USAF School of Aerospace Medicine & Defense Health Agency

DoD Global Respiratory Pathogen Surveillance Program

2017-2018

Cumulative Results

Locations	97
Collected	11,263
Tested	11,144

Influenza A	**2,602**
A(H1N1)pdm09	533
A(H1N1)pdm09 Coinfection	47
A(H1N1)pdm09 & A(H3N2)	3
A(H1N1)pdm09 & B	8
A(H3N2)	1,790
A(H3N2) Coinfection	190
A(H3N2) & B	9
A/not subtyped	19
A/not subtyped Coinfection	3

Influenza B*	**1,406**
B	1,300
B & Coinfection	106

Other Respiratory Pathogens	**3,499**
Adenovirus	122
Chlamydophila pneumoniae	20
Coronavirus	633
Human Bocavirus	26
Human Metapneumovirus	411
Mycoplasma pneumoniae	41
Parainfluenza	189
RSV	542
Rhinovirus/Enterovirus	1,095
Non-influenza Viral Coinfections	410
Non-influenza Bacterial Coinfections	10
-*C. pneumo* coinfections *(3)*	
-*M. pneumo* coinfections *(7)*	

No Pathogen Detected	**3,637**

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
15 - 28 April 2018 (Surveillance Weeks 16 & 17)

- During 15 - 28 April 2018, a total of 222 specimens were collected and received from 45 locations. Results were finalized for 212 specimens from 43 locations. The percent influenza positive for Weeks 16 and 17 were 24% and 13%, respectively. The influenza percent positive for the season is approximately 36%.

Surveillance Week	A(H1N1)pdm09	A(H3N2)	B	A(H3N2) & Rhino/Entero	B & Rhino/Entero	Total
Week 16	7	7	16	1	2	33
Week 17	0	1	6	1	1	9
Total	7	8	22	2	3	42

- This report contains influenza sequence data from 35 locations in five U.S. Global Combatant Commands, collected from specimens sequenced at USAFSAM and data contributed by NAMRU-2 and USAMRD-K. Among the sequences analyzed were 24 influenza A(H1N1)pdm09, 42 influenza A(H3N2), one influenza B/Victoria, and 36 influenza B/Yamagata viruses.

- A recent study examined the possible association between live-attenuated influenza vaccines (LAIVs) and the subsequent development of asthma in children. Researchers from the Kaiser Permanente Vaccine Study Center conducted a placebo-controlled randomized clinical trial among children (younger than three years old) who were enrolled in the LAIV clinical trail and followed up with them until they were no longer enrolled in the health plan, were diagnosed with asthma, or once the study period ended in 2014. Based on results, the researchers did not find any evidence that there was an increased risk of being diagnosed with asthma when children received LAIV compared with those who received a placebo (The Pediatric Infectious Disease Journal, cited 2 May 2018).

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DoD Global Respiratory Pathogen Surveillance Program

Table 1. Finalized results by region and location for specimens collected during Weeks 16 & 17

Region*		A(H1N1)pdm09	A(H3N2)	B	A(H3N2) & Rhino/Entero	B & Rhino/Entero	Adenovirus	*C. pneumoniae*	HBoV	hMPV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	No Pathogen	Total
EUCOM	Landstuhl RMC, Germany	-	-	-	-	-	-	-	-	3	-	-	-	-	-	2	5
	NAS Sigonella, Italy	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NSA Naples, Italy	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	RAF Lakenheath, England	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Ramstein AB, Germany	-	-	-	-	-	1	-	-	-	-	1	-	-	-	1	3
	USAG Grafenwoehr, Germany	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1
	USAG Wiesbaden, Germany	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	2
	Vilseck AHC, Germany	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	2
PACOM	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	1	-	8	9
Region 1	USCG Academy, CT	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1
Region 2	Ft Drum, NY	-	-	3	1	1	1	1	-	1	-	-	-	5	2	4	19
	JB McGuire-Dix-Lakehurst, NJ	-	-	1	-	-	-	-	-	-	-	-	-	1	1	-	3
	USMA - West Point, NY	-	3	3	-	-	-	-	-	-	-	1	-	6	-	7	20
Region 3	Dover AFB, DE	-	1	1	-	-	-	-	-	2	-	-	1	1	-	1	7
	JB Andrews, MD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	JB Langley-Eustis, VA	2	2	3	-	1	-	-	-	-	-	1	-	3	2	6	20
Region 4	JB Charleston (AF), SC	-	-	1	-	-	-	-	-	-	-	-	-	-	-	2	3
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1
	Moody AFB, GA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Robins AFB, GA	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1
	Seymour Johnson AFB, NC	-	-	1	-	-	-	-	-	-	-	-	-	1	-	1	3
	Shaw AFB, SC	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	3

Cont'd on page 3

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

Table 1. Finalized results by region and location for specimens collected during Weeks 16 & 17
Cont'd from page 2

Region*		A(H1N1)pdm09	A(H3N2)	B	A(H3N2) & Rhino/Entero	B & Rhino/Entero	Adenovirus	*C. pneumoniae*	HBoV	hMPV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	No Pathogen	Total
Region 5	Scott AFB, IL	-	-	1	-	-	-	-	-	-	-	-	-	1	-	1	3
	Wright-Patterson AFB, OH	-	-	2	-	1	-	-	-	3	-	4	1	9	-	12	32
Region 6	Altus AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1
	Cannon AFB, NM	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
	Kirtland AFB, NM	-	-	-	-	-	-	-	-	-	-	-	-	2	1	2	5
	Laughlin AFB, TX	-	-	-	-	-	-	-	-	1	-	-	-	1	-	-	2
	Sheppard AFB, TX	-	-	1	-	-	-	-	-	1	1	-	-	1	1	2	7
	Tinker AFB, OK	-	-	1	-	-	-	-	-	-	-	1	-	1	-	5	8
Region 7	McConnell AFB, KS	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	3
Region 8	Ellsworth AFB, SD	5	2	-	-	-	-	-	-	-	-	-	1	3	-	7	18
	Hill AFB, UT	-	-	1	-	-	-	-	-	-	-	-	-	1	-	1	3
	Minot AFB, ND	-	-	1	1	-	-	-	-	-	-	-	-	1	-	1	4
	Peterson AFB, CO	-	-	1	-	-	-	-	-	-	-	-	1	-	-	2	4
	USAF Academy, CO	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	3
Region 9	Luke AFB, AZ	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	2
	Nellis AFB, NV	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	2
Region 10	Fairchild AFB, WA	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Total		7	8	22	2	3	3	1	1	11	1	11	4	49	7	82	212

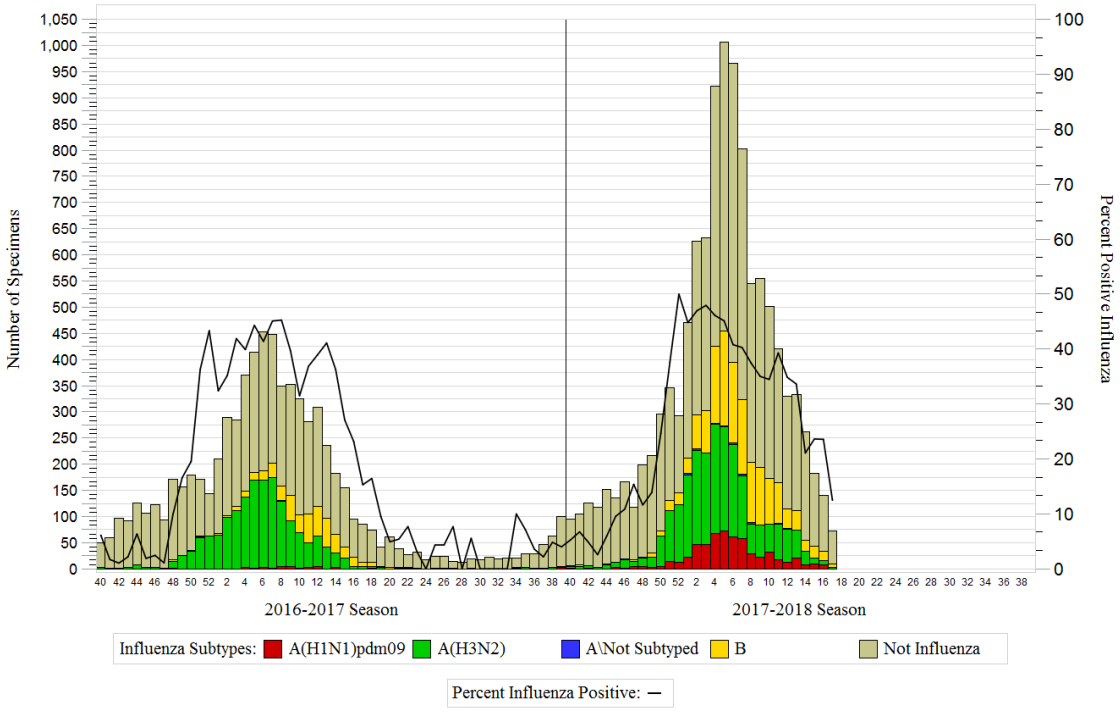
**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

DoD Global Respiratory Pathogen Surveillance Program

Cumulative Laboratory Results

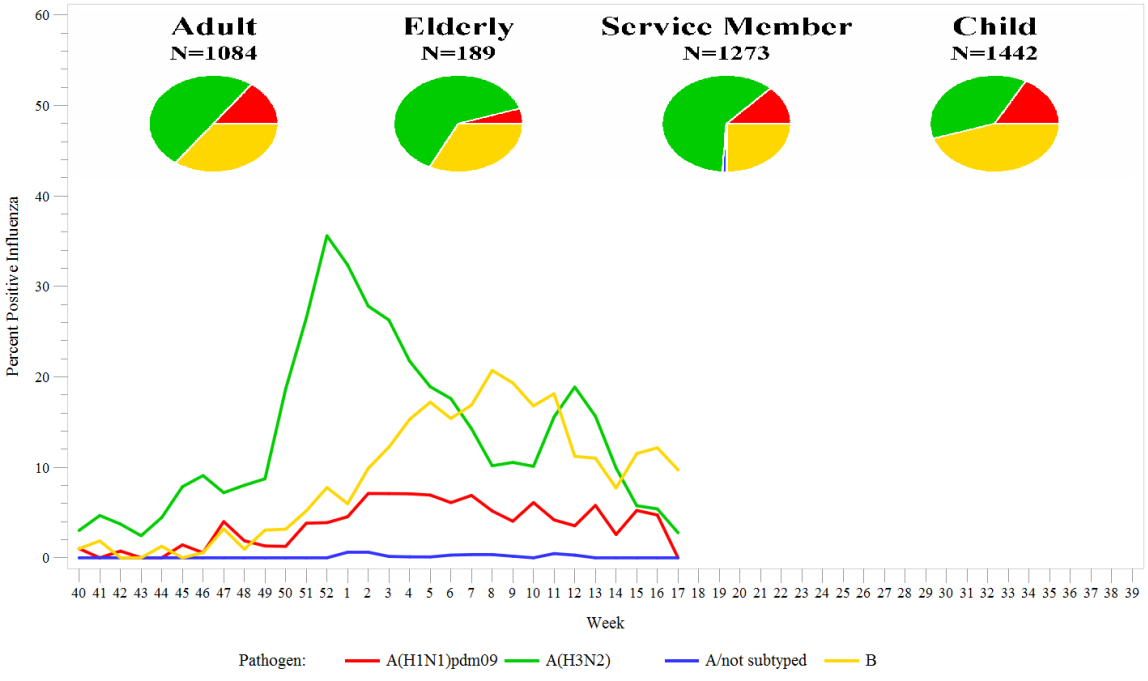
Link to cumulative results by region and location

Graph 1. Percent influenza positive by week: 2016-2017 surveillance year and through Week 17 of the 2017-2018 surveillance year



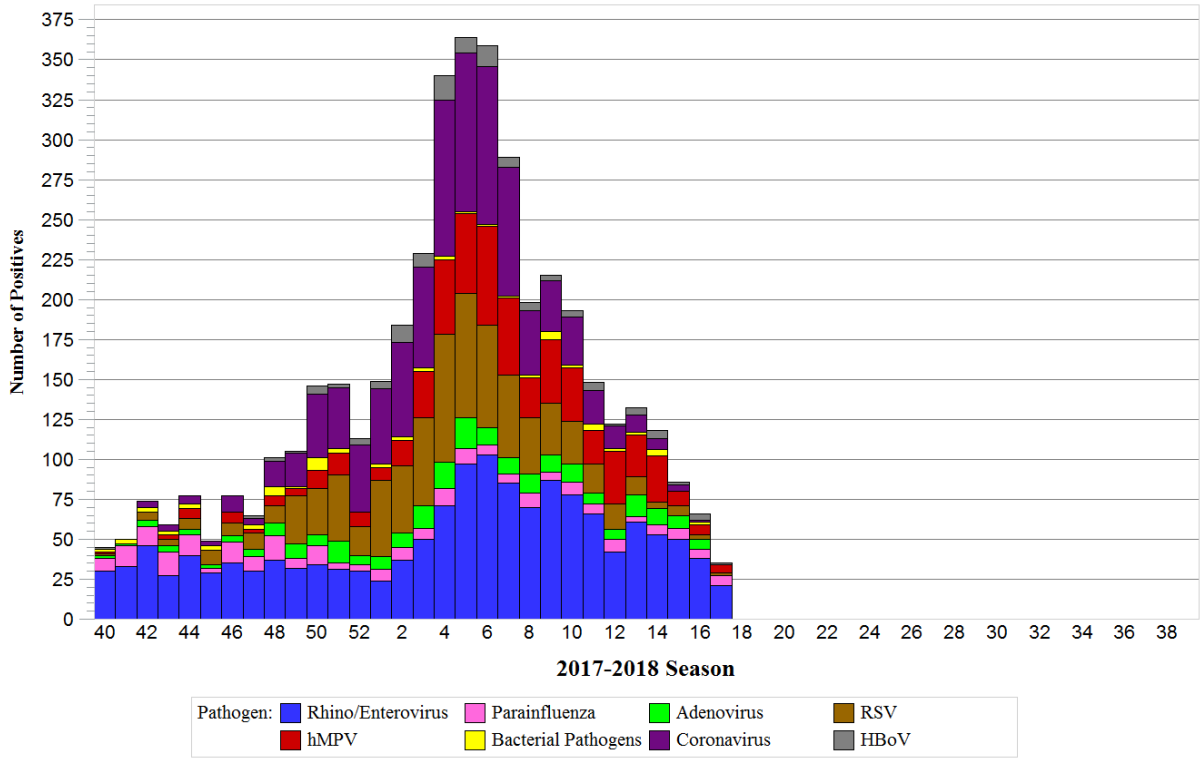
Note: Dual influenza coinfections are excluded from this graph.

Graph 2. Percent positive for influenza through ILI trends by subtype and beneficiary status through Week 17 of the 2017-2018 surveillance year

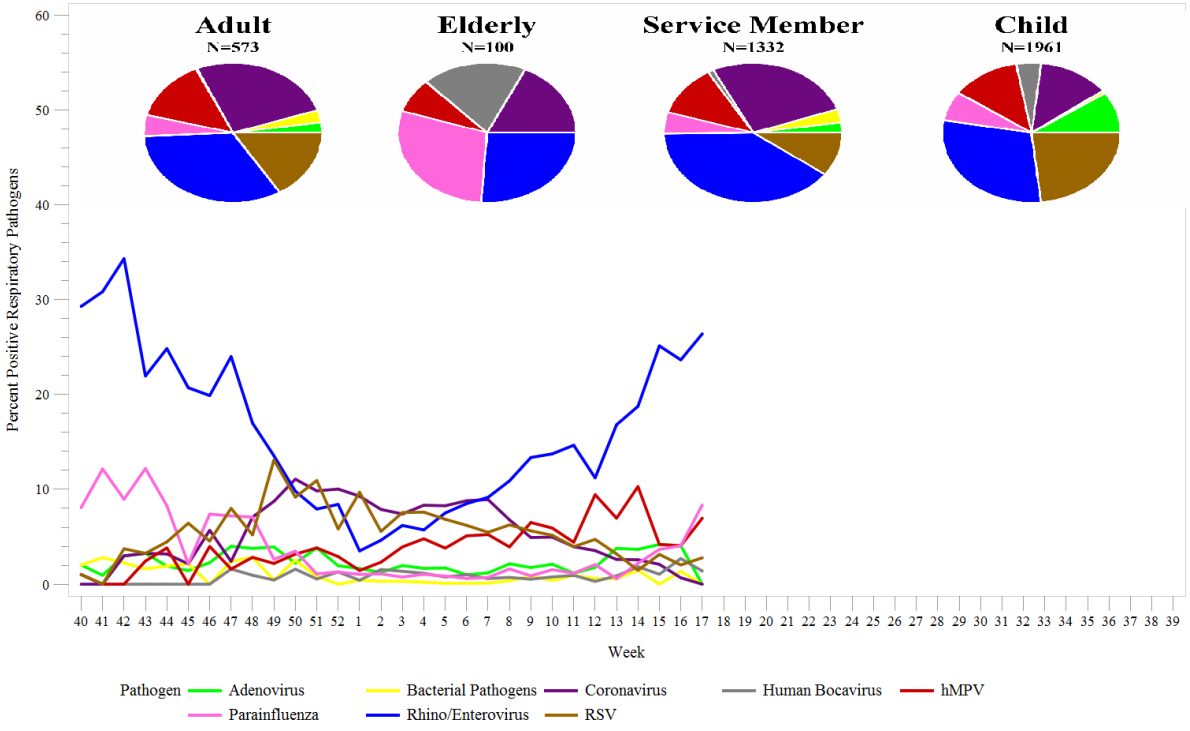


Note: Dual influenza coinfections are excluded from this graph.

Graph 3. Other positive respiratory pathogens through Week 17 of the 2017-2018 surveillance year



Graph 4. Percent positive for respiratory pathogens through ILI trends by week and beneficiary status through Week 17 of the 2017-2018 surveillance year



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

Graph 5. Vaccination status by beneficiary type through Week 17 of the 2017-2018 surveillance year (excluding 'Unknown' beneficiary type)

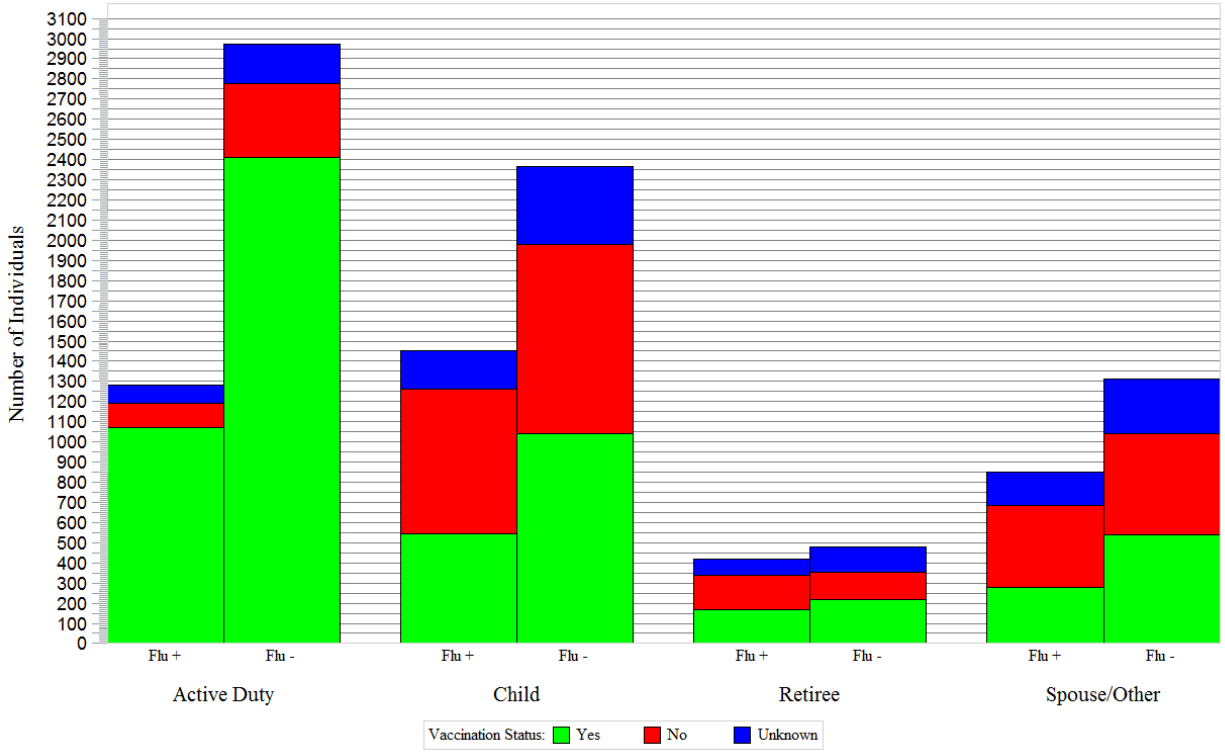
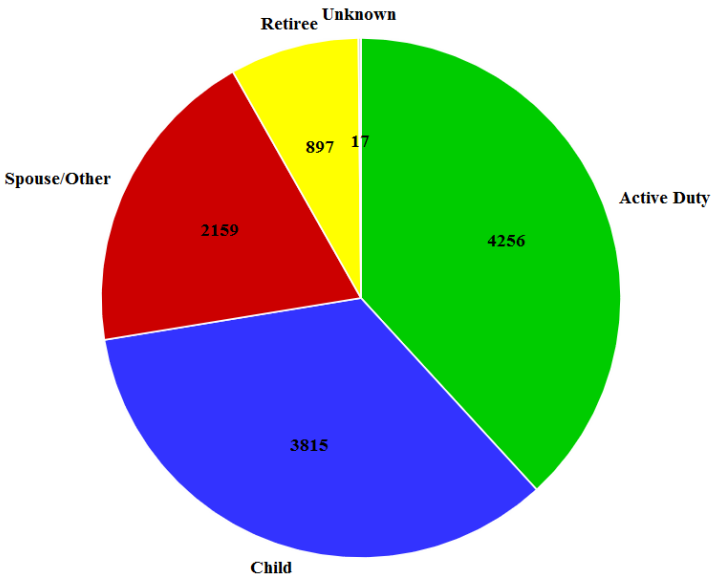


Table 2. ILI by age group through Week 17 of the 2017-2018 surveillance year

Age Group	Frequency	Percent
0-5	2197	19.71
6-9	747	6.70
10-17	944	8.47
18-24	1683	15.10
25-44	3597	32.28
45-64	1441	12.93
65+	535	4.80

Graph 6. ILI by beneficiary status through Week 17 of the 2017-2018 surveillance year

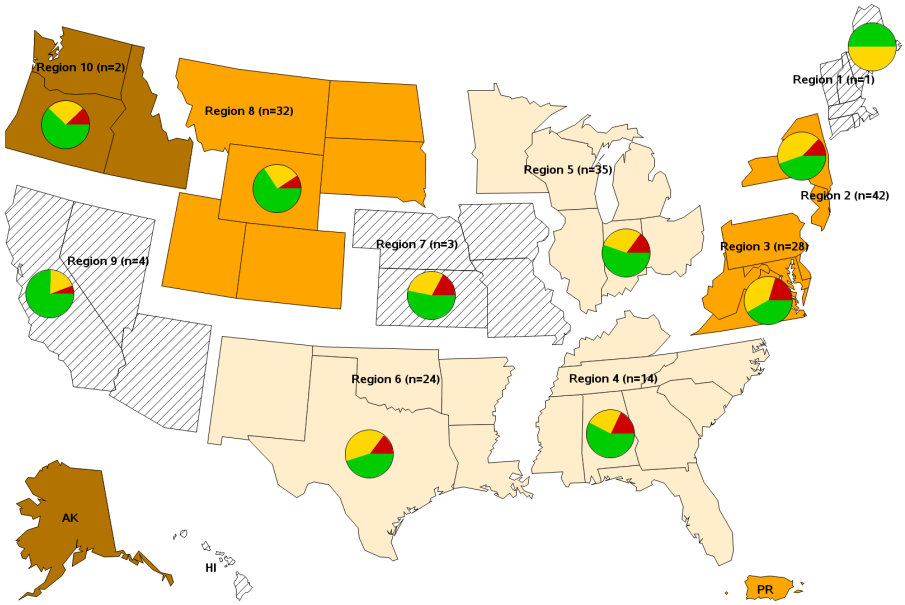


Demographic Summary

Of 11,144 ILI cases, 4,256 are service members (38.2%), 3,815 are children (34.2%), 2,159 are spouse/other beneficiaries (19.4%), 897 are retirees (8.0%), and 17 are unknown (0.2%). The median age of ILI cases with known age (n=11,144) is 25 (range 0, 98).

DoD Global Respiratory Pathogen Surveillance Program

Map 1. Influenza subtypes and activity level by U.S. region through Week 17 of the 2017-2018 surveillance year

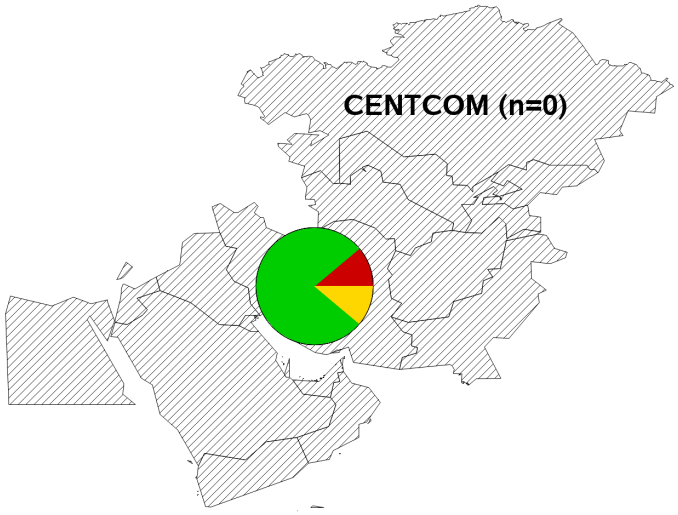


HI - Region 9

AK - Region 10

PR - Region 2

Map 2. Influenza subtypes and activity level for CENTCOM through Week 17 of the 2017-2018 surveillance year



Legend

Influenza Activity - Past 2 weeks

(n = # of submissions)

- No activity (0% +) or no submissions
- Low (<25% +)
- Moderate (25-49% +)
- High (>50% +)

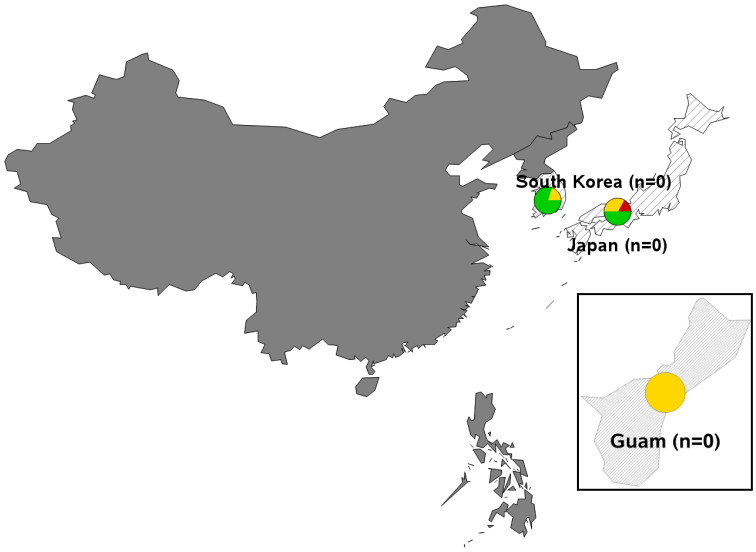
Influenza Results - Cumulative

- Influenza A(H3N2)
- Influenza A(H1N1)pdm09
- Influenza B
- Influenza A/not subtyped

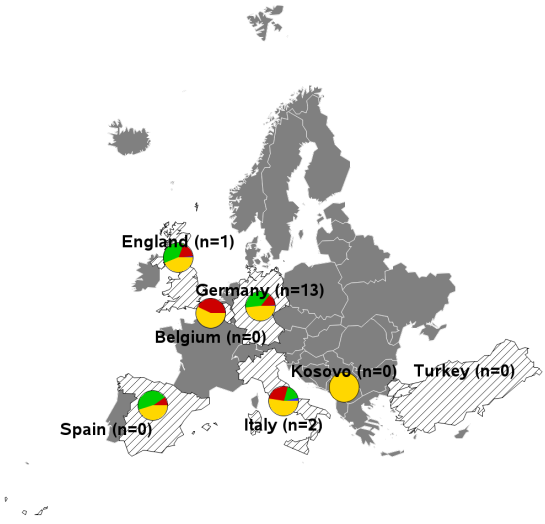
88ABW-2015-5508 and PA email guidance dated 10 November 2015.

DoD Global Respiratory Pathogen Surveillance Program

Map 3. Influenza subtypes and activity level by country through Week 17 of the 2017-2018 surveillance year (Pacific)



Map 4. Influenza subtypes and activity level by country through Week 17 of the 2017-2018 surveillance year (Europe)



Note - Countries shaded in gray do not contain submitting sites and are only displayed for geographical perspective.

Legend

Influenza Activity - Past 2 weeks

(n = # of submissions)

- No activity (0% +) or no submissions
- Low (<25% +)
- Moderate (25-49% +)
- High (>50% +)

Influenza Results - Cumulative

- Influenza A(H3N2)
- Influenza A(H1N1)pdm09
- Influenza B
- Influenza A/not subtyped

Table 3. Cumulative specimens submitted for sequencing only by location through Week 17 of the 2017-2018 surveillance year

Location	Number Received	Number Tested
Aviano AB, Italy	7	1
Brian Allgood ACH, South Korea	184	0
Camp Bondsteel, Kosovo	1	0
Ft Bliss, TX	6	0
Ft Bragg, NC	3	0
Ft Hood, TX	6	3
JB Elmendorf-Richardson, AK	2	0
Keesler AFB, MS	277	121
Landstuhl RMC, Germany	159	8
NAS Sigonella, Italy	16	0
NAVSTA Rota, Spain	13	1
NCRM - Walter Reed NMMC, MD	13	2
NMC Portsmouth, VA	11	0
NSA Naples, Italy	49	0
Nellis AFB, NV	1	1
RAF Lakenheath, England	35	8
Ramstein AB, Germany	33	3
SAMMC, TX	851	87
SHAPE, Belgium	3	1
Spangdahlem AB, Germany	1	0
Tripler AMC, HI	39	3
USAG Baumholder, Germany	4	1
USAG Grafenwoehr, Germany	22	0
USAG Hohenfels, Germany	1	0
USAG Kaiserslautern, Germany	17	0
USAG Stuttgart, Germany	34	4
USAG Vicenza, Italy	32	0
USAG Wiesbaden, Germany	34	1
Vilseck AHC, Germany	39	1
Total	**1893**	**246**

Molecular Sequence Analysis Report #6

This is the sixth USAFSAM influenza sequence surveillance report for the 2017-2018 influenza season. Of the specimens sequenced during this reporting period, results were finalizd for 103 specimens with collection dates between 1 November 2017 and 7 March 2018, with 70 specimens sequenced at USAFSAM, four sequences contributed by the Naval Medical Research Unit 2 (NAMRU-2), and 29 sequences contributed by the United States Army Medical Research Unit Kenya (USAMRD-K). For the 2017-2018 influenza season, 623 sequencing results have been reported.

The 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] 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.

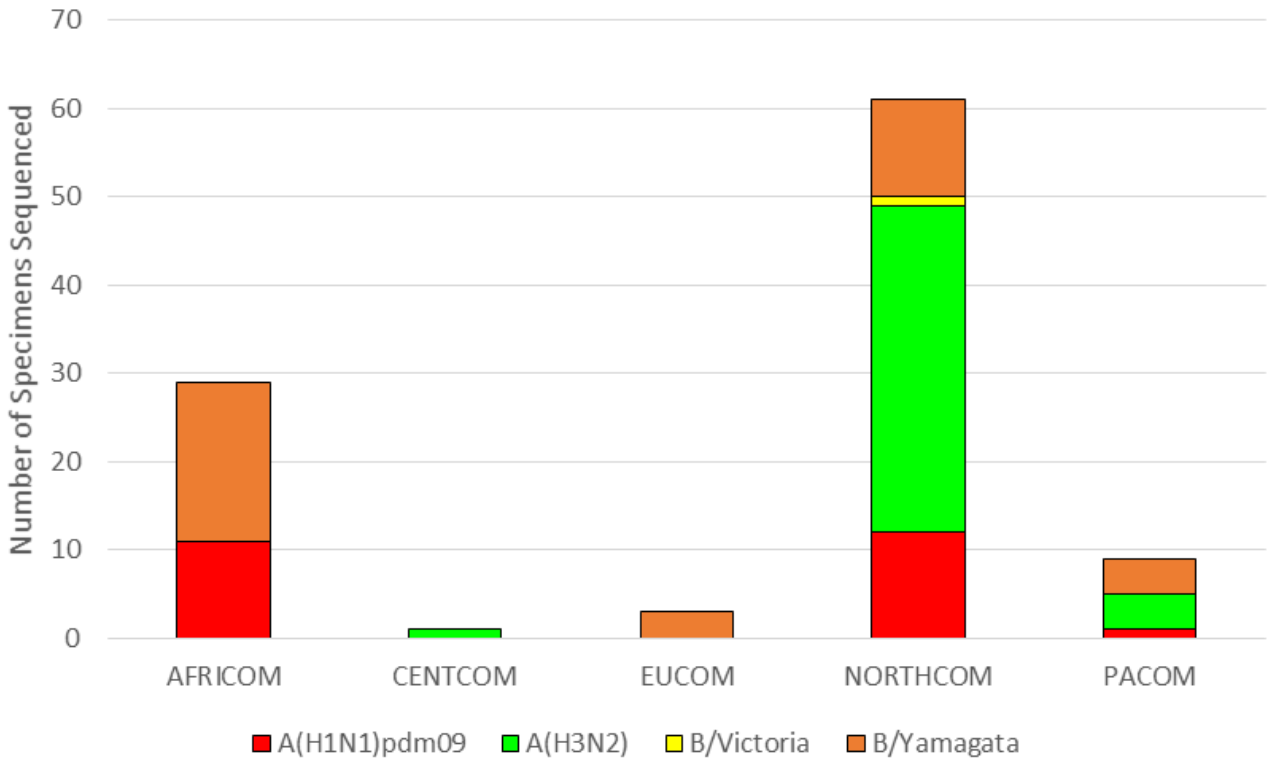


Figure 1. Total influenza sequences from each of the United States Combatant Commands analyzed for this report.

Table 4. Distribution of CONUS and OCONUS sentinel sites that contributed influenza specimens or sequences for this report.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
CONUS					
Arizona					
Davis Monthan AFB		1			1
Luke AFB		1			1
Arkansas					
Little Rock AFB		1			1
California					
Travis AFB		3			3
Colorado					
Peterson AFB		1			1
Delaware					
Dover AFB		1			1
Florida					
Eglin AFB	2	2		1	5
Hurlburt Field		2			2
Tyndall AFB	1				1
Georgia					
Robins AFB		1			1
Idaho					
Mt Home AFB		1			1
Illinois					
Scott AFB		1		1	2
Kansas					
McConnell AFB	2	2			4
Maryland					
JB Andrews	1				1
Mississippi					
Keesler AFB				3	3
New Jersey					
JB McGuire-Dix-Lakehurst	1	2			3
New Mexico					
Cannon AFB		1			1
New York					
Ft Drum		1			1
USMA - West Point		1	1		2
North Carolina					
Seymour Johnson AFB		1			1
North Dakota					
Minot AFB		1			1

Table 4. Distribution of CONUS and OCONUS sentinel sites that contributed influenza specimens or sequences for this report.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
Ohio					
Wright-Patterson AFB	2	2			4
Oklahoma					
Tinker AFB		3			3
Texas					
Lackland AFB	1	2			3
SAMMC	1	1		3	5
Sheppard AFB		2		1	3
Utah					
Hill AFB		1			1
Washington					
NH Bremerton	1				1
Wyoming					
FE Warren AFB		1		2	3
OCONUS					
Cambodia					
NAMRU-2	1	1		2	4
Country 1					
Location B		1			1
Country 2					
Location A		1			1
England					
RAF Lakenheath				3	3
Japan					
Yokota AB		3		2	5
Kenya					
USAMRD-K	11			18	29
Grand Total	**24**	**42**	**1**	**36**	**103**

Table 5. Cumulative protein homologies (percent amino acid match) of 2017-2018 influenza strains relative to vaccine strains. The influenza A (H1N1)pdm09 vaccine strain was changed from A/California/07/2009-like virus to A/Michigan/45/2015-like virus for the 2017-2018 season. Use of the quadrivalent vaccine, which contains strains from each of the influenza B lineages in addition to one A(H1N1)pdm09 and one A(H3N2) virus, began in 2013 for the 2013-2014 influenza season.

Subtype or Lineage	Season(s)	Vaccine Component	Min	Max	Average
A(H1N1)pdm09	2017-2018	A/Michigan/45/2015-like	98.4%	99.5%	98.9%
A(H3N2)	2016-2018	A/Hong Kong/4801/2014-like	96.7%	99.1%	98.3%
B/Victoria	2009-2012 and 2013-2018	B/Brisbane/60/2008-like*	98.4%	99.5%	98.8%
B/Yamagata	2015-2018	B/Phuket/3073/2013-like**	98.8%	99.5%	99.3%

*Quadrivalent only during the 2013-2016 seasons
** Quadrivalent only during the 2016-2018 seasons

Influenza A(H1N1)pdm09

- Among the 66 influenza A HA sequences, 24 (36.3%) 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 previous vaccine strain, A/California/07/2009 [**Figure 2**].
- The influenza A(H1N1)pdm09 sequences characterized for this report exhibited an overall protein homology of 98.4 - 99.3% (average 98.9%) compared to the 2017-2018 influenza vaccine component, A/Michigan/45/2015-like virus. The cumulative protein homology for the season is 98.4 - 99.5% (average 98.9%) [**Table 5**].
- All influenza A(H1N1)pdm09 HA sequences contained mutations consistent with the dominating subgroup referred to as clade 6B and could all be further classified as subclade 6B.1.
- 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 HA sequences characterized in this report, one mutation, S162N (serine to asparagine), was observed that caused a gain of a glycosylation motif.
- Of the 32 mutations present in the influenza A(H1N1)pdm09 sequences, 10 occurred at predicted antigenic sites (none at site A, one at site B, three at site C, two at site D, and four at site E) and two occurred at the receptor binding site.[4,5]

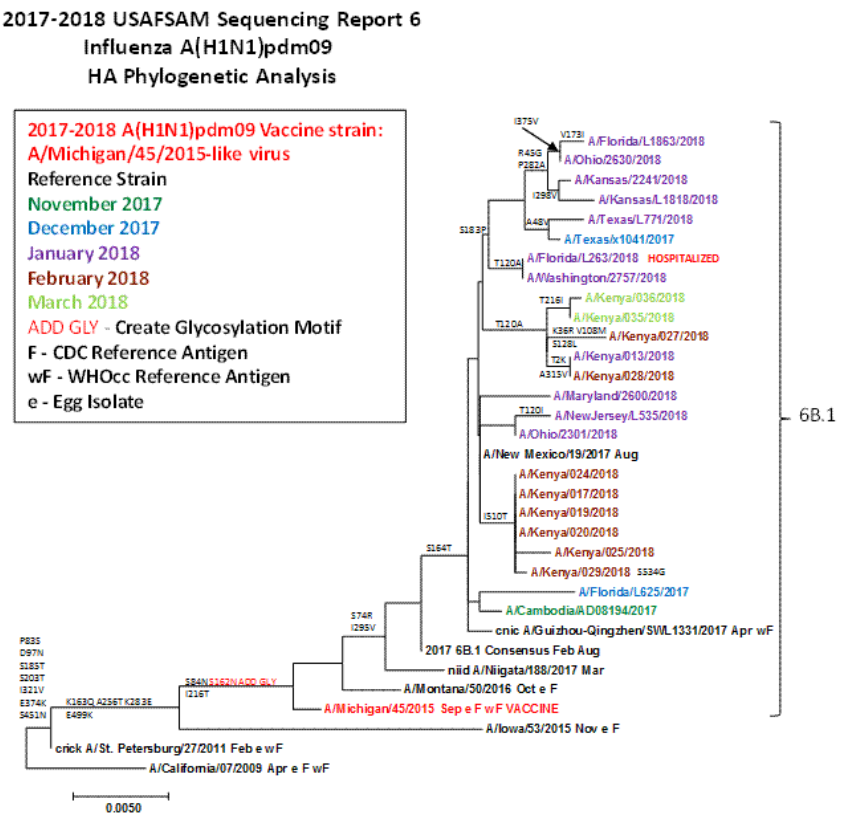


Figure 2. Influenza A(H1N1)pdm09 HA phylogenetic analysis. Twenty-four influenza A(H1N1)pdm09 isolates collected between November 2017 and March 2018 were sequenced and all resided in clade 6B.1, with one shared addition of a glycosylation motif. The vaccine strain A/Michigan/45/2015-like virus was selected again for the 2018-2019 influenza vaccine.

Influenza A(H3N2)

- Among the 66 influenza A HA sequences, 42 (63.6%) 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 4**].

- The influenza A(H3N2) HA sequences characterized in this report have exhibited an overall protein homology of 96.7 - 98.9% (average 98.3%) compared to the 2017-2018 influenza vaccine component, A/Hong Kong/4801/2014-like virus. The cumulative protein homology for the season is 96.7 - 99.1% (average 98.3%) [**Table 5**].

- Thirty-seven of the influenza A(H3N2) viruses sequenced for this report were in clade 3C.2a (88.1%) with four (10.8%) in clade 3C.2a1 and 32 (86.5%) in the newly characterized clade 3C.2a2, distinguished by the mutations T131K, R142K, and R261Q. Among the four in 3C.2a1, two sequences (5.4%) resided in the new subclade 3C.2a1a (distinguished by T135K and G479E) and two (5.4%) resided in the new subclade 3C.2a1b (distinguished by K92R and H311Q). The remaining five sequences resided in clade 3C.3 (11.9%) with four in subclade 3C.3a (80%) and one in the rarely seen subclade 3C.3b (20%).

- Among the influenza A(H3N2) HA sequences characterized in this report, nine mutations; T10M, N122D, S124N, S124R, T135K, N144S, N144K, T160A, and T160K, were observed that caused the loss of a glycosylation motif. Two other mutations, A128T and K160T were observed that caused the gain of a glycosylation motif. One additional mutation, T135N, caused a loss of a glycosylation motif at site 133 and the simultaneous gain of a motif at site 135.

- Of the 51 mutations present in the influenza A(H3N2) sequences, 18 occurred at predicted antigenic sites (six at site A, four at site B, one at site C, two at site D, and five at site E), and two occurred at the receptor binding site.[4,5]

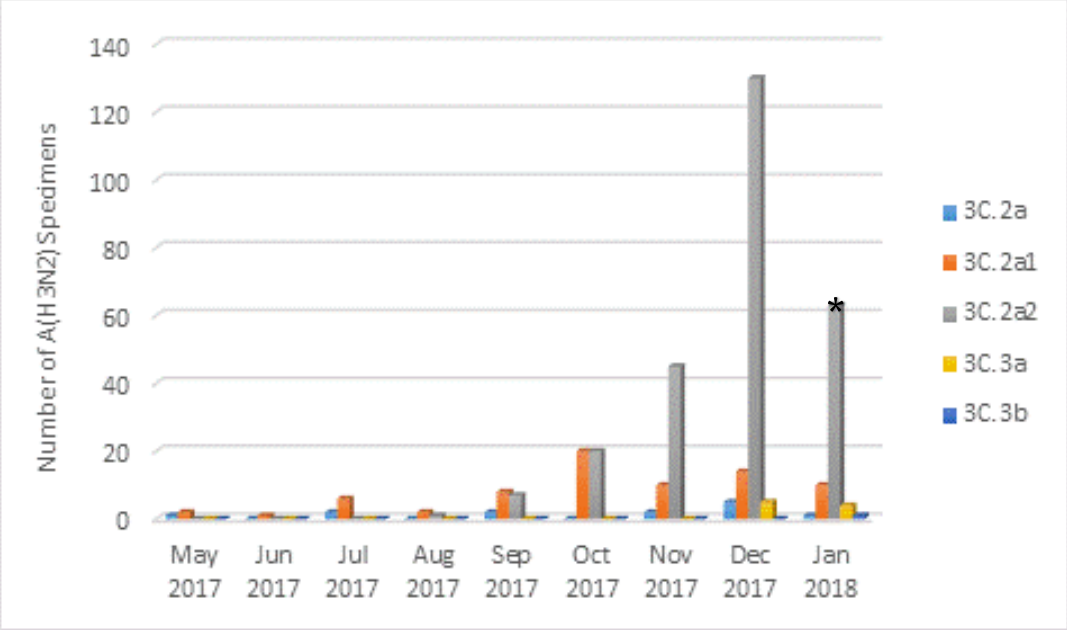


Figure 3. Cumulative proportion of influenza A(H3N2) clades among specimens collected from May 2017 through January 2018. Subclade 3C.2a1 was the dominant A(H3N2) genetic group throughout the 2016-2017 season but declined prior to the start of the 2017-2018 season as clade 3C.2a increased in prevalence. A new subclade of 3C.2a, 3C.2a2, was recently described as well as two new subclades of 3C.2a1, 3C.2a1a and 3C.2a1b (not shown). * - Not all specimens from January have been sequenced as of this report, therefore this figure is not indicative of a decline in influenza A(H3N2) in January 2018.

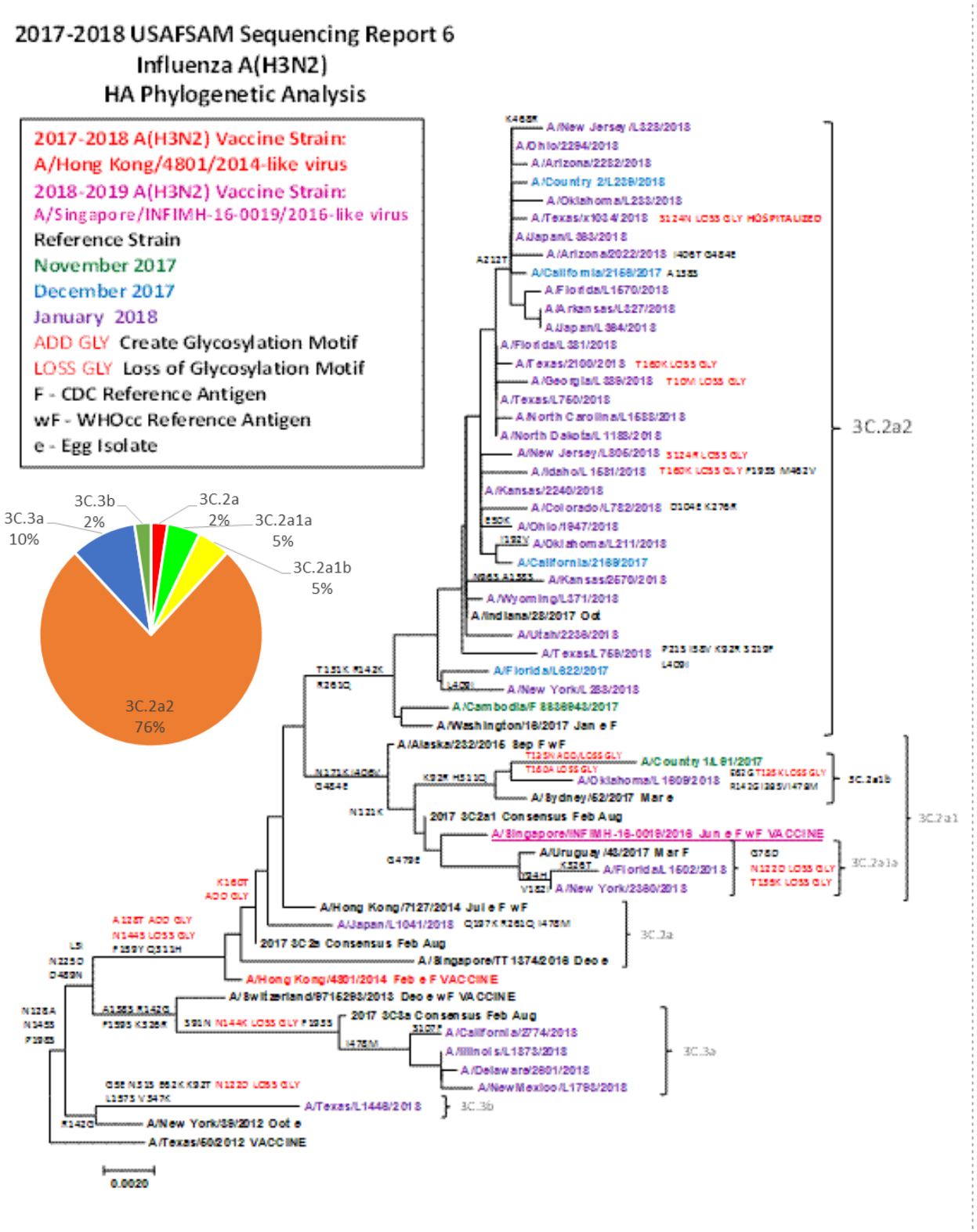


Figure 4. Influenza A(H3N2) HA phylogenetic analysis. Forty-two influenza A(H3N2) specimens collected between November 2017 and January 2018 were sequenced, of which the majority resided in clade 3C.2a2 (76%). Nine mutations caused the loss of glycosylation motifs and two mutations caused the gain of glycosylation motifs, while one mutation caused a simultaneous loss and gain at adjacent sites. The selected strain for the A(H3N2) component of the 2018-2019 influenza vaccine is A/Singapore/INFIMH-16-0019/2016-like virus, underlined (egg propagated).

Influenza B

- The distinguishing characteristic between the two influenza B lineages is defined by an amino acid deletion in viruses belonging to the B/Yamagata lineage.[1] Thirty-six (97.3%) of the 37 influenza B specimens characterized in this report fell into the B/Yamagata lineage and the remaining one (2.7%) fell into the B/Victoria lineage.

- The influenza B/Victoria HA sequence is characterized in a lineage specific, neighbor-joining phylogenetic trees with reference strains and is rooted from the current vaccine strain B/Brisbane/60/2008-like virus [**Figure 5**].

- The influenza B/Victoria sequence characterized for this report exhibited a protein homology of 98.6 % when compared to the 2017-2018 B/Yamagata vaccine component, B/Brisbane/60/2008-like virus. The cumulative protein homology for the season is 98.4 - 99.5% (average 98.8%) [**Table 5**].

- This influenza B/Victoria sequence fell into clade V1A and contained a two amino acid deletion at positions 162-163.

- The influenza B/Yamagata HA sequences are characterized in a lineage specific, neighbor-joining phylogenetic tree with reference strains and are rooted from the previous vaccine seed strain B/Massachusetts/02/2012 [**Figure 6**].

- The influenza B/Yamagata sequences characterized for this report exhibited a protein homology of 98.9 - 99.5% (average 99.4%) when compared to the 2017-2018 B/Yamagata vaccine component, B/Phuket/3073/2013-like virus. The cumulative protein homology for the season is 98.8 - 99.5% (average 99.3%) [**Table 5**].

- All of the B/Yamagata sequences fell into clade Y3 and there was one mutation, D196N that resulted in the addition of a glycosylation motif and one mutation, T169A that resulted in the loss of a glycosylation motif.

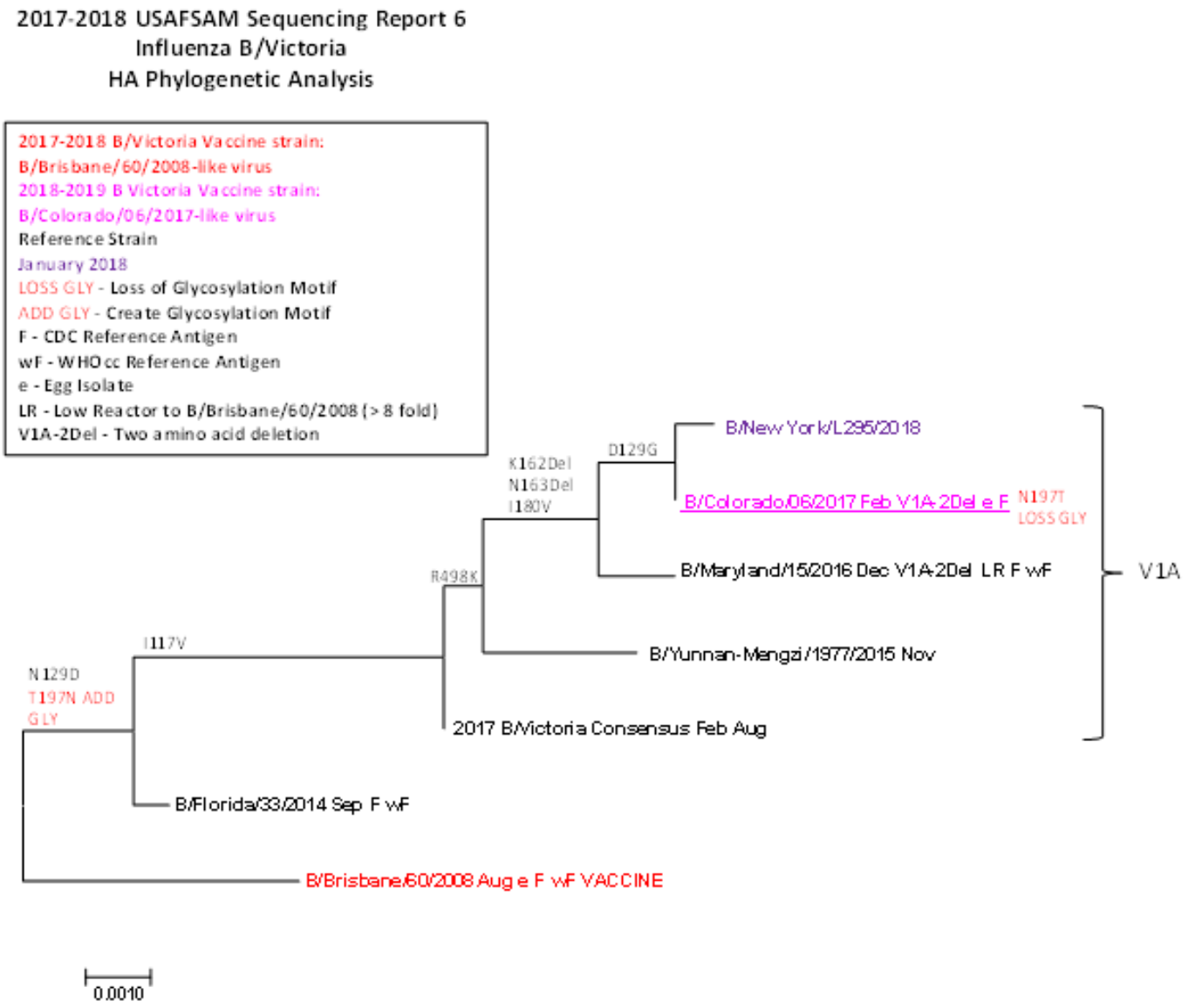


Figure 5. Influenza B/Victoria phylogenetic analysis. One influenza B/Victoria specimen was collected in January 2018 and resided in clade V1A with deletions of amino acid positions 162-163 and the mutations D129G, I180V, and R498K. The selected strain for the B/Victoria component of the 2018-2019 influenza vaccine is B/Colorado/06/2017-like virus, underlined (egg propagated).

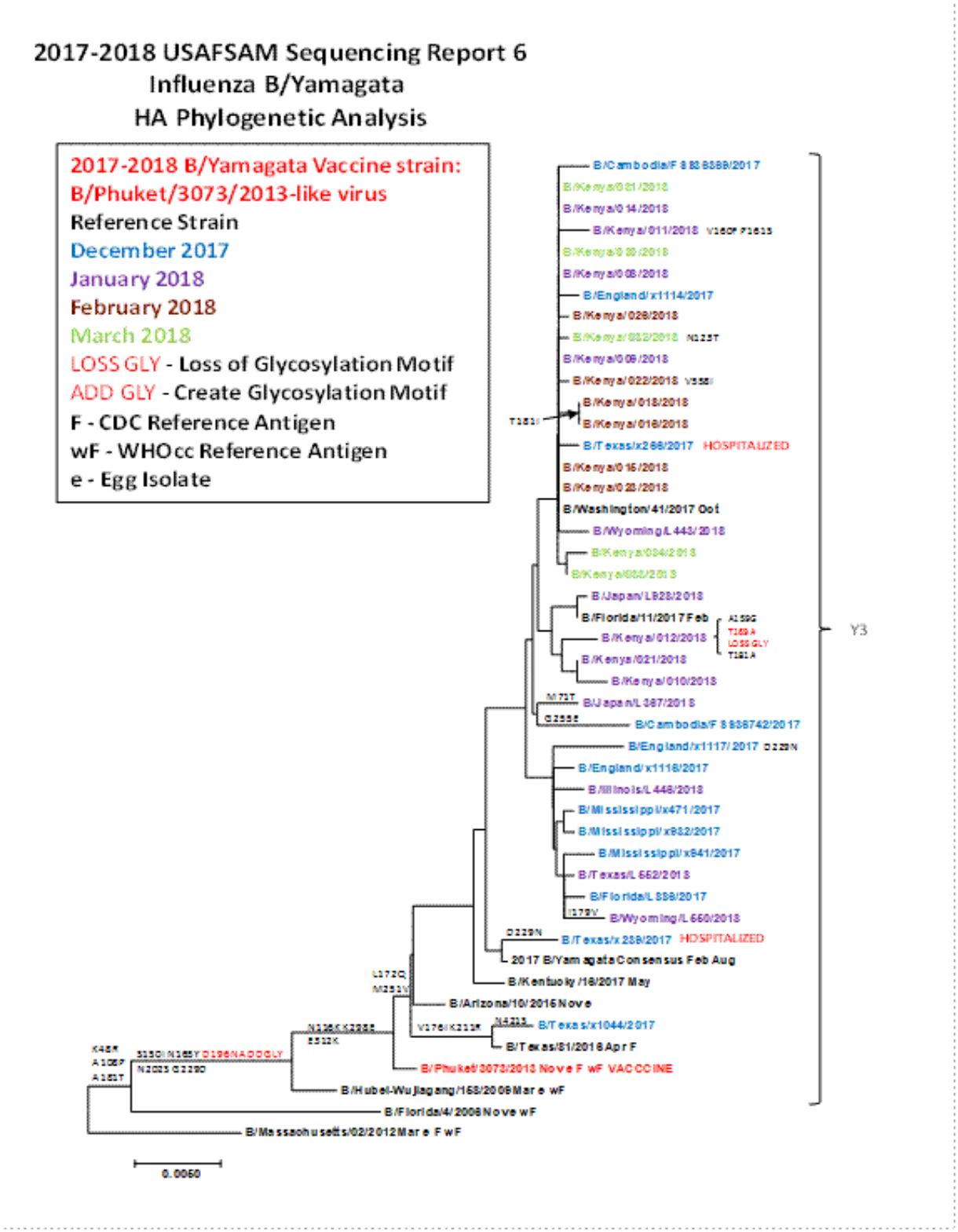


Figure 6. Influenza B/Yamagata phylogenetic analysis. Thirty-six influenza B/Yamagata specimens collected between December 2017 and March 2018 were sequenced and all resided in clade Y3, with one addition of a glycosylation motif and one loss. The vaccine strain B/Phuket/3073/2013-like virus was selected again as the B/Yamagata component of the 2018-2019 influenza vaccine, to be included in the quadrivalent formulation only.

References:

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USAF School of Aerospace Medicine & Defense Health Agency

DoD Global Respiratory Pathogen 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 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 79 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, USAMRD-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. EUCOM respiratory data is obtained from LRMC and incorporated into our weekly report. This process seeks to provide more timely results and efficient transport of specimens.

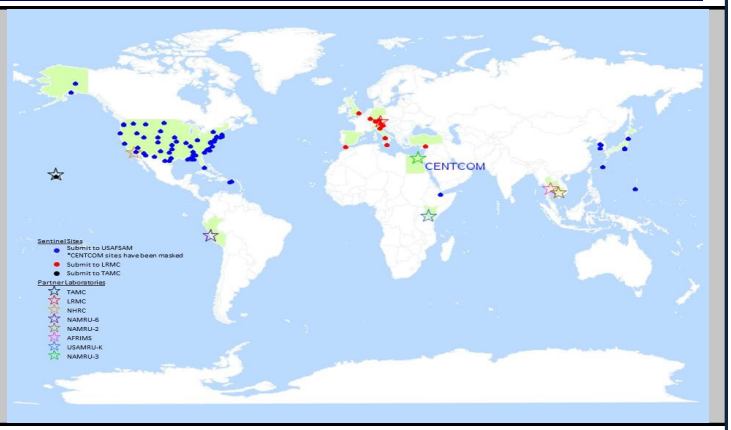
Available on our website (listed below) is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and a dashboard containing respiratory data for our sentinel sites.

Errata:

For Public Health Services
937-938-3196; DSN 798-3196

For Laboratory Services
937-938-4140; DSN 798-4140

USAFSAM.PHRFlu@us.af.mil



Collaborating Partners

In addition to all participating DoD military sentinel sites, collaborating laboratories and medical centers (described above) may be further understood by reviewing the sites' website. Click on the sites' icon to be directed to their webpage.

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