



Cumulative Results

Locations	83
Collected	5,595
Tested	5,530

Influenza A 1,388

A(H1N1)pdm09	28
A(H1N1)pdm09 & Influenza B	1
A(H3N2)	1,352
A(H3N2) & Influenza B	3
A(H3N2) & Coronavirus & RSV	1
A(H3N2) & RSV	1
A(H3N2) & Rhino/Enterovirus	1
A/not subtyped	1

Influenza B* 444

B	443
B & Human Metapneumovirus & Rhino/Enterovirus	1

Other Respiratory Pathogens 1,223

Adenovirus	77
<i>Bordetella pertussis</i>	1
<i>Chlamydomphila pneumoniae</i>	5
Coronavirus	123
Human Metapneumovirus	95
<i>Mycoplasma pneumoniae</i>	40
Parainfluenza	199
RSV	179
Rhinovirus/Enterovirus	363
Non-influenza Viral Coinfections	133
Non-influenza Bacterial Coinfections	8
- <i>M. pneumo</i> coinfections (8)	

Results are preliminary and may change as more results are finalized.
*Influenza B lineages and specimens submitted for sequencing only will be reported in the periodic molecular sequencing reports.

Respiratory Highlights

3 - 30 September 2017 (Surveillance Weeks 36 - 39)

- During 3 - 30 September 2017, a total of 152 specimens were collected and received from 44 locations. Results were finalized for 149 specimens from 43 locations. During Weeks 36 and 37, one influenza A(H1N1) pdm09 virus was identified during each week. During Week 38, three influenza A(H3N2) viruses were identified. During Week 39, two influenza A(H1N1)pmd09 viruses were identified. Approximately 5% of specimens tested positive for influenza during Weeks 36 through 39. The influenza percent positive for the season is currently 33%.
- This report contains the monthly supplemental EUCOM report for surveillance through 30 September 2017.
- This report contains the 13th molecular sequence analysis report which includes 124 specimens collected between 9 January 2017 and 7 September 2017.
- A recent World Health Organization (WHO) report recommended two changes in the composition of the 2018 Southern Hemisphere's vaccine from the 2017-2018 Northern Hemisphere's vaccine. The changes include an A/Singapore/INFIMH-16-0019/2016 (H3N2)-like virus strain instead of the A/Hong Kong/4801/2014 H3N2-like virus strain. Also, the B strains are switched between the trivalent and quadrivalent (WHO, [2018 Southern Hemisphere recommended influenza vaccine composition](#), cited 4 October 2017).
- Signs of an early influenza season are apparent as the state of Alaska reported 274 confirmed cases (PCR or Rapid Test) in September 2017. This is the highest number of cases since April 2017 and more than December 2016 when last season began to peak (Alaska DHSS, [Weekly Report #39](#), cited 4 October 2017).

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DoD Global, Laboratory-Based, Influenza Surveillance Program

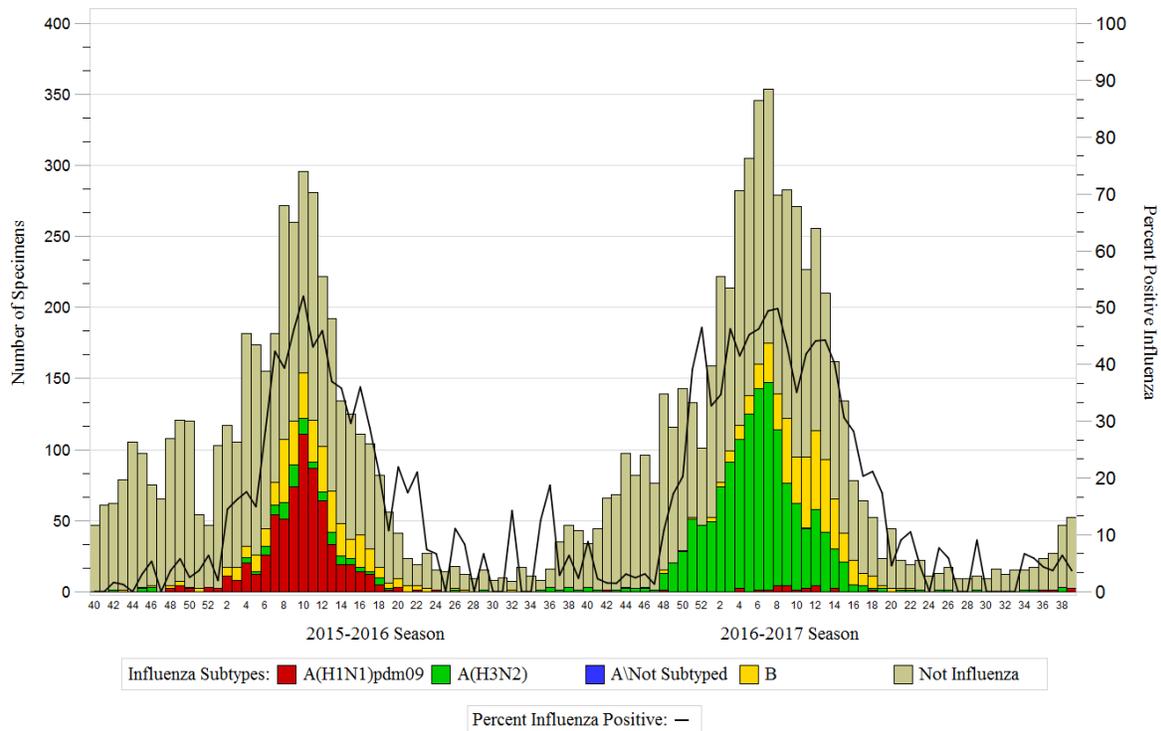
Table 1. Finalized results by region and location for specimens collected during Weeks 36-39

Region*		A(H1N1)pdm09	A(H3N2)	Adenovirus	Coronavirus	hMPV	Parainfluenza	Rhinovirus/Enterovirus	Adeno & Para & Rhino/Enterovirus	Para & Rhino/Enterovirus	No Pathogen	Total
PACOM	JR Marianas - Andersen AFB, Guam	1	-	-	-	-	-	-	-	-	-	1
	Kadena AB, Japan	-	-	-	-	-	-	1	-	-	-	1
	Yokota AB, Japan	-	-	-	-	-	-	2	-	-	5	7
Region 2	Ft Drum, NY	-	-	-	-	-	-	4	-	-	3	7
	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	-	1	-	-	1	2
	USM A - West Point, NY	-	-	-	-	-	-	5	-	-	7	12
Region 3	Dover AFB, DE	-	-	-	-	-	1	1	-	-	-	2
	JB Andrews, MD	-	-	-	-	-	-	-	-	-	1	1
Region 4	Columbus AFB, MS	-	-	-	-	-	-	1	-	-	1	2
	Eglin AFB, FL	-	-	-	-	-	-	-	-	-	1	1
	Ft Bragg, NC	-	-	-	-	-	-	-	-	-	1	1
	Hurlburt Field, FL	3	-	-	-	-	-	1	-	-	1	5
	JB Charleston (AF), SC	-	1	-	-	-	-	-	-	-	-	1
	JB Charleston (Navy), SC	-	-	-	-	-	-	-	-	-	2	2
	Keesler AFB, MS	-	-	-	-	-	-	2	-	-	3	5
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	1	1
	Maxwell AFB, AL	-	-	-	-	-	-	1	-	-	-	1
	Moody AFB, GA	-	-	-	-	-	-	-	-	-	1	1
	NH Beaufort, SC	-	-	-	-	-	-	1	1	-	-	2
	NH Camp Lejeune, NC	-	-	-	-	-	-	1	-	-	-	1
	Robins AFB, GA	-	-	-	-	-	-	-	-	-	3	3
Shaw AFB, SC	-	-	-	-	-	1	-	-	-	-	1	
Region 5	Wright-Patterson AFB, OH	-	-	-	1	-	-	3	-	-	7	11
Region 6	Altus AFB, OK	-	-	1	-	-	-	1	-	-	-	2
	Barksdale AFB, LA	-	-	-	-	-	-	1	-	-	-	1
	Laughlin AFB, TX	-	-	-	-	-	-	1	-	-	-	1
	Sheppard AFB, TX	-	-	-	-	1	-	4	-	-	7	12
	Tinker AFB, OK	-	-	-	-	-	-	2	-	-	3	5
	Vance AFB, OK	-	-	-	-	-	-	1	-	-	4	5
Region 7	Offutt AFB, NE	-	-	-	-	-	-	3	-	-	-	3
Region 8	Ellsworth AFB, SD	-	1	-	-	-	-	-	-	-	1	2
	FE Warren AFB, WY	-	-	-	-	-	1	1	-	-	3	5
	Hill AFB, UT	-	-	-	-	-	-	3	-	-	3	6
	Minot AFB, ND	-	-	-	-	-	-	2	-	-	1	3
	Peterson AFB, CO	-	-	-	-	-	1	2	-	-	5	8
	USAF Academy, CO	-	-	-	-	-	-	1	-	1	-	2
Region 9	Davis-Monthan AFB, AZ	-	-	-	-	-	-	-	-	-	4	4
	Los Angeles AFB, CA	-	1	-	-	-	-	-	-	-	-	1
	Nellis AFB, NV	-	-	-	-	-	-	1	-	-	1	2
	Travis AFB, CA	-	-	-	-	-	-	1	-	-	2	3
Region 10	Fairchild AFB, WA	-	-	1	-	-	-	2	-	-	1	4
	McChord AFB, WA	-	-	-	-	-	-	-	-	-	2	2
	NH Bremerton, WA	-	-	-	-	-	-	5	-	-	2	7
Total		4	3	2	1	1	4	55	1	1	77	149

*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: 2015-2016 surveillance year and through Week 39 of the 2016-2017 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.

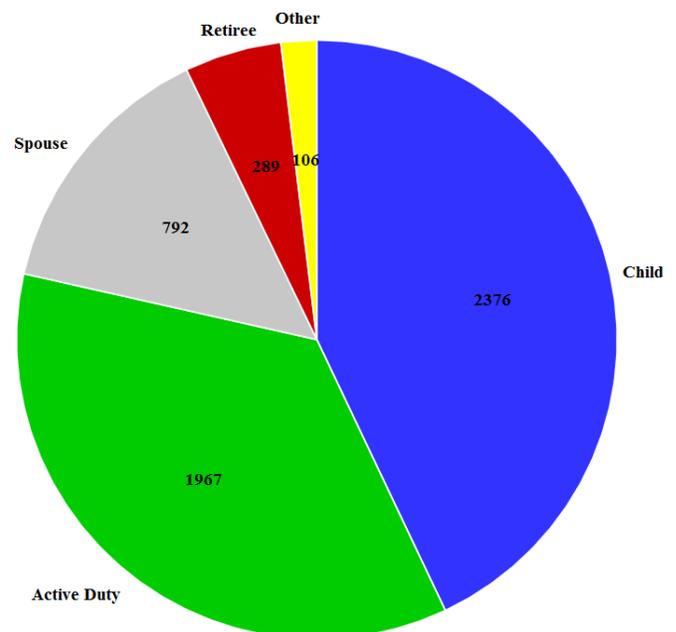
Table 2. ILI by age group for the 2016-2017 surveillance year through Week 39

Age Group	Frequency	Percent
0-5	1240	22.42
6-9	493	8.92
10-17	650	11.75
18-24	774	14
25-44	1717	31.05
45-64	532	9.62
65+	124	2.24

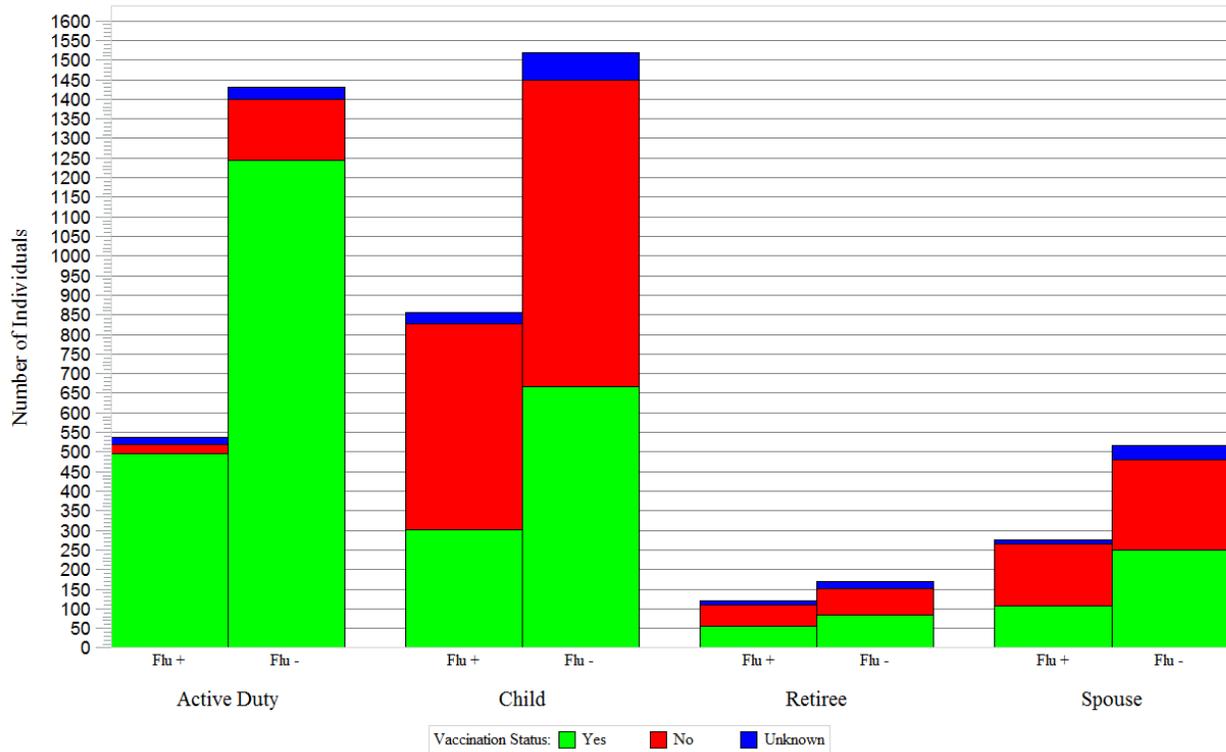
Demographic Summary

Of 5,530 ILI cases, 1,967 are service members (35.6%), 2,376 are children (43.0%), 792 are spouses (14.3%), and 395 (7.1%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=5,530) is 21 (range 0, 96).

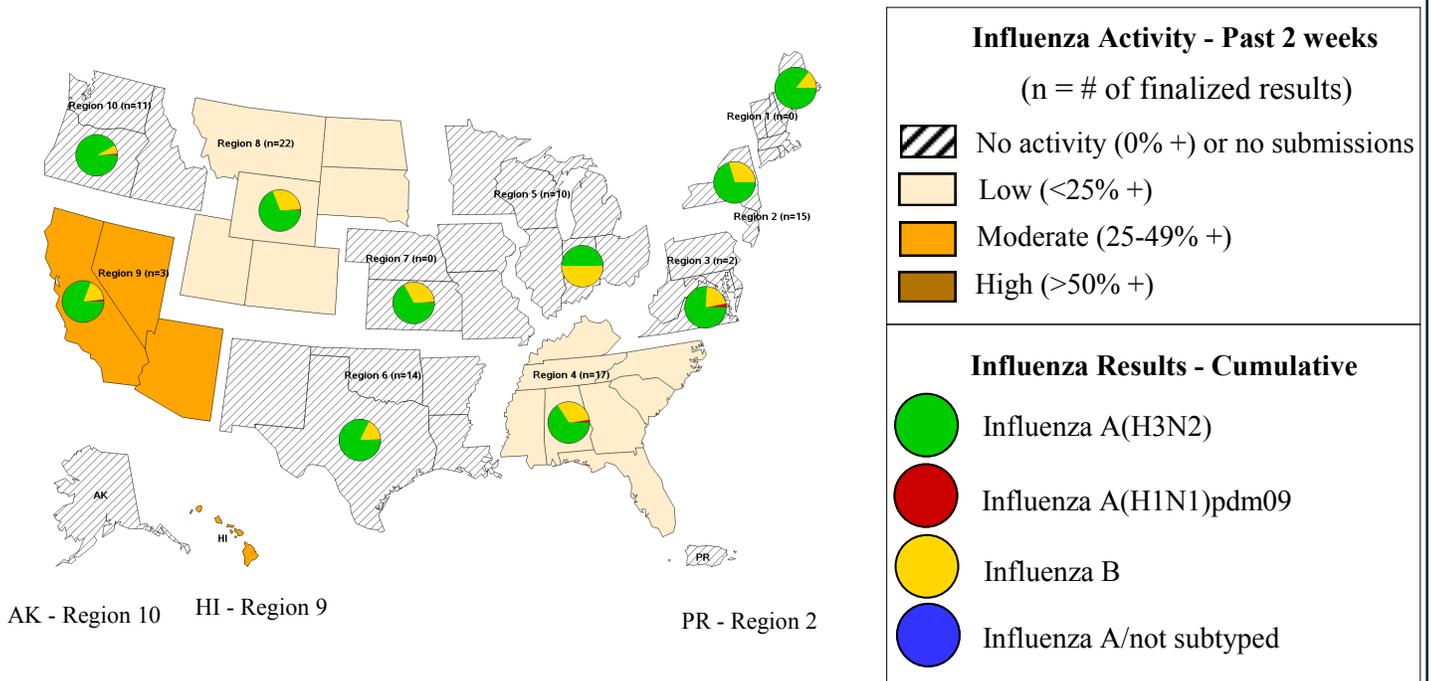
Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 39



Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 39 (excluding 'Other' beneficiary type)



Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 39



DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 39

Table 3. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & hMNV & Rhino/Entero	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 1, Location A	-	3	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	-	-	7	12	
	Country 1, Location B	-	14	-	-	-	-	-	9	-	-	-	-	-	2	-	-	-	1	2	1	-	-	11	40
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	33	1	-	-	-	1	1	-	-	-	-	-	6	-	-	-	-	6	2	-	-	16	66
EUCOM	Incirlik AB, Turkey	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5	
	NH Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
PACOM	Eielson AFB, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	2	-	7	12	
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	4	6	
	JR Marianas - Andersen AFB, Guam	1	-	-	-	-	-	-	1	-	2	-	-	-	-	1	1	-	-	-	-	-	7	13	
	Kadena AB, Japan	-	4	-	-	-	-	-	1	-	-	-	-	-	1	-	3	-	3	1	1	1	24	38	
	Kunsan AB, South Korea	-	2	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	5	
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	
	Osan AB, South Korea	-	4	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	9	14	
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3	
	Yokota AB, Japan	-	36	-	-	-	-	-	6	1	-	1	-	-	3	1	2	3	2	11	5	-	75	145	
	Region 1	Hanscom AFB, MA	-	3	-	-	-	-	1	-	1	-	-	-	-	1	1	2	-	-	1	-	4	13	
USCG Academy, CT		-	9	-	-	-	-	1	-	-	-	-	-	1	1	1	-	-	3	-	2	6	24		
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	Ft Drum, NY	1	49	-	-	1	-	-	62	-	7	-	1	5	10	1	9	8	11	5	-	101	271		
	JB McGuire-Dix-Lakehurst, NJ	-	54	-	-	-	-	-	2	3	-	-	6	9	2	10	6	13	5	-	87	197			
	USM A - West Point, NY	-	86	-	-	-	-	-	15	12	-	-	5	7	3	11	13	19	8	-	166	345			
Region 3	Dover AFB, DE	-	19	-	-	-	-	11	2	-	-	2	1	1	1	1	1	7	-	-	-	52	97		
	JB Anacostia-Bolling, DC	-	14	-	-	-	-	4	-	-	-	-	-	-	-	-	-	1	-	-	-	-	19		
	JB Andrews, MD	2	23	-	-	-	-	12	-	-	-	2	1	-	3	2	1	2	-	44	92				
	JB Langley-Eustis, VA	6	149	-	1	1	-	31	1	-	4	10	2	12	21	38	11	-	262	549					
	NCRM - Walter Reed NM MC, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2		
	NM C Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3		
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1		
Region 4	CGSMobile, AL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	
	Columbus AFB, MS	-	5	-	-	-	-	1	-	-	-	-	-	2	-	-	-	-	2	-	-	21	31		
	Eglin AFB, FL	1	15	-	-	-	-	5	7	-	2	2	2	2	5	12	6	-	49	108					
	Ft Bragg, NC	1	8	-	-	-	-	6	-	-	1	1	1	3	2	7	4	3	40	77					
	Ft Campbell, KY	1	15	-	-	-	-	9	1	2	-	-	1	-	3	-	4	-	17	53					
	Hurlburt Field, FL	3	19	-	-	-	-	6	3	-	1	-	1	1	2	5	1	-	30	72					
	JB Charleston (AF), SC	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	19		
	JB Charleston (Navy), SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2		
	Keesler AFB, MS	-	2	-	-	1	-	-	-	-	-	-	-	-	1	3	3	8	3	-	22	43			
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	1	-	-	-	8	11		
	Maxwell AFB, AL	-	10	-	-	-	-	2	-	-	-	-	-	-	1	-	2	-	2	-	-	15	32		
	Moody AFB, GA	-	36	-	-	-	-	45	1	-	2	7	1	15	9	18	14	1	96	245					
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	5	7		
	NH Camp Lejeune, NC	-	2	-	-	1	-	-	-	-	-	-	-	-	-	2	-	1	1	-	12	19			
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	4	6		
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	
	Robins AFB, GA	-	25	-	-	-	-	8	-	-	-	-	-	-	2	1	3	3	-	34	76				
	Seymour Johnson AFB, NC	3	17	-	-	-	-	1	2	-	-	-	-	-	1	1	2	1	-	24	52				
	Shaw AFB, SC	-	71	-	-	-	-	34	1	-	1	7	5	1	6	1	13	2	-	73	215				
	Tyndall AFB, FL	-	11	-	-	-	-	5	1	-	-	-	-	-	-	-	-	-	-	-	-	1	18		

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

(Cont'd on page 6)

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 39

Table 3. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year
(Cont'd from page 5)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	A(H3N2) & Rhino/Enterovirus	B	B & hMN & Rhino/Enterovirus	Adenovirus	B. pertussis	C. pneumoniae	Coronavirus	hMN	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	Non-Influenza Bacterial Coinfection	No Pathogen	Total		
Region 5	Scott AFB, IL	-	3	-	-	-	-	-	-	3	-	-	-	-	-	-	1	3	1	1	-	1	9	22		
	Wright-Patterson AFB, OH	-	10	-	-	-	-	-	-	10	-	-	-	-	2	1	1	2	-	5	2	-	-	49	82	
Region 6	Altus AFB, OK	-	7	-	-	-	-	-	-	1	-	2	-	-	1	1	-	1	5	8	4	-	-	41	71	
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	2	-	2	-	-	-	8	13	
	Cannon AFB, NM	-	13	-	-	-	-	-	-	4	-	-	-	-	2	-	1	3	-	5	1	-	-	42	71	
	Ft Polk, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	3	
	JBSA Lackland, TX	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	
	Laughlin AFB, TX	1	-	-	-	-	-	-	-	1	-	-	-	-	1	2	-	-	-	-	1	-	-	7	13	
	Little Rock AFB, AR	-	12	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	13	26	
	Sheppard AFB, TX	-	60	-	-	-	-	-	-	9	-	1	-	-	10	6	1	6	2	13	-	-	-	-	97	205
	Tinker AFB, OK	1	99	-	-	-	-	1	-	25	-	2	-	-	10	4	1	9	7	14	6	-	-	152	331	
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	16	17	
Region 7	McConnell AFB, KS	-	25	-	-	-	-	-	18	-	1	-	-	4	-	1	4	5	9	3	-	-	-	37	107	
	Offutt AFB, NE	1	32	-	-	-	-	-	9	-	1	-	-	6	2	-	2	1	13	1	-	-	-	62	130	
Region 8	Ellsworth AFB, SD	-	15	-	-	-	-	-	15	-	-	-	-	3	-	-	3	1	4	-	-	-	-	42	83	
	FE Warren AFB, WY	-	36	-	-	-	-	-	7	-	3	-	-	4	1	2	5	6	5	-	-	-	-	59	128	
	Hill AFB, UT	-	30	-	-	-	-	-	5	-	-	-	-	3	1	1	8	4	8	2	-	-	-	51	113	
	Malmstrom AFB, MT	-	7	-	-	-	-	-	3	-	-	-	-	-	-	-	1	-	-	1	-	-	-	9	21	
	Minot AFB, ND	1	25	-	-	-	-	-	15	-	-	-	-	3	2	1	1	6	10	3	-	-	-	50	117	
	Peterson AFB, CO	1	19	-	-	-	-	-	12	-	-	1	-	3	-	-	4	11	6	4	-	-	-	38	99	
USAF Academy, CO	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2	1	-	-	5	11		
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	
	Davis-Monthan AFB, AZ	1	16	-	-	-	-	-	4	-	-	-	-	-	2	-	5	1	8	5	-	-	-	46	88	
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2	
	Los Angeles AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	Luke AFB, AZ	-	-	-	-	-	-	-	5	-	1	-	-	2	-	-	1	3	3	1	-	-	-	23	39	
	Nellis AFB, NV	1	3	-	-	-	-	-	4	-	3	-	-	1	-	-	5	4	6	7	-	-	-	35	69	
	Travis AFB, CA	-	58	-	-	-	-	-	5	-	1	-	1	6	8	-	7	13	17	5	-	-	-	51	172	
Vandenberg AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	7		
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4	
	Fairchild AFB, WA	2	17	-	-	-	-	-	2	-	5	-	-	3	-	1	5	2	6	-	-	-	-	56	99	
	JB Lewis-McChord, WA	-	2	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	3	
	Mont Home AFB, ID	-	23	-	-	-	-	-	1	-	1	-	1	1	1	-	1	23	12	12	5	-	-	81	161	
	NH Bremerton, WA	-	67	-	-	-	-	-	5	-	8	-	1	3	1	2	8	7	12	4	-	-	-	29	147	
Total		28	1352	1	1	3	1	1	1	443	1	77	1	5	123	95	40	199	179	363	133	8	2475	5530		

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

Monthly EUCOM Respiratory Surveillance Supplemental Report Through 30 September 2017

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 finalized.

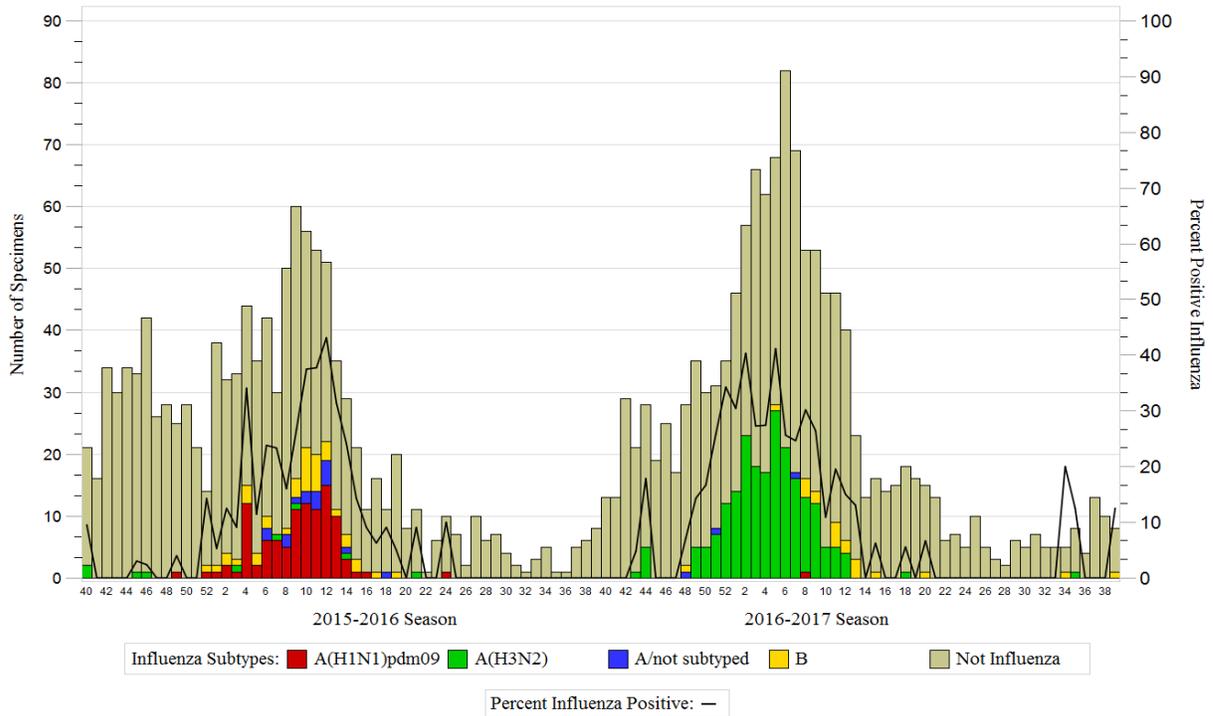
Table 4. Finalized results by region and location for specimens collected during Weeks 36-39

Region		B	Parainfluenza	Rhinovirus/Enterovirus	Para & Rhino/Entero	No Pathogen	Total
Deployed	Country 6, Location A	-	-	-	-	1	1
EUCOM	Landstuhl RMC, Germany	1	2	2	-	6	11
	NAVSTA Rota, Spain	-	-	1	-	3	4
	NSA Naples, Italy	-	-	1	-	1	2
	RAF Lakenheath, England	-	-	1	-	2	3
	Ramstein AB, Germany	-	-	2	-	3	5
	USAG Stuttgart, Germany	-	-	3	-	2	5
	USAG Vicenza, Italy	-	-	-	1	2	3
	Vilseck AHC, Germany	-	-	-	-	1	1
Total		1	2	10	1	21	35

Table 5. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

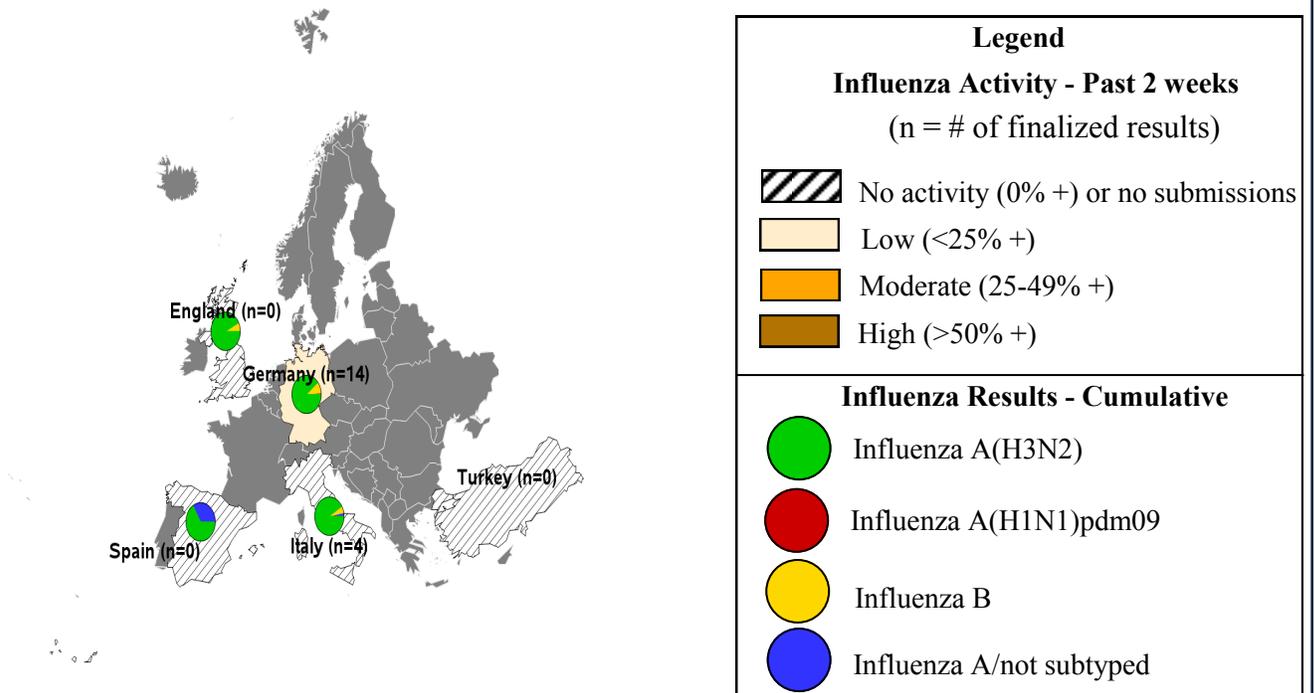
Region		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H3N2) & Adeno	A(H3N2) & hMNV & Rhino/Entero	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & Rhino/Entero	Adenovirus	hMNV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & RSV	Adeno & RSV & Rhino/Entero	Adeno & Rhino/Entero	hMNV & RSV	hMNV & Rhino/Entero	Para & RSV	Para & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total		
Deployed	Country 2, Location A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2	
	Country 6, Location A	-	3	-	-	-	2	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	20	29	
EUCOM	Aviano AB, Italy	-	-	-	-	-	-	2	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	11	15	
	Landstuhl RMC, Germany	1	58	-	-	-	2	1	7	-	2	12	12	17	46	1	-	3	-	1	1	-	-	3	190	357	
	NAS Sigonella, Italy	-	6	-	-	-	-	-	-	-	-	1	-	3	4	-	-	-	-	-	-	-	-	-	5	19	
	NAVSTA Rota, Spain	-	2	1	-	-	-	-	-	-	-	2	4	5	11	-	-	-	-	-	-	-	-	-	-	35	60
	NSA Naples, Italy	-	10	-	-	-	-	1	-	-	-	2	4	4	11	-	-	-	-	-	-	-	-	-	-	34	66
	RAF Lakenheath, England	-	24	-	-	-	-	1	2	-	3	11	5	14	29	-	1	1	-	1	-	-	-	2	94	188	
	Ramstein AB, Germany	-	24	1	-	-	-	-	3	-	1	8	3	12	23	-	-	1	-	-	-	-	1	-	63	140	
	Spangdahlem AB, Germany	-	1	-	-	-	-	1	-	-	-	-	-	1	2	-	-	-	-	-	-	-	-	-	6	11	
	USAG Stuttgart, Germany	-	17	-	-	-	-	-	1	1	-	5	3	7	20	-	-	-	-	-	-	-	-	-	-	35	89
	USAG Vicenza, Italy	-	14	1	2	-	-	-	-	-	-	3	-	2	2	-	-	-	-	-	-	-	1	-	29	54	
	Vilseck AHC, Germany	-	41	-	-	1	-	-	4	-	1	14	16	31	30	-	-	1	1	-	2	3	-	94	239		
Total		1	200	3	2	1	2	6	19	1	7	58	47	96	184	1	1	6	1	2	3	5	5	618	1269		

Graph 4. Percent influenza positive by week: 2015-2016 surveillance year and through Week 39 of the 2016-2017 surveillance year (EUCOM)



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

Map 4. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 39 (Europe)



Molecular Sequence Analysis Report #13

This is the thirteenth USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 124 influenza specimens collected between 9 January 2017 and 7 September 2017, with 53 specimens sequenced at USAFSAM, five hemagglutinin sequences provided by the United States Army Medical Research Directorate in Kenya (USAMRU-K), and 66 hemagglutinin sequences provided by the Naval Health Research Center (NHRC) in San Diego, California. Ten (8.1%) of these specimens were influenza A(H1N1)pdm09, 68 (54.8%) were influenza A(H3N2), 34 (27.4%) were influenza B/Victoria lineage, and 12 (9.7%) were influenza B/Yamagata lineage. Figure 1 shows the distribution of all specimens by US Combatant Command. The number of sequences in this report is shown for each sentinel site in Table 1. Figures 2-5 display the phylogenetic relationships among HA sequences for the influenza A(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata specimens,

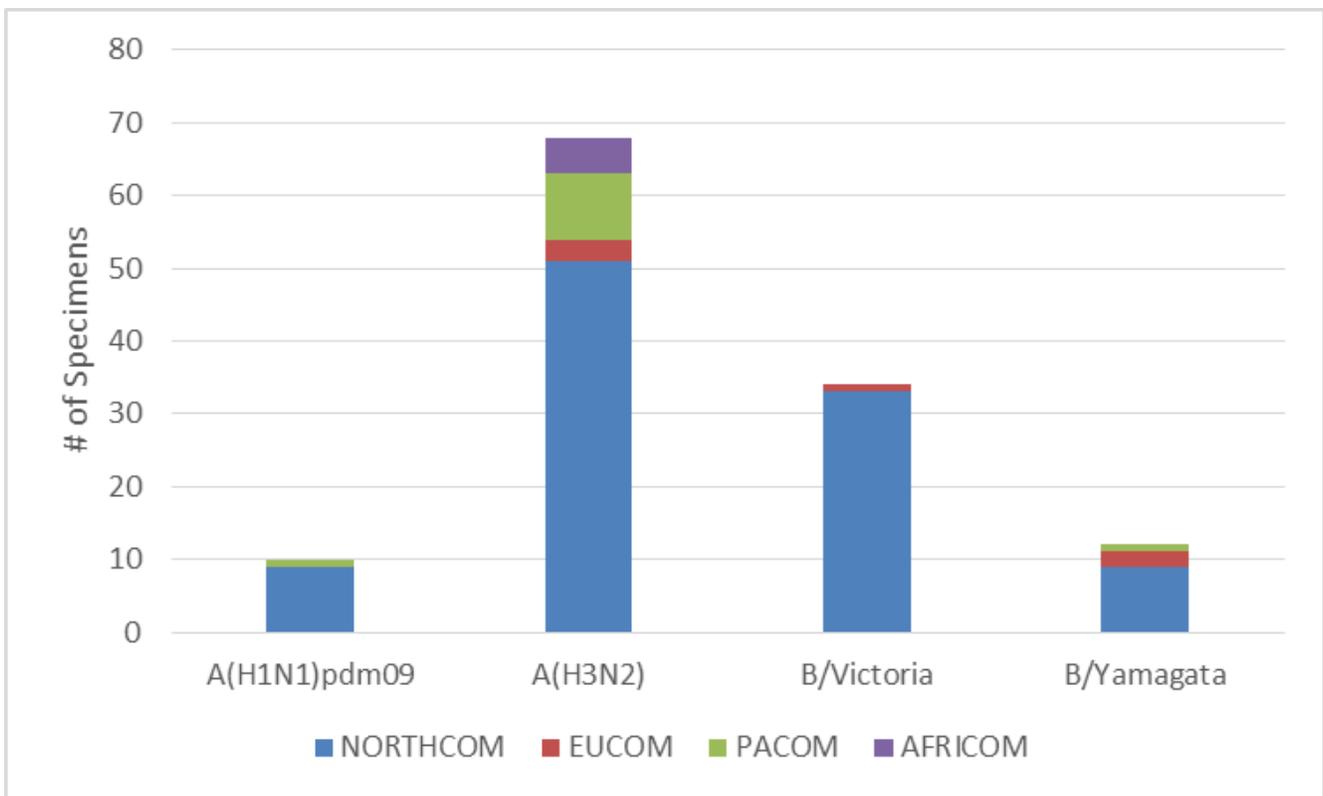


Figure 1. The total HA sequences of influenza A(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata from each of the United States Combatant Commands listed in this report.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1: Distribution of CONUS and OCONUS sentinel sites that contributed influenza A(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata specimens or sequences for this report.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
CONUS					
Arizona					
Luke AFB			1		1
California					
Travis AFB		2			2
NHRC	6	21	2	4	33
Colorado					
Peterson AFB			1		1
Delaware					
Dover AFB		1	1		2
Florida					
Eglin AFB			1		1
Hurlburt Field		1	1		2
Georgia					
Moody AFB			12	1	13
NHRC		3			3
Illinois					
NHRC		5	5	2	12
Kentucky					
Ft Campbell			1		1
Maryland					
NCRM - Walter Reed NMMC		1			1
Mississippi					
Keesler AFB			3		3
Missouri					
NHRC	1	2			3
Nevada					
Nellis AFB			1		1
New Jersey					
NHRC		3			3
New York					
Ft Drum			1		1
USMA - West Point			1		1
Oklahoma					
Tinker AFB		2			2
South Carolina					
Shaw AFB		1	2		3

DoD Global, Laboratory-Based, Influenza Surveillance Program

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
NHRC		8		2	10
Texas					
Ft Bliss	1				1
SAMMC		1			1
Virginia					
NMC Base Portsmouth	1				1
OCONUS					
Alaska					
Eielson AFB		1			1
Germany					
Landstuhl RMC		2	1		3
Ramstein AB		1			1
Vilseck AHC				1	1
Guam					
JB Marianas-Andersen	1				1
Italy					
Aviano AB				1	1
Japan					
NH Okinawa		1			1
NHRC		2			2
Yokota AB		1			1
Kenya					
USAMRD-K		5			5
South Korea					
Brian Allgood ACH		4		1	5
Total	10	68	34	12	124

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 contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

Influenza A(H1N1)pdm09

- Among the 78 influenza A isolates, 10 (12.8% of A, 8.1% of total influenza) were influenza A(H1N1)pdm09. The influenza A(H1N1)pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the 2016-2017 influenza vaccine strain, A/California/07/2009-like virus [Figure 2].
- The influenza A(H1N1)pdm09 isolates characterized for this report exhibited an overall protein homology of 96.9 – 97.4% (average 97.1%) compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus. In addition, overall protein homology of 99.3 – 99.8% (average 99.5%) was observed between the influenza A(H1N1)pdm09 isolates and the 2017-2018 influenza vaccine component, A/Michigan/45/2015-like virus. Only full-length coding sequences were used for protein homology calculations (3 of 10).
- All influenza A(H1N1)pdm09 HA sequences contained mutations consistent with the dominating subgroup referred to as clade 6B, and all could be further classified as subclade 6B.1 (distinguished by the mutations S162N and I216T).
- Gain or loss of *N*-linked glycosylation sites has been shown to alter HA protein surface topology. A gain in glycosylation could be advantageous to the virus by virtue of a masking effect on important antibody recognition sites, thus potentially modulating viral antigenicity.⁴ Observations are based solely on sequence motifs. For the influenza A(H1N1)pdm09 isolates 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 influenza A(H1N1)pdm09 isolates, nine occurred at predicted antigenic sites (none at site A, none at site B, two at site C, three at site D, and four at site E) and two occurred at the receptor binding sites.^{2,5}
- Two of the sequenced influenza A(H1N1)pdm09 specimens were isolated from hospitalized patients.

Figure 2. Recent 2016-2017 Influenza A(H1N1)pdm09 HA Phylogenetic Analysis

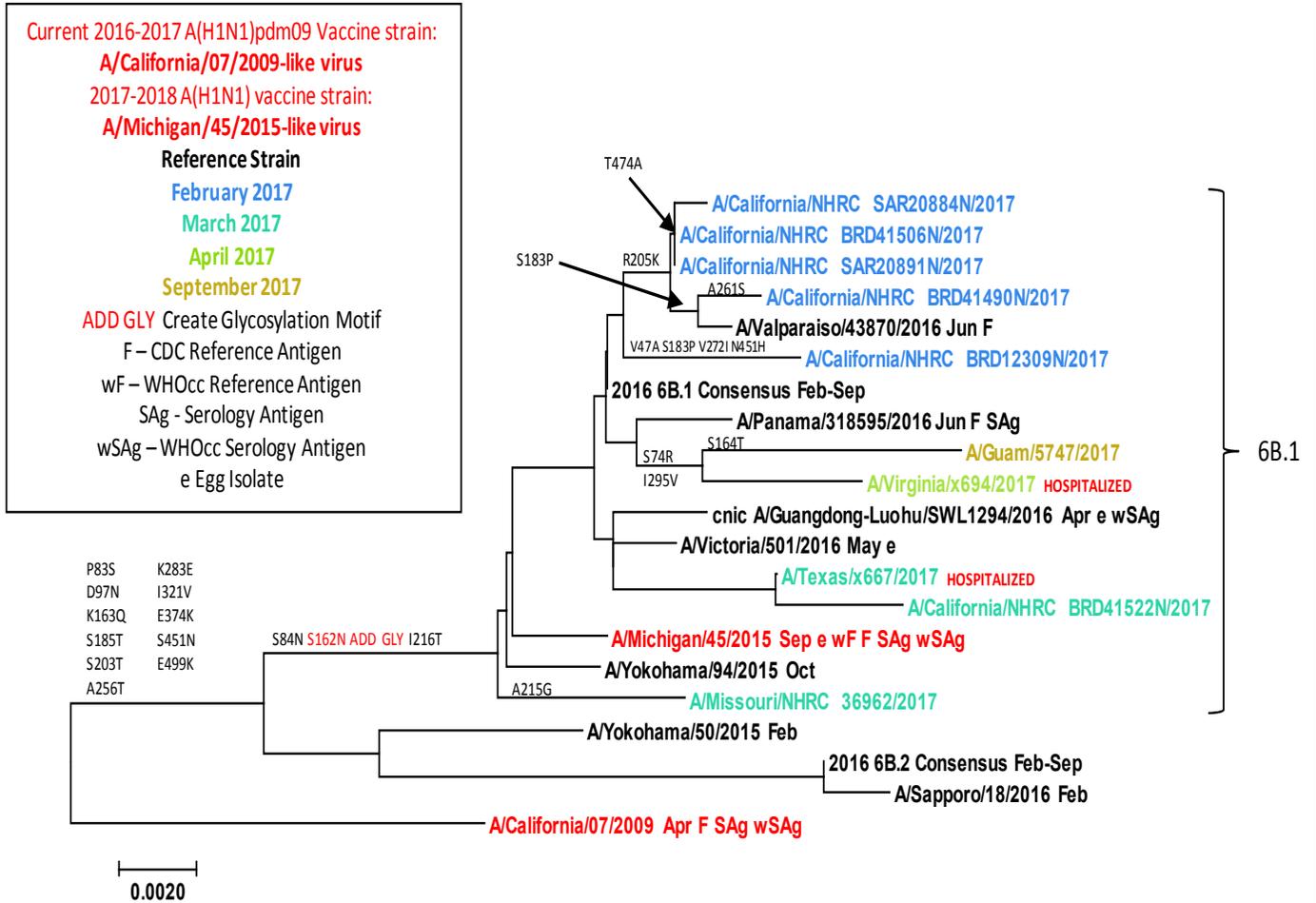


Figure 2. 2016-2017 USAFSAM Report 13 influenza A(H1N1)pdm09 HA phylogenetic analysis. Ten influenza A(H1N1)pdm09 isolates collected between February 2017 and September 2017 were sequenced and all resided in clade 6B.1, with one shared addition of a glycosylation motif. The influenza vaccine A(H1N1)pdm09 component for the 2016-2017 season is A/California/07/2009-like virus but was changed to A/Michigan/45/2015-like virus for the 2017-2018 season.

Influenza A(H3N2)

- Among the 78 influenza A isolates, 68 (87.2% of A, 54.8% of total influenza) were influenza A(H3N2). The influenza A(H3N2) HA sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from a previous vaccine strain, A/Texas/50/2012 [Figure 3].
- The influenza A(H3N2) isolates characterized for this report exhibited an overall protein homology of 97.3 – 98.9% (average 98.1%) compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014-like virus. Only full-length coding sequences were used for protein homology calculations (57 of 68).
- All of the influenza A(H3N2) isolates sequenced for this report were in clade 3C with three (4.4%) in clade 3C.3a and 65 (95.6%) in clade 3C.2a. Forty-one of the 65 3C.2a (63.1%) further classified as the 3C.2a1 subclade of 3C.2a. The mutation N121K was present in 39 (95.1%) of the 3C.2a1 isolates and 45 (66.2%) of the total influenza A(H3N2) isolates. The mutation T135K was present in 15 isolates (36.6% of 3C.2a1 and 22.1% of total).
- Among the influenza A(H3N2) isolates characterized in this report, eight mutations; T10M (threonine to methionine), N22K (asparagine to lysine), N122D (asparagine to aspartic acid), T128N (threonine to asparagine), T135K (threonine to lysine), N144S (asparagine to serine), N144K (asparagine to lysine), and N144R (asparagine to arginine) 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 67 mutations present in the influenza A(H3N2) specimens, 21 occurred at predicted antigenic sites (six at site A, four at site B, two at site C, two at site D, and seven at site E) and three occurred at the receptor binding site.^{2,5}
- Three of the sequenced influenza A(H3N2) specimens were isolated from hospitalized patients.

Figure 3. Recent 2016-2017 Influenza A(H3N2) HA Phylogenetic Analysis

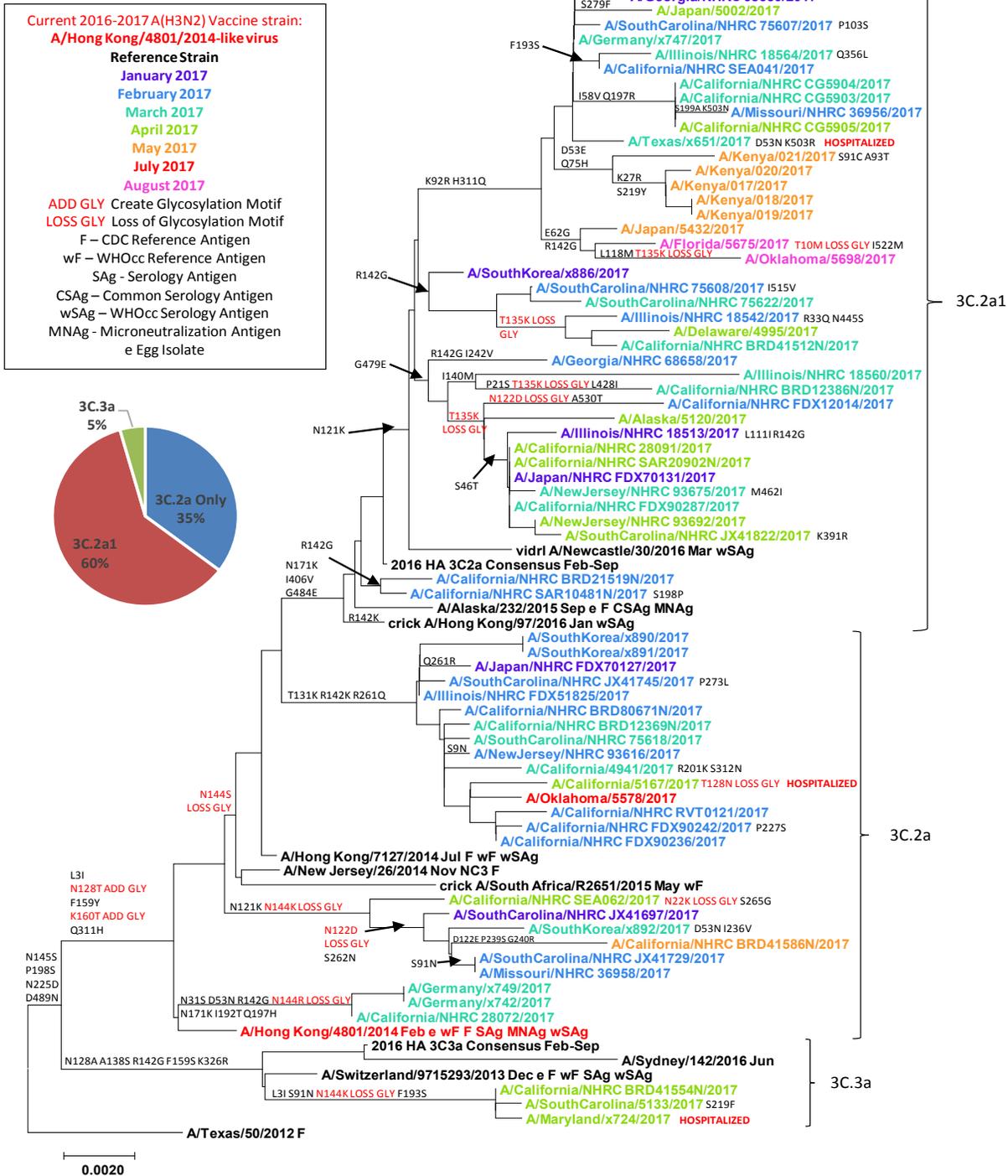


Figure 3. 2016-2017 USAFSAM Report 13 influenza A(H3N2) HA phylogenetic analysis. Sixty-eight influenza A(H3N2) isolates collected between January 2017 and August 2017 were sequenced, of which the majority resided in subclade 3C.2a1 (60.3%), followed by 3C.2a only (35.3%), and 3C.3a (4.4%). Eight mutations caused the loss of glycosylation motifs while two mutations caused the gain of glycosylation motifs.

Influenza B

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees and are rooted from the reference strain B/Ohio/01/2005 for the B/Victoria isolates [Figure 4] and from the previous vaccine strain B/Massachusetts/02/2012-like virus for the B/Yamagata isolates [Figure 5].
- The distinguishing characteristic between the two influenza B lineages (B/Victoria & B/Yamagata) is defined by an amino acid deletion in viruses belonging to the B/Yamagata lineage.¹ Thirty-four (73.9%) of the 46 influenza B isolates characterized in this report fell into the B/Victoria lineage and 12 (26.1%) fell into the B/Yamagata lineage.
- Of interest, 18 (52.9%) of the influenza B/Victoria isolate sequences contained a six base pair deletion causing a double amino acid deletion (positions K162 – N163), which fall in the same region as the single amino acid deletion at 162 observed in Yamagata lineage specimens. All of these B/Victoria deletion specimens also shared the mutations I180V, and R498K and 15 (83.3%) shared the mutation D129G.
- Additionally, one B/Yamagata lineage isolate showed a deletion at position D527.
- The influenza B/Victoria isolates characterized for this report exhibited a protein homology from 98.4 – 99.5% (average 98.9%) when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-like virus.
- The influenza B/Yamagata isolates characterized for this report exhibited a protein homology of 99.1 – 99.3% (average 99.3%) when compared to the 2016-2017 B/Yamagata vaccine component, B/Phuket/3073/2013-like virus.
- All of the influenza B/Victoria isolates fell into clade V1A and all of the B/Yamagata isolates fell into clade Y3. For the B/Victoria isolates, one mutation, A199T (alanine to threonine), adds a glycosylation motif while one mutation, N145D, could cause the loss of a glycosylation motif. For the B/Yamagata isolates, one mutation, D197N (aspartic acid to asparagine), adds a glycosylation motif.

Figure 4. Recent 2016-2017 Influenza B/Victoria HA Phylogenetic Analysis

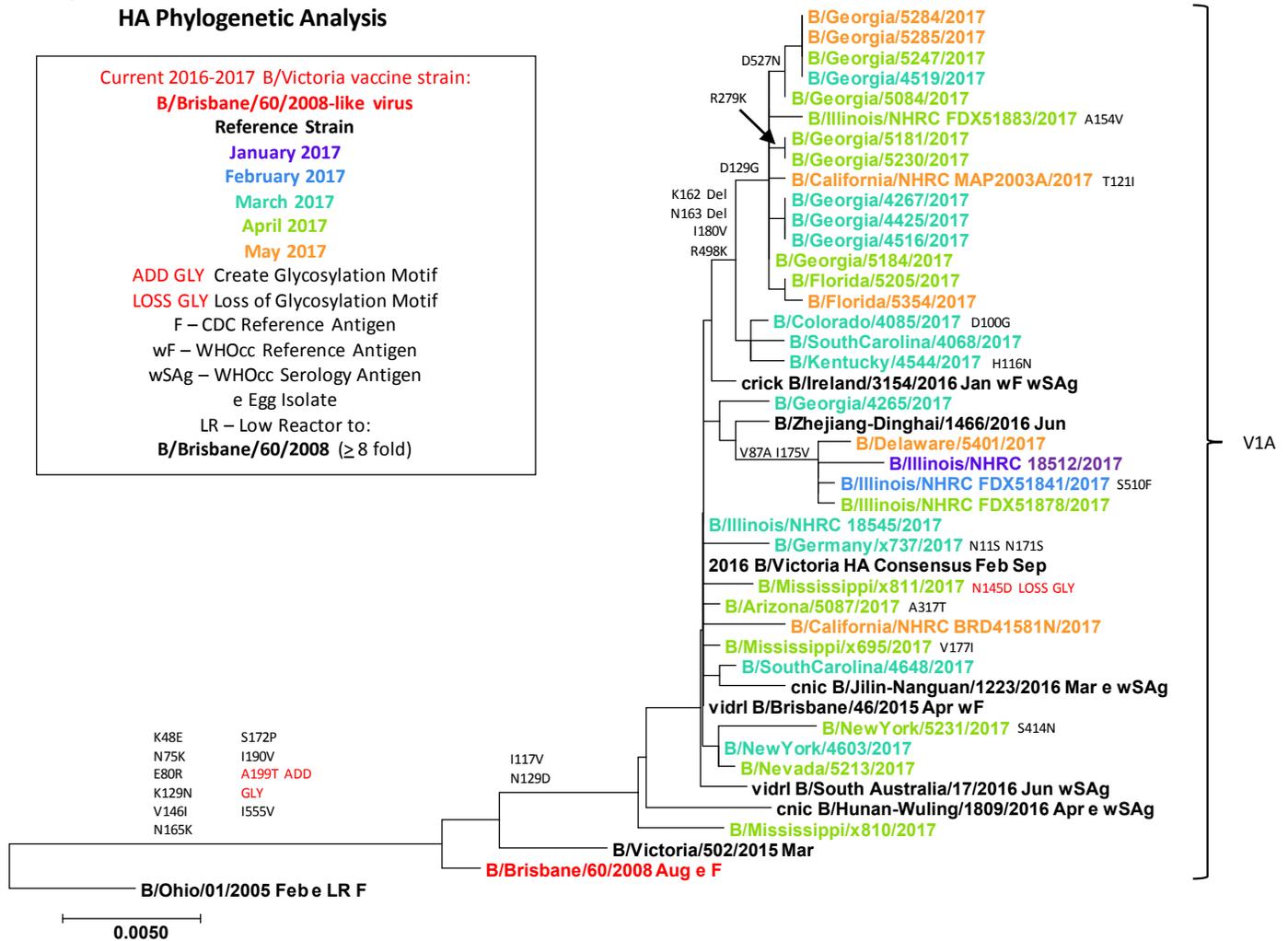


Figure 4. 2016-2017 USAFSAM Report 13 influenza B/Victoria HA phylogenetic analysis. Thirty-four influenza B/Victoria isolates collected between January 2017 and May 2017 were sequenced and all resided in clade V1A, with one shared addition of a glycosylation motif. Eighteen of these isolates had a double deletion at amino acid positions 162-163.

References:

1. Wright, P., Neumann, G., and Kaqaoka, Y. (2007). Orthomyxoviruses 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 hemagglutinin H5 in viral sequences derived from human tissues. *Journal of Gen. Vir.* **89**, 1805-1810.
3. Cherry, J.L., Lipman, D.J., Nikolskaya, A., and Wolf, Y.I. (2009). Evolutionary Dynamics of N-Glycosylation Sites of Influenza Virus Hemagglutinin. *PLoS Curr Influenza*. 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, Y.I., Viboud, C., Holmes, E.C., Koonin, E.V., and Lipman, D.J. (2006). Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol Direct.*; **1**: 34. doi: 10.1186/1745-6150-1-34.

Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the Defense Health Agency/Armed Forces Health Surveillance Branch—Air Force Satellite Cell (DHA/AFHSB-AF) and 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).

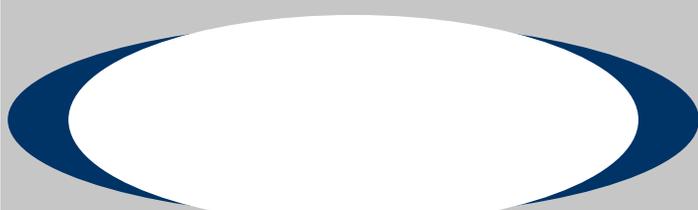
Sentinel Site Surveillance

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. DHA/AFHSB-AF and 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 the program 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.

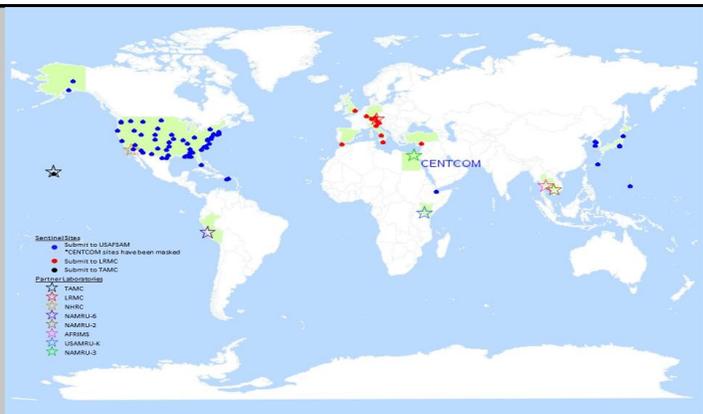
Errata:



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.

