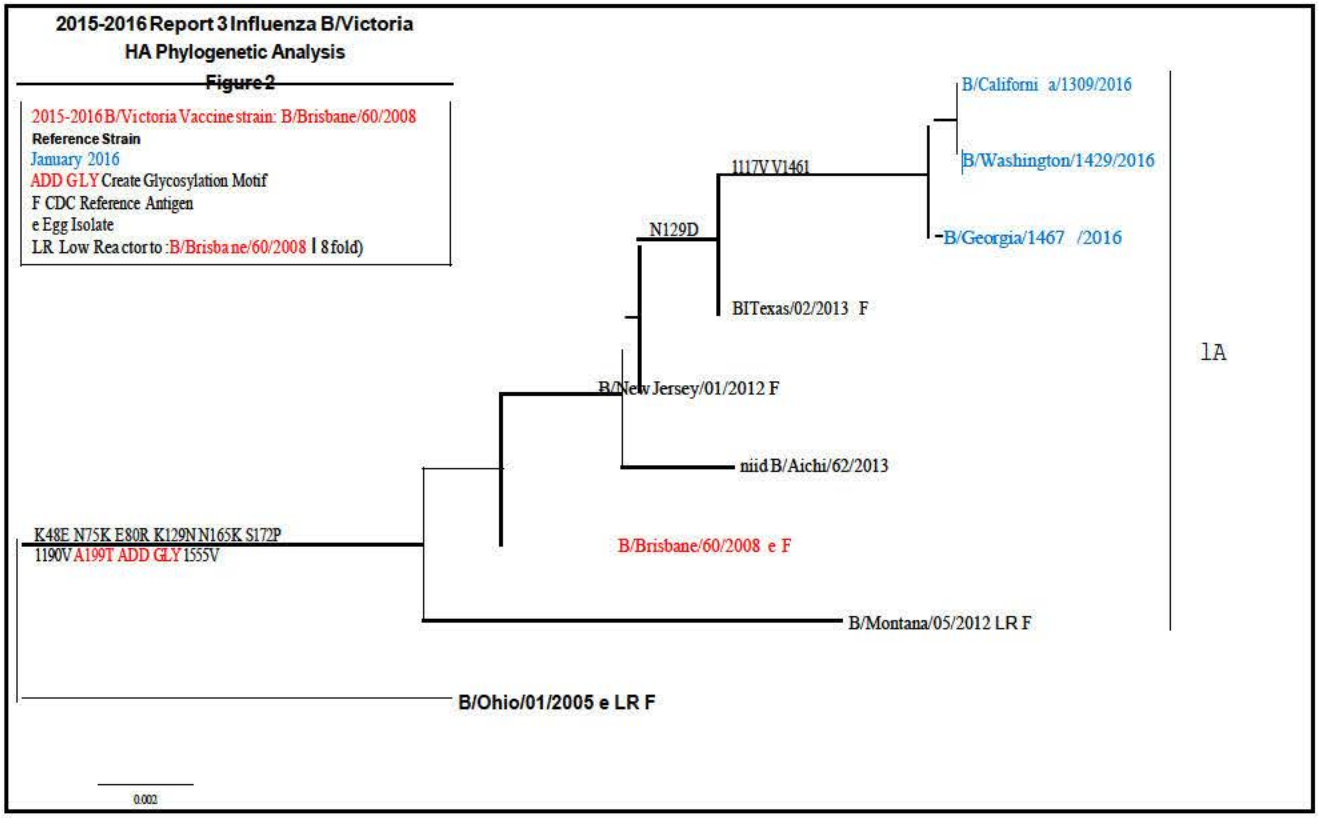
- All three of the influenza B/Victoria specimens classify into group 1A, while all six influenza B/Yamagata specimens classify into group 3.

- Among the influenza B/Victoria specimens one mutation, A199T (alanine to threonine), was observed that could cause the gain of a glycosylation motif. For the influenza B/Yamagata specimens, the mutation D197N (aspartic acid to asparagine) was observed that could lead to the gain of a glycosylation motif. Both of these mutations impact the same glycosylation motif for influenza B hemagglutinin.

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

Figure 2

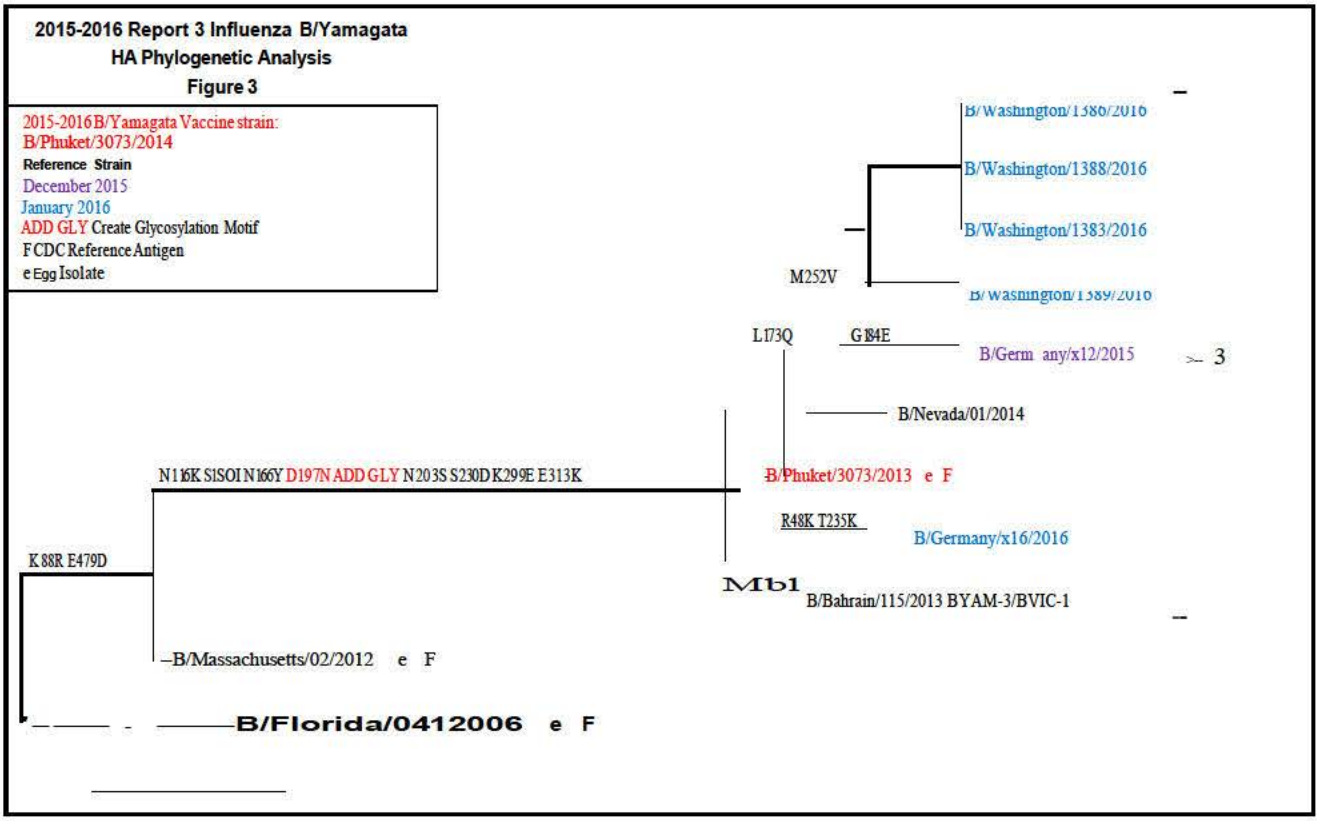
2015-2016 B/Victoria Vaccine strain: B/Brisbane/60/2008
Reference Strain
January 2016
ADD GLY Create Glycosylation Motif
F CDC Reference Antigen
e Egg Isolate
LR Low Reactor to :B/Brisbane/60/2008 | 8 fold)



2015-2016 Report 3 Influenza B/Yamagata HA Phylogenetic Analysis

Figure 3

2015-2016 B/Yamagata Vaccine strain:
B/Phuket/3073/2014
Reference Strain
December 2015
January 2016
ADD GLY Create Glycosylation Motif
F CDC Reference Antigen
e Egg Isolate



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.
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.
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.

[redacted]

Molecular Sequence Analysis Report

Fourth USAFSAM Epidemiology Laboratory Service

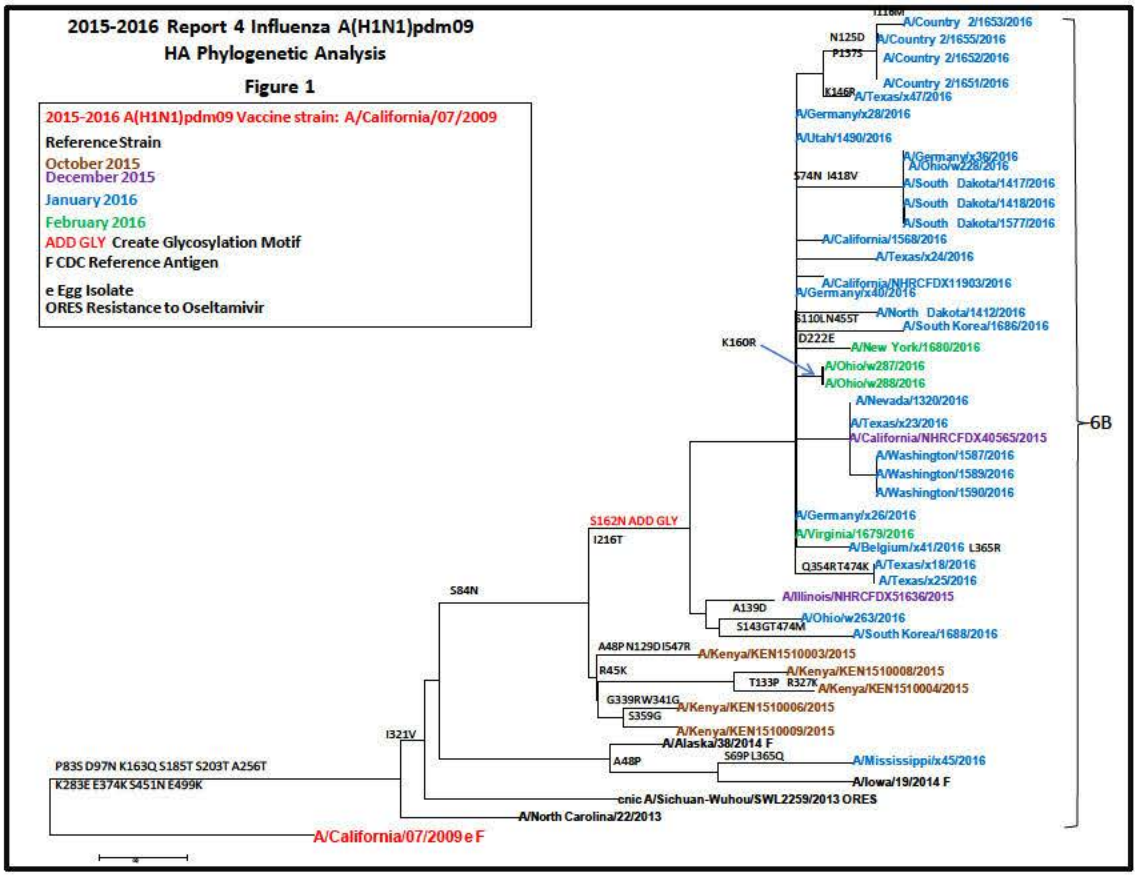
This is the fourth USAFSAM Sequencing report for the 2015-2016 influenza season, and includes 72 sequences from specimens collected between 1 October 2015 and 5 February 2016. Fifty influenza positive specimens were collected from 20 sites and subsequently sequenced and analyzed at USAFSAM. Twenty-two additional sequences were submitted to USAFSAM from partner labs at NHRC (Naval Health Research Center) and USAMRU-K (United States Army Medical Research Unit in Kenya) and were included in this analysis. Among the sequences analyzed for this report, 41 (56.9%) were influenza A(H1N1)pdm09, 12 (16.7%) were influenza A(H3N2), two (2.8%) were influenza B/Victoria, and 17 (23.6%) 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	**Arizona,** Luke AFB				2
	California, NHRC	2	8		2
	California, Travis AFB	1	1		
	Illinois, NHRC	1			
	Mississippi, Keesler AFB	1			
	Nebraska, Offutt AFB				1
	Nevada, Nellis AFB	1			
	New York, USMA – West Point	1			
	North Dakota, Minot AFB	1			
	Ohio, Wright-Patterson AFB	4			
	Oklahoma, Tinker AFB				1
	South Dakota, Ellsworth AFB	3			
	Texas, Laughlin AFB		1		
	Texas, SAMMC	5			1
	Utah, Hill AFB	1			
	Virginia, NMC Portsmouth	1			
	Washington, NH Bremerton	3			7
OCONUS	**Belgium,** Shape AHC	1			
	Country 2, Location A	4			
	Germany, Landstuhl RMC	4		2	
	Kenya, USAMRU-K	5	1		3
	South Korea, Brian Allgood ACH		1		
	South Korea, Osan AB	2			
TOTAL		41	12	2	17

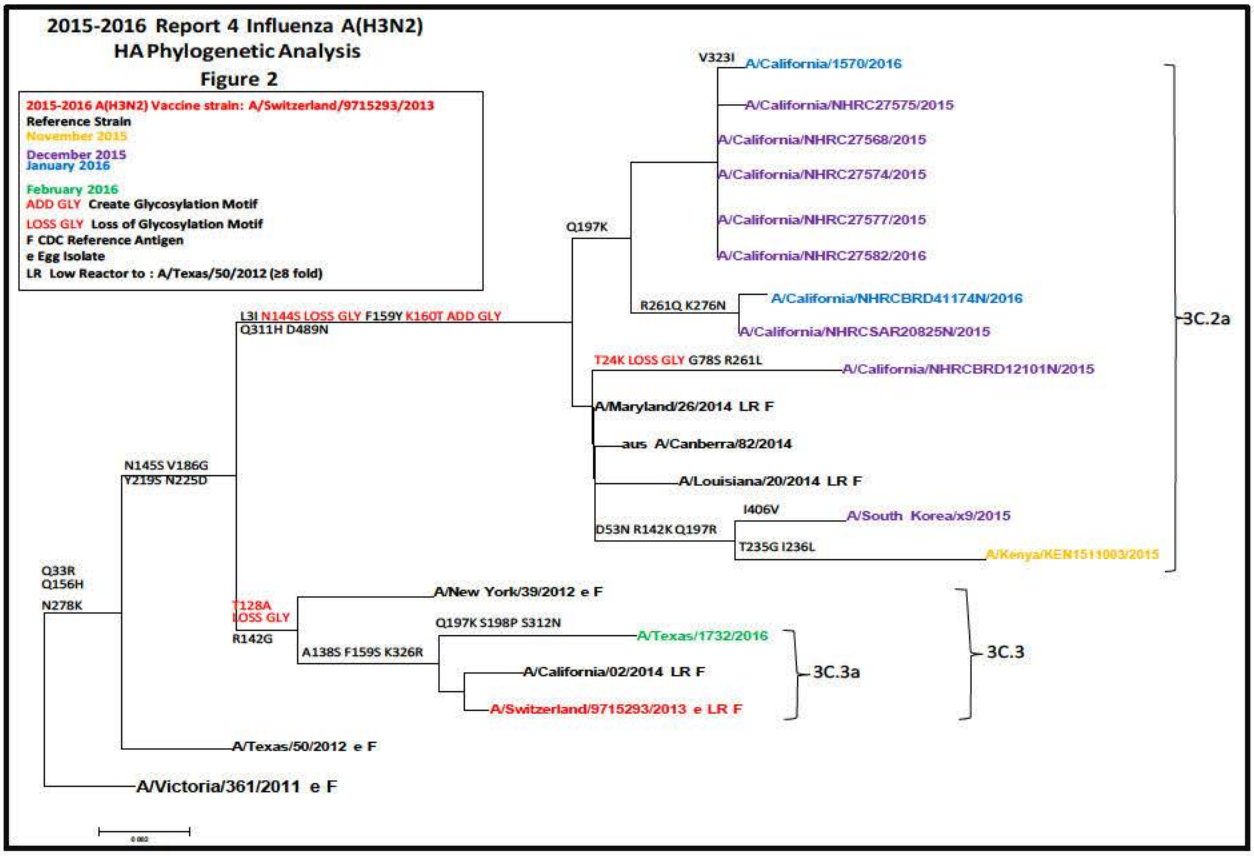
Influenza A(H1N1)pdm09

- The influenza A(H1N1)pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009-like virus [Figure 1].
- The A(H1N1)pdm09 specimens characterized for this report exhibited an overall protein homology of 95.8-97.1% 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, S162N (serine to asparagine), was observed that could cause a gain of a glycosylation motif.
- Of the 39 mutations present in the A(H1N1)pdm09 specimens, 14 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 96.7-98.7% compared to the 2015-2016 influenza vaccine component, A/Switzerland/9715293/2013-like virus.
- Eleven of the influenza A(H3N2) sequences classified as clade 3C.2a, while one sequence classified as clade 3C.3a.
- Among the influenza A(H3N2) specimens characterized in this report, three mutations; T24K (threonine to lysine), 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 29 mutations present in the A(H3N2) specimens, 12 occurred at predicted antigenic sites and three at the receptor binding site.[2,5]



Influenza B

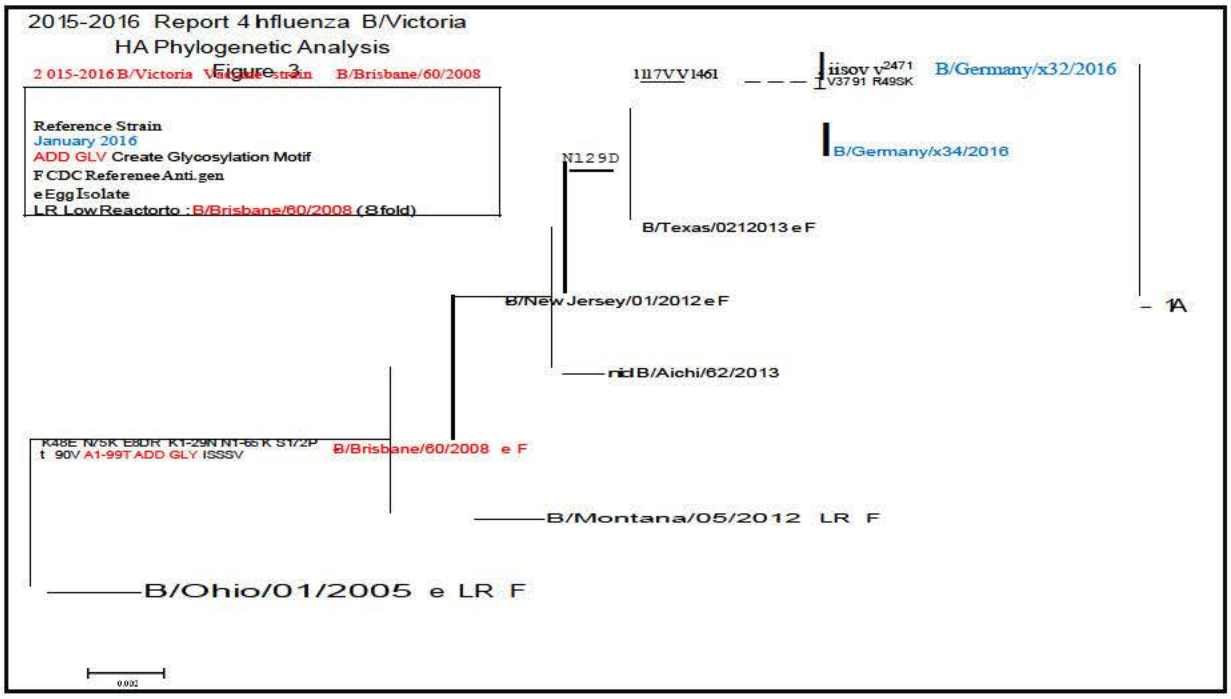
- The influenza B isolates are characterized in lineage specific; neighbor-joining phylogenetic trees with reference strains and are rooted from previous vaccines; B/Ohio/01/2005-like virus for B/Victoria specimens [Figure 3] and B/Florida/04/2006-like virus for B/Yamagata specimens [Figure 4].

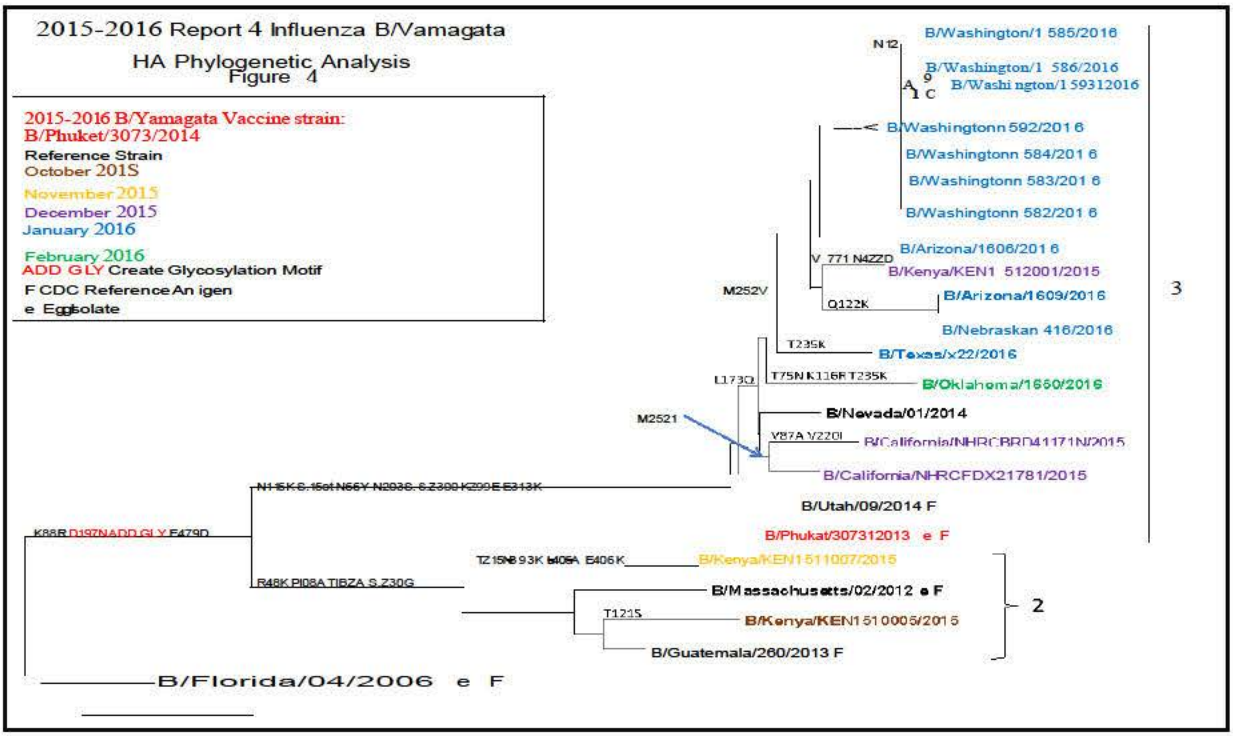
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.[1] Two of the influenza B viruses characterized in this report fall into the Victoria lineage, while the other 17 fall into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

- The influenza B/Victoria specimens characterized for this report exhibited a protein homology of 98.6-99.3% 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 97.0-99.1% when compared to the 2015-2016 B/Yamagata vaccine strain, B/Phuket/3073/2013-like virus.

- Both of the influenza B/Victoria specimens classify into group 1A, distinguished by the mutations N75K (asparagine to lysine), N165K (asparagine to lysine), and S172P (serine to proline). Fifteen of the influenza B/Yamagata sequences classified into group 3, while the remaining two classified into group 2.

- Among the influenza B/Victoria specimens one mutation, A199T (alanine to threonine), was observed that could cause the gain of a glycosylation motif. For the influenza B/Yamagata specimens, the mutation D197N (aspartic acid to asparagine) was observed that could lead to the gain of a glycosylation motif. Both of these mutations impact the same glycosylation motif for influenza B hemagglutinin.


2015-2016 Report 4 hfluenza B/Victoria
HA Phylogenetic Analysis
Figure 3
2 015-2016 B/Victoria Vaccine strain B/Brisbane/60/2008
Reference Strain
January 2016
ADD GLV Create Glycosylation Motif
F CDC Referenee Anti.gen
eEggIsolate
LR LowReactorto : B/Brisbane/60/2008 (8fold)
1117VV1461
iisov V2471 B/Germany/x32/2016
V3791 R49SK
B/Germany/x34/2016
N129D
B/Texas/0212013 e F
B/New Jersey/01/2012 e F
1A
nid B/Aichi/62/2013
K48E N/5K E8DR K1-29N N1-65 K S172P
t 90V A1-99T ADD GLY ISSSV
B/Brisbane/60/2008 e F
B/Montana/05/2012 LR F
B/Ohio/01/2005 e LR F
0.002


2015-2016 Report 4 Influenza B/Vamagata
HA Phylogenetic Analysis
Figure 4
2015-2016 B/Yamagata Vaccine strain:
B/Phuket/3073/2014
Reference Strain
October 201S
November 2015
December 2015
January 2016
February 2016
ADD GLY Create Glycosylation Motif
F CDC Reference An igen
e Eggsolate
N12
B/Washington/1 585/2016
B/Washington/1 586/2016
B/Washi ngton/1 59312016
B/Washingtonn 592/201 6
B/Washingtonn 584/201 6
B/Washingtonn 583/201 6
B/Washingtonn 582/201 6
B/Arizona/1606/201 6
V 771 N4ZZD
B/Kenya/KEN1 512001/2015
M252V
Q122K
B/Arizona/1609/2016
3
B/Nebraskan 416/2016
T235k
B/Texas/x22/2016
L173Q
T75N K116R T235K
B/Oklahoma/1660/2016
M2521
B/Nevada/01/2014
V87A V220I
B/California/NHRCFDX21781/2015
B/Utah/09/2014 F
N156K 8.45et N66Y N203S. 8.Z300 KZ99E E313K
K88R D197NADD GLY E479D
B/Phukat/307312013 e F
TZ15N693K 1405A E406K
B/Kenya/KEN1511007/2015
R48K P108A TIBZA S.Z30G
B/Massachusetts/02/2012 e F
T121S
B/Kenya/KEN1510005/2015
2
B/Guatemala/260/2013 F
B/Florida/04/2006 e 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.
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.
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.

[redacted]

USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the U.S. Air Force School of Aerospace Medicine (USAFSAM) (sentinel site respiratory surveillance), the Naval Health Research Center (recruit and shipboard population-based respiratory surveillance), the Naval Medical Research Unit (NAMRU-3) in Cairo, Egypt, the Naval Medical Research Unit (NAMRU-2) in Phnom Penh, Cambodia, the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Bangkok, Thailand, the Naval Medical Research Unit-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.

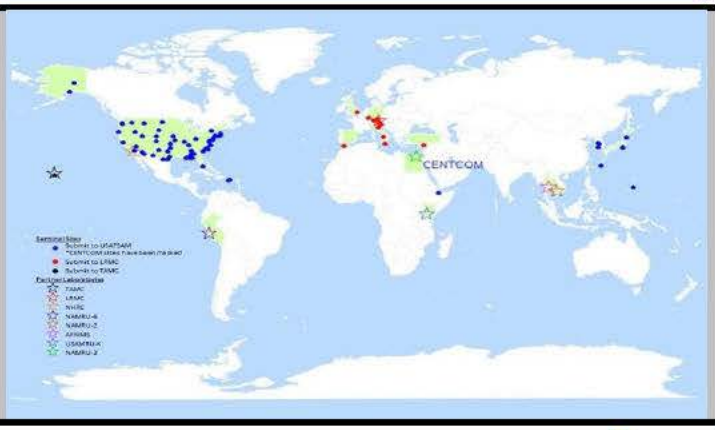
For an expanded view of this report, visit our website. Also available on the website is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and an overview of historical data. Please visit the AFHSC/GEIS 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 10November 2015.