



**Cumulative Results**

Locations	79
Collected	4,395
Tested	4,340

**Influenza A 745**

A(H1N1)pdm09	637
A(H1N1)pdm09 & B	1
A(H1N1)pdm09 & Coronavirus	1
A(H1N1)pdm09 & Parainfluenza	1
A(H3N2)	104
A(H3N2) & B	1

**Influenza B\* 374**

B	373
B & Adenovirus	1

**Other Respiratory Pathogens 1,074**

Adenovirus	163
<i>Bordetella pertussis</i>	1
<i>Chlamydomphila pneumoniae</i>	2
Coronavirus	86
Human Metapneumovirus	86
<i>Mycoplasma pneumoniae</i>	57
Parainfluenza	120
RSV	130
Rhinovirus/Enterovirus	289
Non-influenza Viral Coinfections	124
Non-influenza Bacterial Coinfections	16
-B. pertussis (3)	
-B. pertussis & M. pneumo (1)	
-C. pneumo (2)	
-C. pneumo & M. pneumo (1)	
-M. pneumo (9)	

Lab data are current as of 5 July 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**

5 June - 2 July 2016 (Surveillance Weeks 23 - 26)

- During 5 June - 2 July 2016, a total of 68 specimens were collected and received from 27 locations. Results were finalized for 61 specimens from 26 locations. During Week 23, two influenza B viruses were identified. One influenza A(H1N1)pdm09 was identified in Week 24. One influenza A(H3N2) and one influenza B virus was identified during Week 26. Approximately 7% of specimens tested positive for influenza during Weeks 23 and 24. The percent positive for Week 26 increased to approximately 17% as fewer specimens were received. The influenza percent positive for the season is currently 26%.
- A study recently published in *National Climate Change* reported an association between cold winter temperatures and flu fatality rates in Europe; thus, warmer winters may mean fewer deaths attributable to influenza. Regional mortality data from 1998-2005 for 405 million people in 16 European nations were analyzed to reach this conclusion (Ballester, et al. European seasonal mortality and influenza incidence due to winter temperature variability. National Climate Change. Published 4 July 2016 Cited 7 July 2016).
- This report contains the monthly supplemental EUCOM report for surveillance through 2 July 2016. See page 14 for more details.
- This report contains the ninth molecular sequence analysis report and includes 99 specimens collected between 4 January 2016 and 29 March 2016. See page 8 for further details.

**Table of Contents**

Respiratory Highlights	Page 1
Results by Region and Location for Specimens Collected during Weeks 23-26	Page 2
Laboratory Results - Cumulative for Season and Demographic Summary	Page 3
Vaccination Status by Beneficiary Type	Page 4
Geographic distribution of influenza subtype and activity level maps	Pages 4 & 5
Cumulative Results by Region and Location	Pages 6 & 7
Molecular Sequence Analysis Report #9	Pages 8-13
Monthly Supplemental EUCOM Report	Pages 14 & 15
DoD Global, Laboratory-Based, Influenza Surveillance Program Background	Page 16

# DoD Global, Laboratory-Based, Influenza Surveillance Program

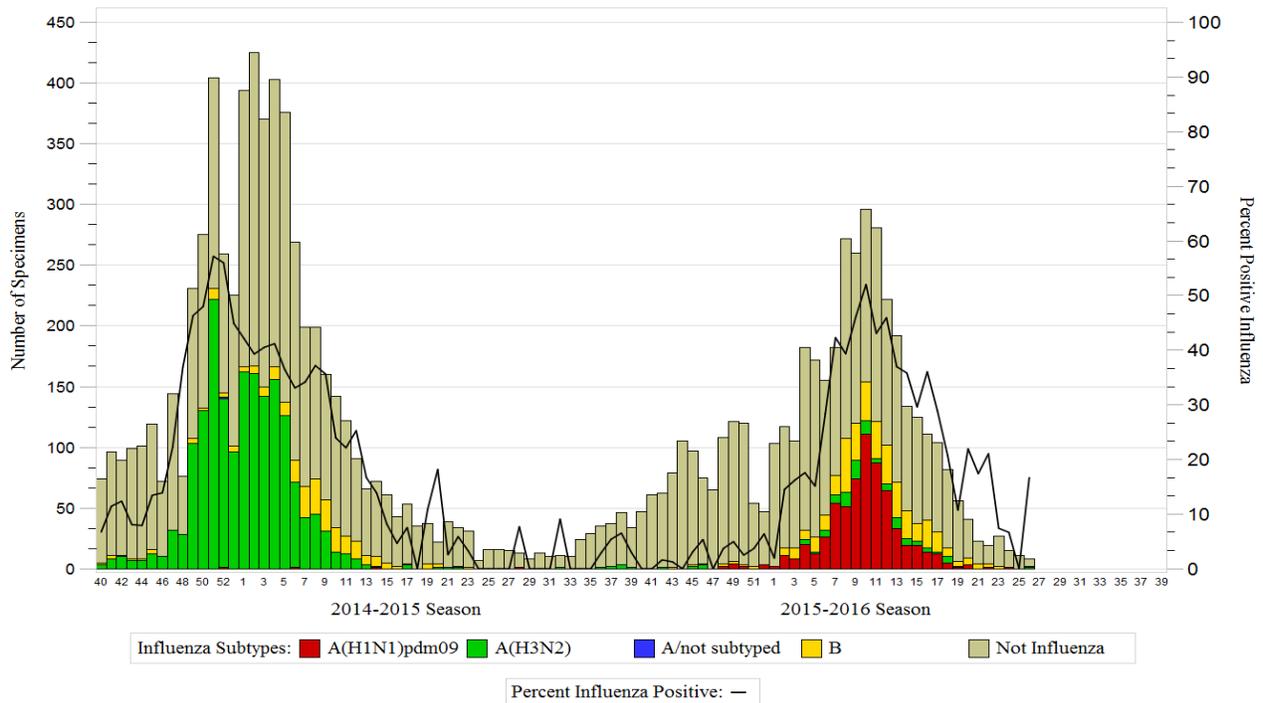
**Table 1.** Results by region and location for specimens collected during Weeks 23-26

Region*		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	Coronavirus	<i>M. pneumoniae</i>	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Rhino/Entero	Para & Rhino/Entero	No Pathogen	Total
PACOM	Eielson AFB, AK	1	-	-	-	-	-	-	-	-	-	-	1	2
	Kadena AB, Japan	-	-	-	-	-	-	-	-	2	-	-	1	3
	Yokota AB, Japan	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 2	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	-	-	-	-	-	-	2	2
	USMA - West Point, NY	-	-	-	1	-	-	1	-	-	1	1	-	4
Region 3	JB Langley-Eustis, VA	-	-	-	-	-	-	-	1	-	-	-	1	2
Region 4	Columbus AFB, MS	-	-	-	-	1	-	-	-	-	-	-	1	2
	Eglin AFB, FL	-	-	-	-	-	-	1	-	-	-	-	3	4
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	-	1	1
	Maxwell AFB, AL	-	-	-	-	-	-	-	-	1	-	-	1	2
	Moody AFB, GA	-	-	-	-	-	-	2	-	2	-	-	2	6
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	1	-	-	1
	Robins AFB, GA	-	-	-	-	-	-	-	-	1	-	-	-	1
	Shaw AFB, SC	-	-	1	-	-	-	-	-	-	-	-	-	1
Region 5	Scott AFB, IL	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 6	Cannon AFB, NM	-	-	-	1	-	-	-	-	1	-	1	-	3
	Laughlin AFB, TX	-	-	2	-	-	-	-	-	1	-	-	-	3
	Sheppard AFB, TX	-	-	-	-	-	-	-	-	1	-	-	3	4
	Tinker AFB, OK	-	-	-	-	-	-	-	-	-	-	-	1	1
	Vance AFB, OK	-	-	-	-	-	-	1	-	-	-	-	1	2
Region 7	McConnell AFB, KS	-	-	-	-	-	-	-	-	-	-	-	1	1
	Offutt AFB, NE	-	-	-	-	-	-	1	-	1	-	-	2	4
Region 9	Luke AFB, AZ	-	-	-	-	-	-	-	-	-	-	-	1	1
	Nellis AFB, NV	-	-	-	-	-	-	1	-	-	-	-	1	2
	Travis AFB, CA	-	-	-	-	-	1	-	-	1	-	-	1	3
Region 10	Mt Home AFB, ID	-	1	-	-	-	-	-	-	-	-	-	-	1
<b>Total</b>		1	1	3	2	1	1	7	1	11	2	2	29	61

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

## Laboratory Results - Cumulative for Season

**Graph 1.** Percent influenza positive by week: 2014-2015 surveillance year and through Week 26 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.

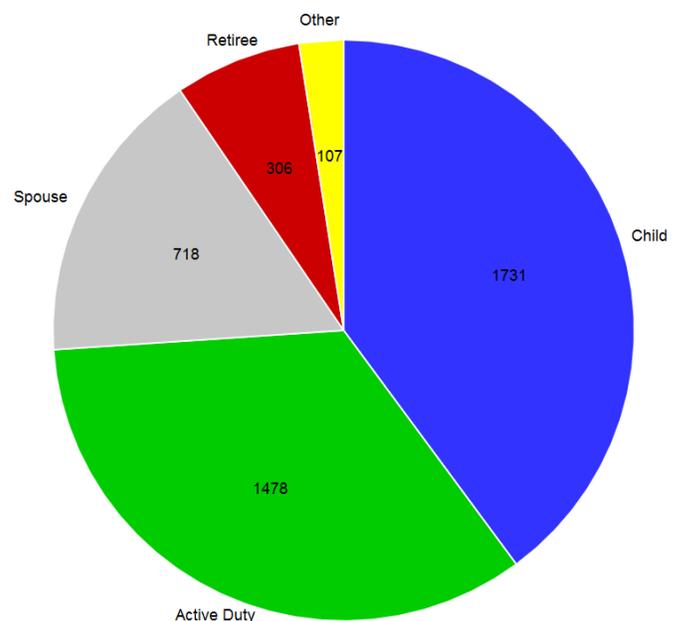
**Table 2.** ILI by age group for the 2015-2016 surveillance year through Week 26

Age Group	Frequency	Percent
0-5	984	22.67
6-9	339	7.81
10-17	411	9.47
18-24	590	13.59
25-44	1390	32.03
45-64	510	11.75
65+	116	2.67

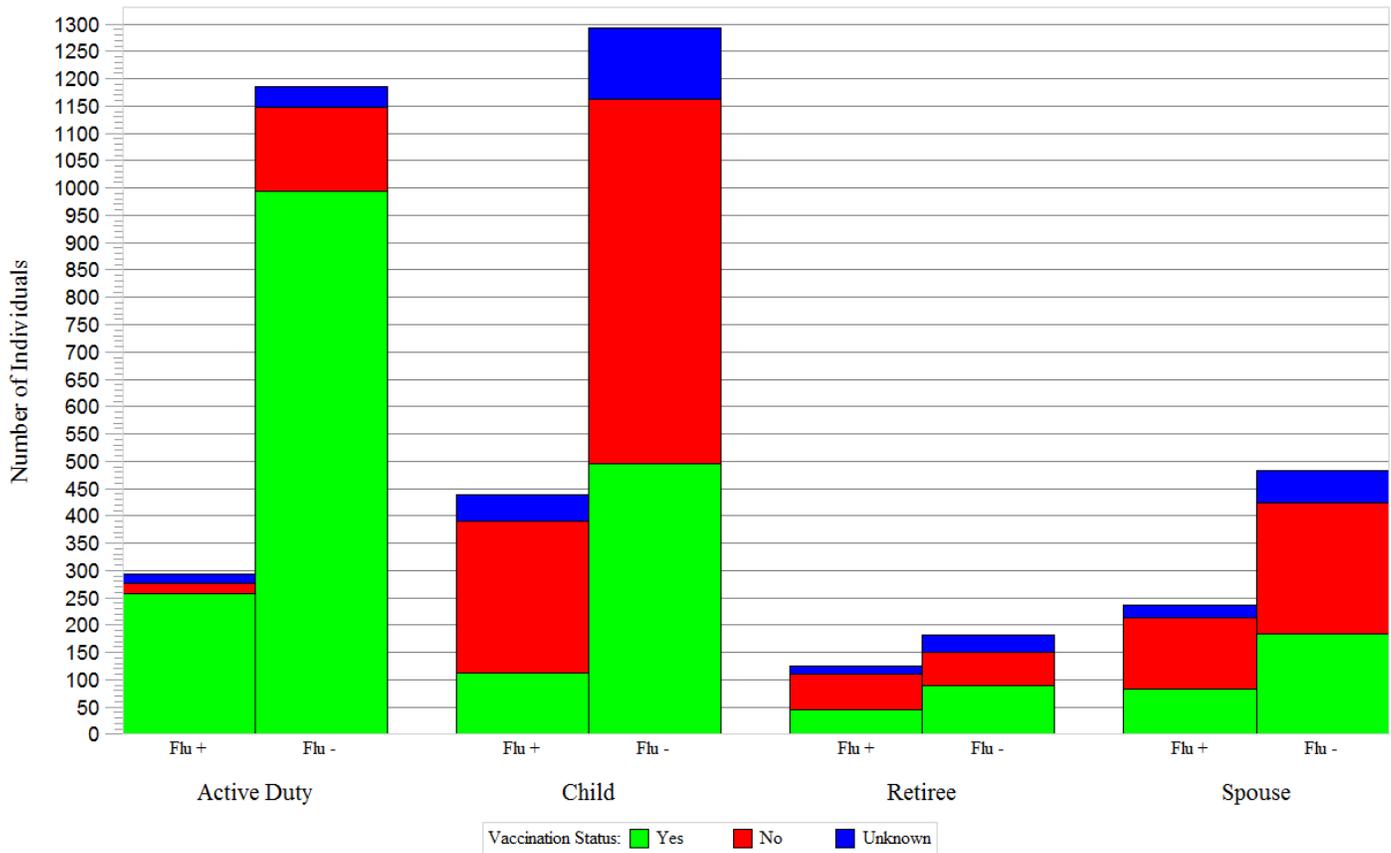
### Demographic Summary

Of 4,340 ILI cases, 1,478 are service members (34.0%), 1,731 are children (40.0%), 718 are spouses (16.5%), and 413 (9.5%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=4,340) is 23 (range 0, 95).

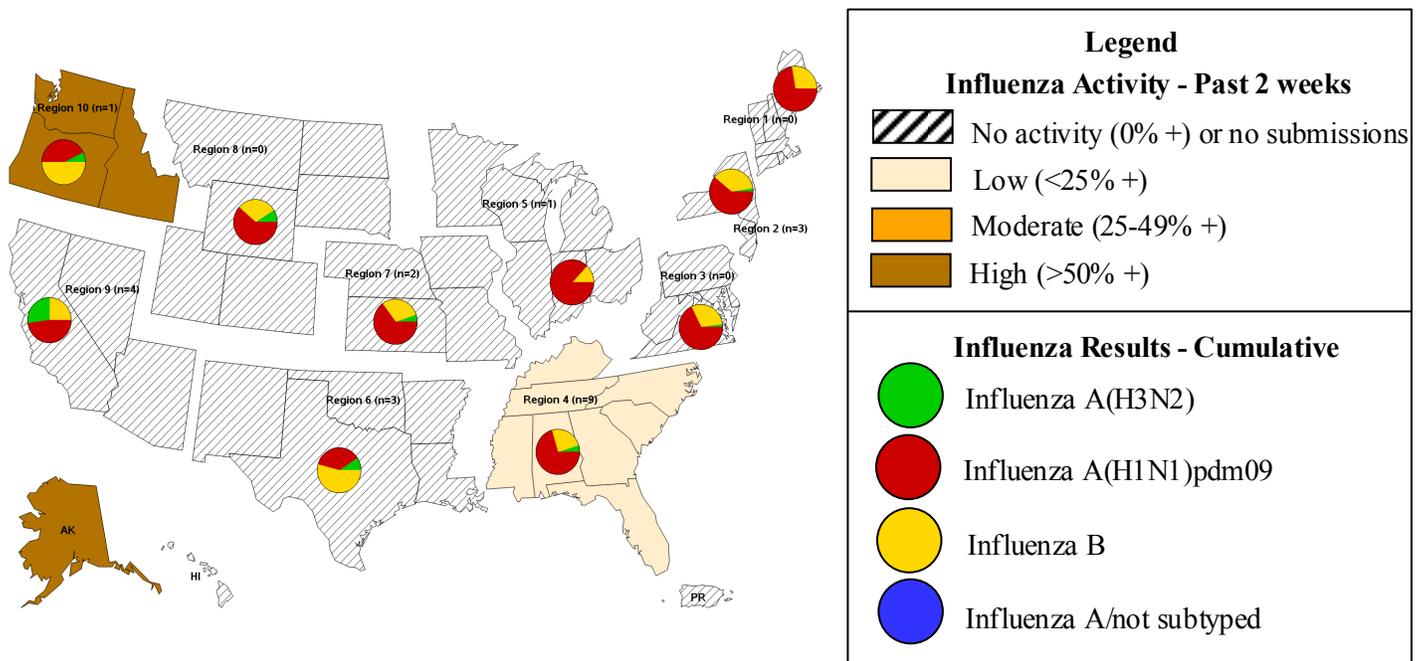
**Graph 2.** ILI by beneficiary status for the 2015-2016 surveillance year through Week 26



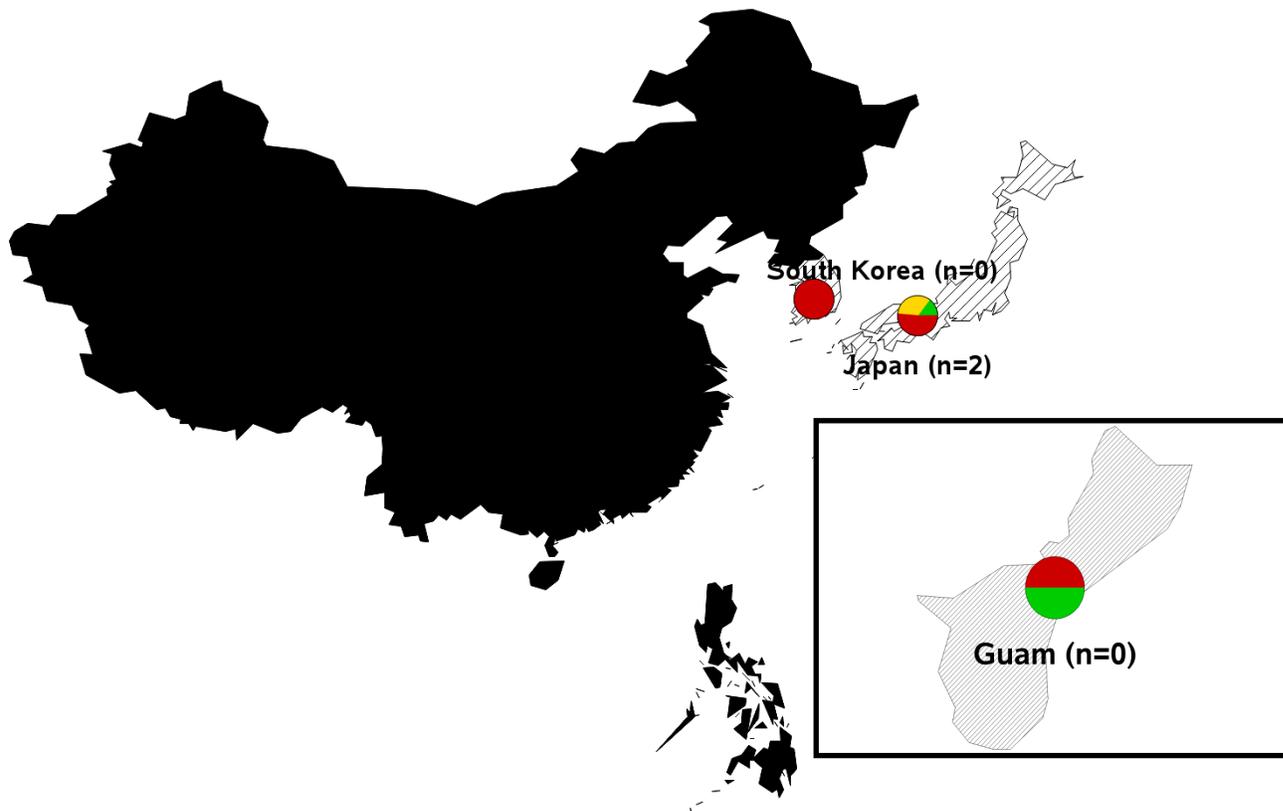
**Graph 3.** Vaccination status by beneficiary type for the 2015-2016 surveillance year through Week 26



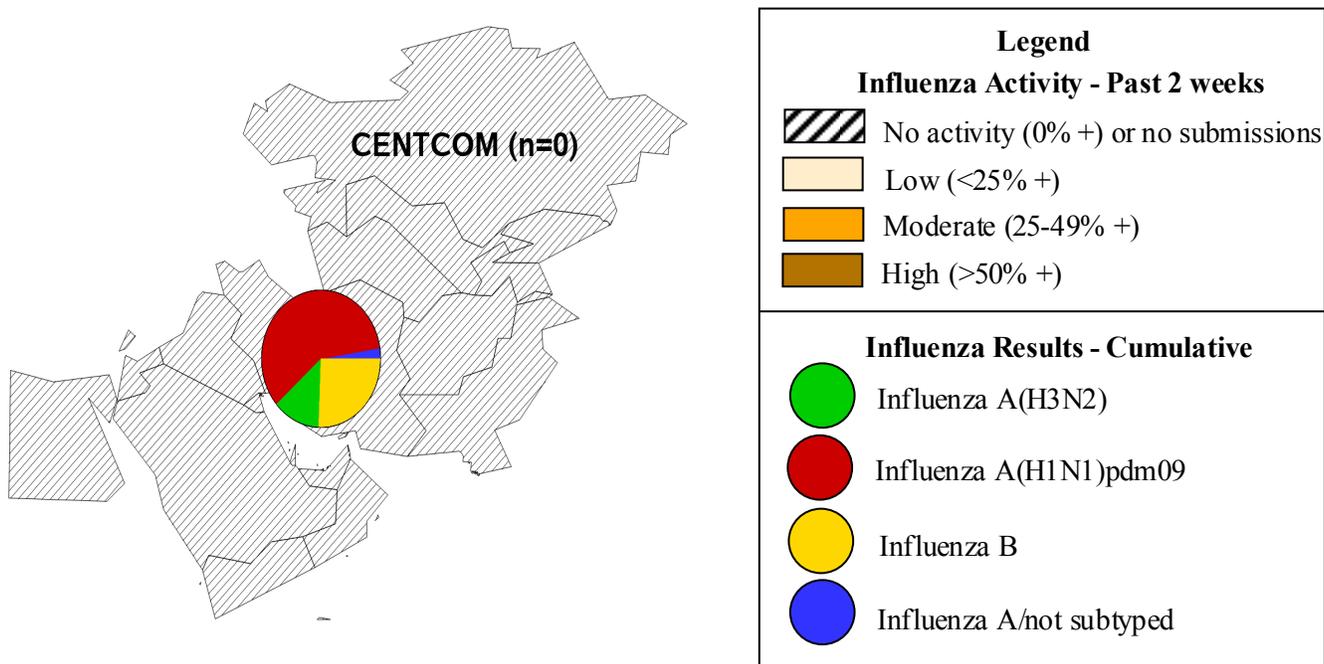
**Map 1.** Influenza subtypes and activity level by region for the 2015-2016 surveillance year through Week 26



**Map 2.** Influenza subtypes and activity level by country for the 2015-2016 surveillance year through Week 26 (Pacific)



**Map 3.** Influenza subtypes and activity level for CENTCOM for the 2015-2016 surveillance year through Week 26



Note - Specimens for CENTCOM were tested at USAFSAM or Landstuhl Regional Medical Center (LRMC).

**Laboratory Results—Through Current Surveillance Week 26**

**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	Influenza	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	-	-	6	14	
	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	1
	Kadena AB, Japan	2	1	-	-	-	-	3	-	-	-	-	-	2	-	3	-	-	5	-	1	22	39
	Kunsan AB, South Korea	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Misawa AB, Japan	2	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	3	-	-	5	12
	Osan AB, South Korea	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	6
	USCG Base Kodiak, AK	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	20	5	-	-	-	-	13	-	8	-	-	-	4	-	2	5	2	5	-	2	37	103
	Region 1	Hanscom AFB, MA	9	-	-	-	-	-	5	-	4	-	-	-	-	1	2	2	-	-	2	26	51
NHCNE Newport, RI		-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	1	-	11	14	
USCG Academy, CT		4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	11	
Region 2	Ft Drum, NY	12	-	-	-	-	2	-	-	-	-	-	1	-	-	-	-	3	-	-	7	25	
	JB McGuire-Dix-Lakehurst, NJ	31	1	-	-	-	20	1	3	-	-	1	4	3	2	-	13	1	3	51	134		
	USMA - West Point, NY	56	3	-	1	-	38	-	25	-	-	10	9	5	13	11	18	3	11	170	373		
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	65	150		
	NCRM - Walter Reed NMMC, MD	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5	
	NMC Portsmouth, VA	6	1	-	-	-	4	-	4	-	-	-	1	1	5	1	2	3	1	1	24	54	
Region 4	CGS Mobile, AL	1	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	2	7	
	Columbus AFB, MS	6	-	-	-	-	-	2	-	-	-	2	1	-	-	2	4	-	-	-	24	41	
	Eglin AFB, FL	10	1	-	-	-	3	-	6	-	-	1	1	1	5	7	7	-	1	69	112		
	Ft Bragg, NC	9	-	-	-	-	12	-	4	-	-	4	1	1	-	3	2	1	2	40	79		
	Ft Campbell, KY	24	1	-	-	-	9	-	1	-	-	4	2	-	2	1	4	-	-	43	91		
	Hurlburt Field, FL	7	1	-	-	-	2	-	5	-	1	-	2	4	1	1	1	-	2	34	61		
	JB Charleston (AF), SC	4	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	5	5	
	Keesler AFB, MS	-	-	-	-	-	-	-	1	-	-	-	-	-	2	1	-	2	-	1	33	40	
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-	-	-	1	4	
	Maxwell AFB, AL	23	1	-	1	-	2	-	6	-	-	-	1	-	1	1	2	9	-	1	65	113	
	Moody AFB, GA	13	1	-	-	-	9	-	8	-	-	-	2	1	2	7	6	18	-	6	40	113	
	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	-	-	-	17	30	
	Seymour Johnson AFB, NC	12	-	-	-	-	1	-	2	-	-	-	2	-	-	1	-	4	1	1	13	37	
	Shaw AFB, SC	2	1	-	-	-	2	-	-	-	-	-	4	-	4	-	-	5	1	1	12	32	
Tyndall AFB, FL	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	3	6		
Region 5	Scott AFB, IL	5	-	-	-	-	1	-	2	-	-	-	1	-	1	-	1	-	-	21	32		
	Wright-Patterson AFB, OH	15	-	-	-	-	2	-	3	-	-	-	1	1	1	1	4	-	-	31	59		

\*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM. (Cont'd on page 7)

# DoD Global, Laboratory-Based, Influenza Surveillance Program

## Laboratory Results—Through Current Surveillance Week 26

**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	hMPV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Bacterial Coinfection	Non-Influenza Viral Coinfection	No Pathogen	Total
Region 6	Altus AFB, OK	7	-	-	-	-	4	-	4	-	-	3	5	-	6	10	12	-	5	73	129
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	5	6
	Cannon AFB, NM	13	4	1	-	-	12	-	3	-	-	2	4	-	2	2	7	-	12	45	107
	Laughlin AFB, TX	1	5	-	-	-	5	-	2	-	-	1	-	-	-	2	4	-	-	9	29
	Little Rock AFB, AR	5	1	-	-	-	1	-	-	-	-	1	1	-	-	-	4	-	1	27	41
	Sheppard AFB, TX	8	-	-	-	-	32	-	10	-	-	3	3	3	2	5	22	-	6	107	201
	Tinker AFB, OK	4	-	-	-	-	3	-	6	-	-	1	-	1	7	7	7	1	7	52	96
	USCG New Orleans, LA	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	1	-	-	-	-	1	-	2	-	-	-	2	-	2	-	2	-	-	47	57
Region 7	Ft Leavenworth, KS	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	9	11
	McConnell AFB, KS	5	-	-	-	-	4	-	1	-	-	1	-	2	2	-	7	1	-	37	60
	Offutt AFB, NE	19	2	-	-	-	6	-	2	-	-	2	2	-	4	1	8	-	-	81	127
Region 8	Ellsworth AFB, SD	16	2	-	-	-	2	-	3	-	-	1	4	1	7	2	1	-	5	44	88
	FE Warren AFB, WY	19	3	-	-	-	7	-	3	1	-	3	2	1	3	7	5	-	3	54	111
	Hill AFB, UT	38	6	-	-	-	33	-	3	-	-	2	3	1	-	2	14	1	1	122	226
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Minot AFB, ND	7	-	-	-	-	-	-	-	-	-	2	1	-	1	2	3	-	1	12	29
	Peterson AFB, CO	14	3	-	-	-	1	2	-	2	-	5	1	-	-	1	5	-	5	40	79
	USAF Academy, CO	-	-	-	-	-	1	-	-	-	-	-	-	-	4	-	1	-	-	12	18
Region 9	Beale AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	CGS Humboldt Bay, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Davis-Monthan AFB, AZ	4	8	-	-	-	1	-	-	-	-	4	-	-	-	-	1	-	1	17	36
	Edwards AFB, CA	1	-	-	-	-	1	-	-	-	-	1	-	-	-	1	1	-	-	8	13
	Luke AFB, AZ	30	24	-	-	-	21	-	3	-	-	9	1	1	9	6	-	10	54	168	
	NH Twentynine Palms, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	19	2	-	-	-	4	-	6	-	-	3	-	-	8	4	8	-	8	86	148
	Travis AFB, CA	19	8	-	-	-	13	-	3	-	-	2	9	2	5	7	16	-	6	52	142
	USCG Island Alameda, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Vandenberg AFB, CA	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	11	14
Region 10	Fairchild AFB, WA	6	1	-	-	-	6	-	1	-	-	-	1	-	-	-	2	-	-	16	33
	JB Lewis-McChord, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Mt Home AFB, ID	1	1	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	8	12
	NH Bremerton, WA	44	7	-	-	-	57	-	5	-	-	2	2	2	12	6	15	1	12	80	245
<b>Total</b>	<b>637</b>	<b>104</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>373</b>	<b>1</b>	<b>163</b>	<b>1</b>	<b>2</b>	<b>86</b>	<b>86</b>	<b>57</b>	<b>120</b>	<b>130</b>	<b>289</b>	<b>16</b>	<b>124</b>	<b>2147</b>	<b>4340</b>

\*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 ninth USAFSAM influenza sequence surveillance report for the 2015-2016 influenza season, and includes 99 specimens collected between 4 January 2016 and 29 March 2016. USAFSAM sentinel sites submitted specimens from which 94 of these sequences were determined, while the remaining five sequences were data obtained from the Navy Medical Research Unit-2 (NAMRU-2) in Cambodia. Among the sequences analyzed for this report, 59 (59.6%) were influenza A(H1N1)pdm09, three (3.0%) were influenza A(H3N2), 11 (11.1%) were influenza B/Victoria, and 26 (26.3%) were influenza B/Yamagata.

The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously published experimental evidence.<sup>1,3,4</sup> 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
<b>CONUS</b>	<b>Alabama</b> , Maxwell AFB	1			
	<b>Arizona</b> , Luke AFB	2	1		6
	<b>Arkansas</b> , Little Rock AFB	1			
	<b>California</b> , Beale AFB	1			
	<b>California</b> , Travis AFB	3			
	<b>Colorado</b> , Peterson AFB	1			
	<b>Florida</b> , Eglin AFB	2			
	<b>Florida</b> , Hurlburt Field	1			
	<b>Florida</b> , Tyndall AFB	1			
	<b>Kentucky</b> , Ft Campbell	9			1
	<b>Massachusetts</b> , Hanscom AFB	3			
	<b>Nebraska</b> , Offutt AFB	1			2
	<b>Nevada</b> , Nellis AFB	1			
	<b>New Jersey</b> , JB McGuire-Dix-Lakehurst	5			1
	<b>New Mexico</b> , Cannon AFB	1			
	<b>New York</b> , USMA – West Point	8		1	
	<b>North Carolina</b> , Seymour Johnson AFB	1			
	<b>North Carolina</b> , Ft Bragg			2	
	<b>Ohio</b> , Wright-Patterson AFB	5	1		
	<b>Oklahoma</b> , Tinker AFB				1
	<b>Texas</b> , Sheppard AFB			6	1
	<b>Utah</b> , Hill AFB	3			5
	<b>Washington</b> , Fairchild AFB	2		1	1
	<b>Washington</b> , NH Bremerton				5
<b>OCONUS</b>	<b>Alaska</b> , Eielson AFB	1			
	<b>Cambodia</b> , NAMRU-2	2			3
	<b>England</b> , RAF Lakenheath	2			
	<b>Guam</b> , JR Marianas – NH Guam	1			
	<b>Italy</b> , USAG Vicenza		1		
	<b>Japan</b> , Yokota AB	1		1	
<b>TOTAL</b>		<b>59</b>	<b>3</b>	<b>11</b>	<b>26</b>

## Influenza A(H1N1)pdm09

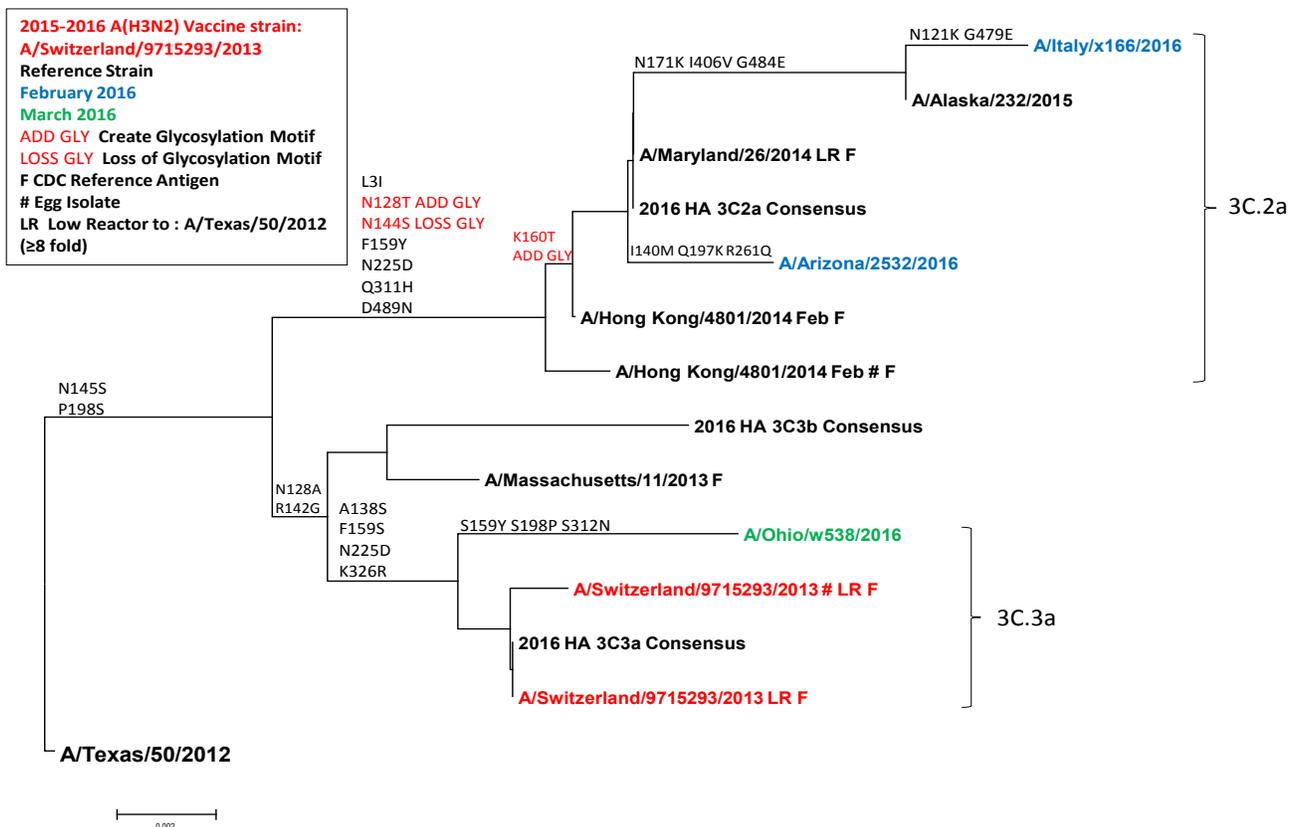
- The influenza A(H1N1)pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009-like virus [Figure 1].
- The A(H1N1)pdm09 specimens characterized for this report exhibited an overall protein homology of 96.5-96.9% compared to the 2015-2016 influenza vaccine component, A/California/07/2009-like virus.
- All of the A(H1N1)pdm09 viruses sequenced for this report contain mutations consistent with one of the circulating 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). Fifty-eight (98.3%) of the influenza A(H1N1)pdm09 specimens sequenced for this report were in subgroup 6B.1, while the remaining specimen resided in subgroup 6B.2.
- 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.<sup>4</sup> 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 36 mutations present in the A(H1N1)pdm09 specimens, 12 occurred at predicted antigenic sites (one at site A, one at site B, three at site C, three at site D, and four at site E) and one occurred at the receptor binding site.<sup>2,5</sup>
- One specimen, A/New Mexico/2358/2016, showed evidence of an influenza B and influenza A(H1N1)pdm09 coinfection based on RT-PCR results; however, a successful sequence for influenza B was not able to be obtained.
- Another specimen, A/Florida/2660/2016, was collected from a hospitalized patient that presented symptoms of cough, fever of 103°F, rigors, nausea, loose (non-bloody) stool, and fatigue/malaise, and was admitted for a one day hospital stay. An initial chest x-ray was negative, however a second x-ray indicated pneumonia and the patient was prescribed antibiotics.



## Influenza A(H3N2)

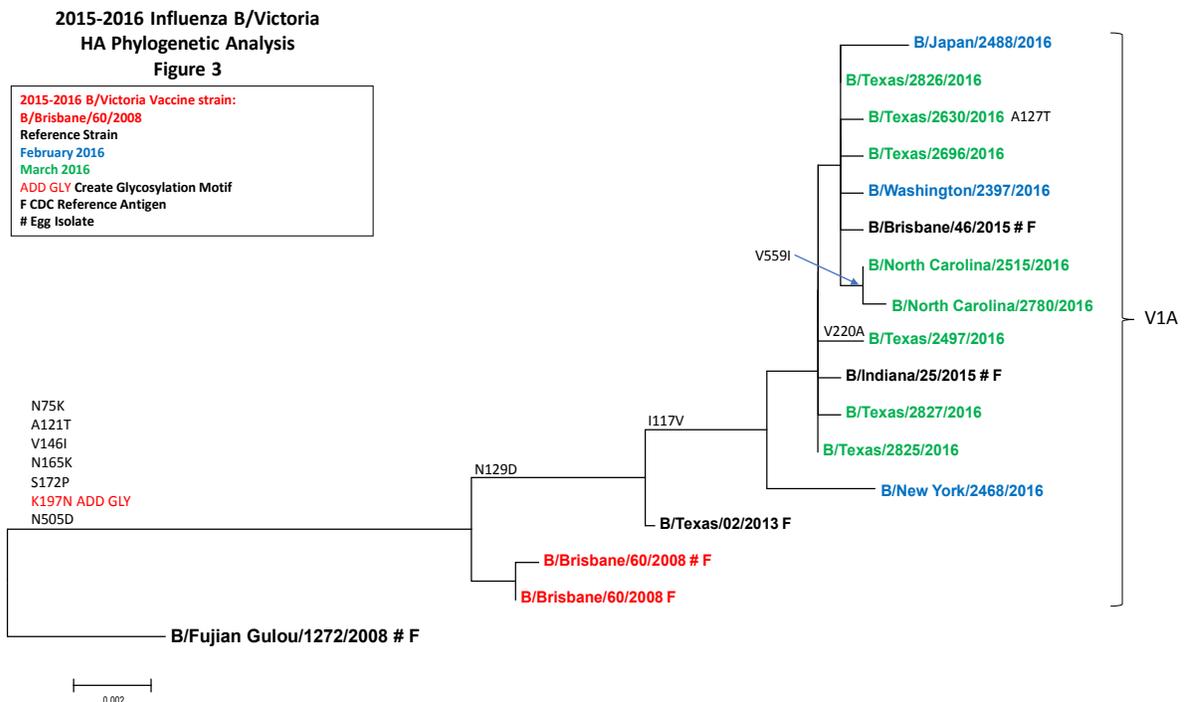
- The influenza A(H3N2) sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from a previous vaccine strain, A/Texas/50/2012-like virus [Figure 2].
- The A(H3N2) specimens characterized for this report exhibited an overall protein homology of 96.6-98.7% compared to the 2015-2016 influenza vaccine component, A/Switzerland/9715293/2013-like virus.
- All of the influenza A(H3N2) specimens sequenced for this report were in clade 3C. Two of the influenza A(H3N2) sequences classified as subclade 3C.2a and the remaining specimen classified as subclade 3C.3a.
- Among the influenza A(H3N2) specimens characterized in this report, one mutation, N144S (asparagine to serine), was 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 22 mutations present in the A(H3N2) specimens, eight occurred at predicted antigenic sites (five at site A, two at site B, and one at site E) and two occurred at the receptor binding site.<sup>2,5</sup>

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



## Influenza B

- The influenza B isolates are characterized in lineage specific; neighbor-joining phylogenetic trees with reference strains and are rooted from the reference strain B/Fujian Gulou/1272/2008 for B/Victoria specimens [Figure 3] and from the previous 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.<sup>1</sup> Eleven (30%) of the 37 influenza B viruses characterized in this report fall into the Victoria lineage, while the other 26 (70%) fall into the Yamagata lineage.
- The influenza B/Victoria specimens characterized for this report exhibited a protein homology of 99.1-99.3% 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
- One mutation in the Victoria lineage, K197N (lysine to asparagine) was observed that adds a glycosylation motif.
- The influenza B/Yamagata specimen B/New Jersey/2681/2016 tested positive for a coinfection of influenza B and adenovirus.



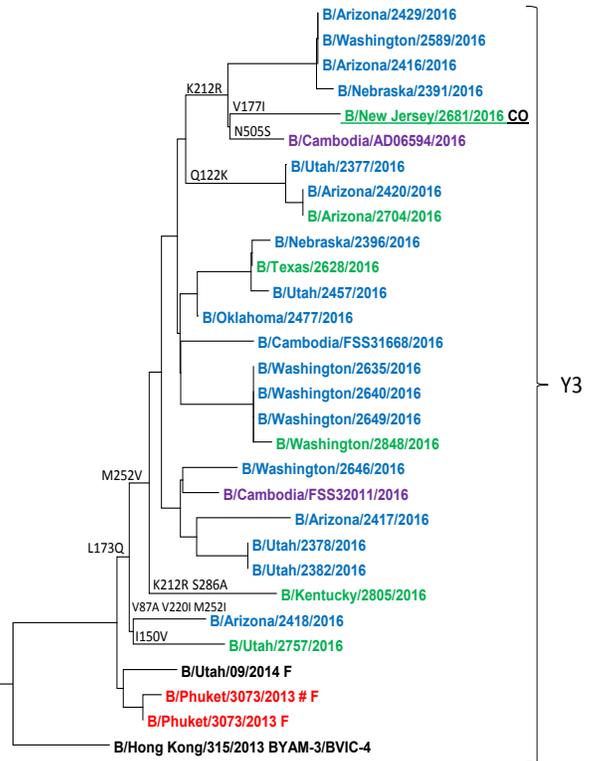
2015-2016 Influenza B/Yamagata  
HA Phylogenetic Analysis  
Figure 4

2015-2016 B/Yamagata Vaccine strain:  
B/Phuket/3073/2013  
Reference Strain  
January 2016  
February 2016  
March 2016  
F CDC Reference Antigen  
# Egg Isolate

K48R  
A108P  
N116K  
S150I  
N166Y  
A182T  
N203S  
G230D  
K299E  
E313K

B/Massachusetts/02/2012 F

0.005



References:

1. Wright, P, Neumann, G, Kaqaoka, Y 2007. Oorthomyxoviruses 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.

USAFSAM POCs for sequence data and analysis are:

Mr. Jim Hanson: [james.hanson.7@us.af.mil](mailto:james.hanson.7@us.af.mil)

Mr. Bill Gruner: [william.gruner.1.ctr@us.af.mil](mailto:william.gruner.1.ctr@us.af.mil)

Ms. Marie Powell: [marie.powell.2@us.af.mil](mailto:marie.powell.2@us.af.mil)

**Monthly EUCOM Respiratory Surveillance Supplemental Report Through  
2 July 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.

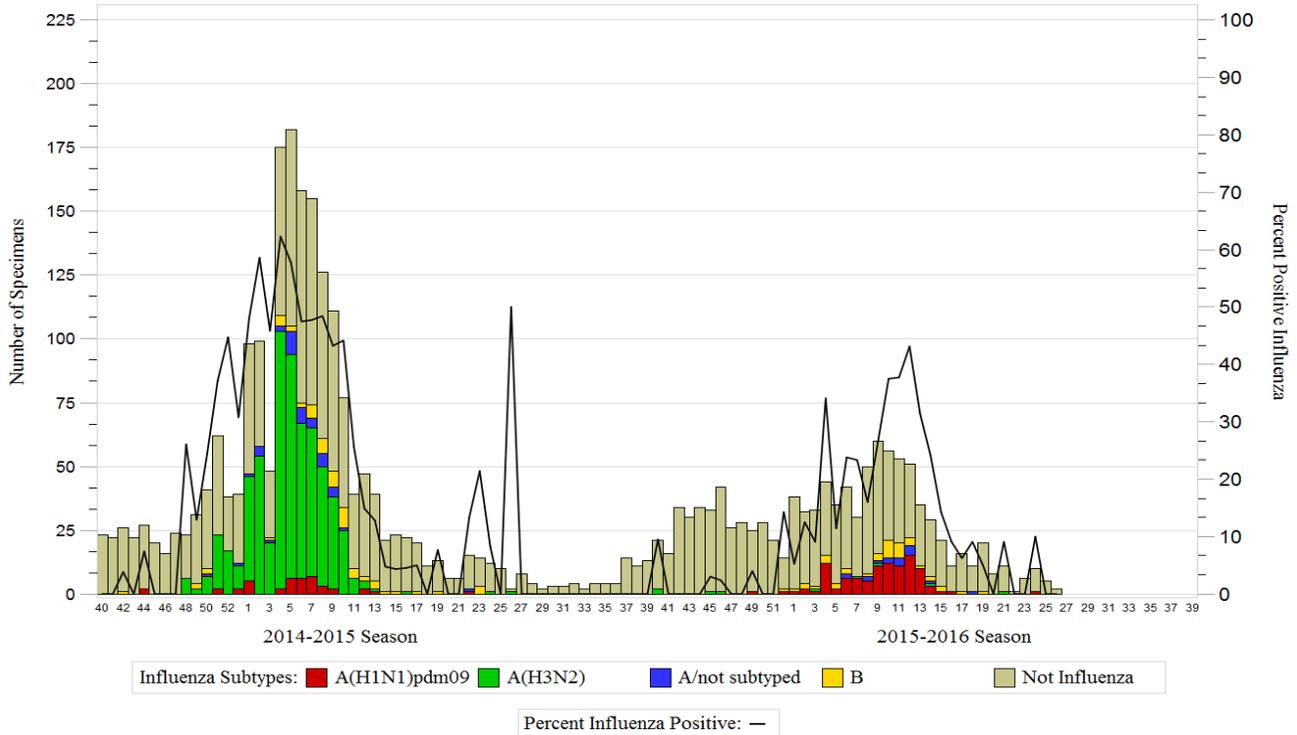
**Table 4.** Results by region and location for specimens collected and finalized during Weeks 23-26

Region		A(H1N1)pdm09 & Rhino/Enterovirus	Adenovirus	Rhinovirus/Enterovirus	Para & Rhino/Enterovirus	No Pathogen	Total
EUCOM	Landstuhl RMC, Germany	1	-	1	-	5	7
	RAF Lakenheath, England	-	1	2	-	2	5
	Ramstein AB, Germany	-	-	1	-	-	1
	USAG Stuttgart, Germany	-	-	2	-	3	5
	Vilseck AHC, Germany	-	-	1	1	3	5
<b>Total</b>		<b>1</b>	<b>1</b>	<b>7</b>	<b>1</b>	<b>13</b>	<b>23</b>

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

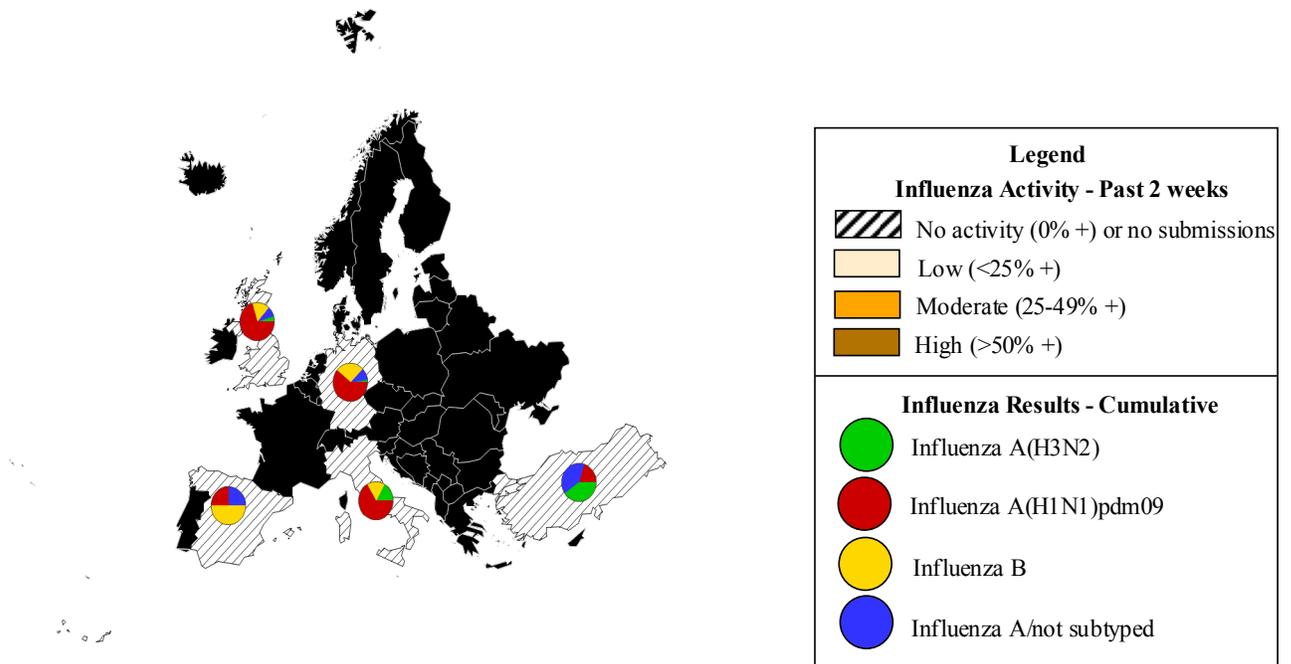
Region	A(H1N1)pdm09	A(H3N2)	A/not subtyped	A/not subtyped & Adeno	A/not subtyped & hMNV	A/not subtyped & Para	A/not subtyped & RSV	A/not subtyped & Rhino/Enterovirus	A(H1N1)pdm09 & B	A(H1N1)pdm09 & hMNV	A(H1N1)pdm09 & Para & Rhino/Enterovirus	A(H1N1)pdm09 & RSV	A(H1N1)pdm09 & Rhino/Enterovirus	A(H3N2) & Rhino/Enterovirus	A/not subtyped & B	B	B & hMNV	B & Rhino/Enterovirus	Adenovirus	hMNV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & RSV	Adeno & RSV & Rhino/Enterovirus	Adeno & Rhino/Enterovirus	hMNV & Para	hMNV & Rhino/Enterovirus	Para & Rhino/Enterovirus	RSV & Rhino/Enterovirus	No Pathogen	Total																								
AFRICOM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2																							
Deployed	Camp Lemonnier, Djibouti																		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2						
	Country 2, Location A																		1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7				
	Country 6, Location A																		14	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2	1	4	-	-	-	-	-	-	-	-	-	-	65	120		
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	32	-	-	1	-	1	3	3	127	233						
	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	58	1	-	-	-	2	3	19	112	296							
	Ramstein AB, Germany																		3	-	2	-	-	-	-	-	-	-	-	-	-	-	4	-	-	1	2	2	3	12	-	-	-	-	-	-	-	1	24	54						
	Spangdahlem AB, Germany																		-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	1	-	-	-	-	-	-	-	-	-	-	6	11			
	USAG Stuttgart, Germany																		13	-	1	-	-	-	-	-	-	1	-	-	-	1	2	-	-	2	6	3	5	18	-	-	-	-	-	1	-	-	-	-	-	-	40	93		
	USAG Vicenza, Italy																		1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	1	5	-	-	-	-	-	-	-	-	-	-	-	10	19			
	Vilseck AHC, Germany																		12	-	1	-	-	1	-	1	-	-	-	-	2	-	1	8	-	-	1	5	6	13	26	1	1	2	1	3	4	2	49	140						
<b>Total</b>	<b>91</b>	<b>7</b>	<b>9</b>	<b>1</b>	<b>2</b>	<b>1</b>	<b>2</b>	<b>1</b>	<b>1</b>	<b>3</b>	<b>1</b>	<b>1</b>	<b>6</b>	<b>2</b>	<b>3</b>	<b>36</b>	<b>2</b>	<b>1</b>	<b>17</b>	<b>46</b>	<b>35</b>	<b>75</b>	<b>199</b>	<b>2</b>	<b>1</b>	<b>3</b>	<b>1</b>	<b>8</b>	<b>10</b>	<b>25</b>	<b>474</b>	<b>1066</b>																								

**Graph 4.** Percent influenza positive by week: 2014-2015 surveillance year and through Week 26 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 26 (Europe)



## 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.

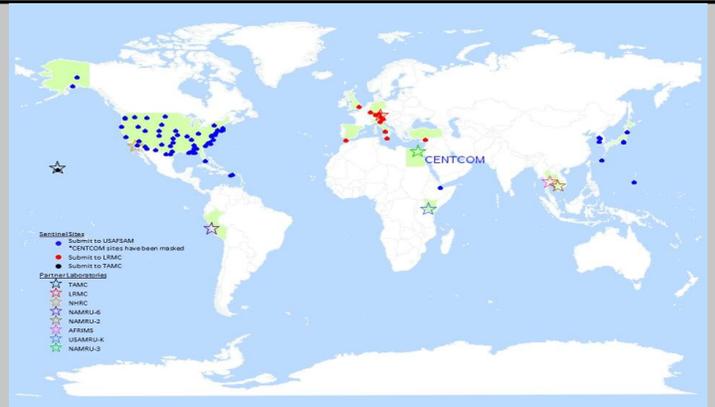
Landstuhl Regional Medical Center (LRMC) and Tripler Army Medical Center (TAMC) assist USAFSAM by processing DoD specimens for the EUCOM region and the State of Hawaii, respectively. This process seeks to provide more timely results and efficient transport of specimens.

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.

