USAF School of Aerospace Medicine & Defense Health Agency

DoD Global Respiratory Pathogen Surveillance Program

2017-2018

Cumulative Results

Locations	90
Collected	2,505
Tested	2,409

Influenza A	**413**
A(H1N1)pdm09	38
A(H1N1)pdm09 Coinfection	6
A(H3N2)	347
A(H3N2) Coinfection	19
A(H3N2) & B	1
A/not subtyped	2
Influenza B*	**68**
B	64
B & Coinfection	4
Other Respiratory Pathogens	**943**
Adenovirus	39
Chlamydophila pneumoniae	5
Coronavirus	128
Human Bocavirus	4
Human Metapneumovirus	52
Mycoplasma pneumoniae	24
Parainfluenza	96
RSV	133
Rhinovirus/Enterovirus	343
Non-influenza Viral Coinfections	113
Non-influenza Bacterial Coinfections	6
-*C. pneumo* coinfections *(2)*	
-*M. pneumo* coinfections *(4)*	
No Pathogen Detected	**985**

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

24 December 2017 - 6 January 2018 (Surveillance Weeks 52 & 1)

- During 24 December 2017 - 6 January 2018, a total of 442 specimens were collected and received from 56 locations. Results were finalized for 381 specimens from 51 locations. During Week 52, there were 92 influenza viruses detected: 69 influenza A(H3N2) (including six coinfections), seven influenza A(H1N1)pdm09 (including three coinfections), one influenza A/not subtyped, and 15 influenza B (including one coinfection). During Week 52, the influenza percent positive was approximately 47%. During Week 1, there were 77 influenza viruses detected: 62 influenza A(H3N2) (including two coinfections), six influenza A(H1N1)pdm09, one influenza A/not subtyped, and eight influenza B viruses. During Week 1, the influenza percent positive was approximately 42%. The influenza percent positive for the season is 20%.
- According to the CDC FluView, influenza activity increased during Week 1 in the U.S. with influenza A(H3) remaining the predominant virus type. Positive clinical respiratory specimens for influenza continued to be elevated. "The proportion of deaths attributed to pneumonia and influenza (P&I) was at the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System". There were seven influenza-associated pediatric deaths. The proportion of outpatient Influenza-like Illness (ILI) visits was 5.8%, continuing to exceed the national baseline of 2.2%. All 10 of the Health and Human Services regions reported ILI at or above region-specific baseline levels. New York City and 26 states experienced high ILI activity. Forty-nine states reported widespread influenza activity with regional activity reported in Guam and one other state. (CDC, FluView Report Week 1, cited 12 January 2018).

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Table 1. Finalized results by region and location for specimens collected during Weeks 52 & 1

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & Corona	A(H3N2) & Corona	A(H3N2) & Rhino/Entero	B	B & Rhino/Entero	Adenovirus	Coronavirus	HBoV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & HBoV & Rhino/Entero	Adeno & Para	Adeno & Para & Rhino/Entero	Adeno & RSV	Adeno & RSV & Rhino/Entero	Corona & HBoV	Corona & RSV	Corona & Rhino/Entero	HBoV & RSV & Rhino/Entero	hMPV	hMPV & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
EUCOM	Landstuhl RMC, Germany	-	-	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	3	6
	NAVSTA Rota, Spain	-	-	-	-	-	-	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	NSA Naples, Italy	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	RAF Lakenheath, England	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Ramstein AB, Germany	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	1	4
	Spangdahlem AB, Germany	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	USAG Baumholder, Germany	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2
	USAG Grafenwoehr, Germany	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	USAG Stuttgart, Germany	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	USAG Wiesbaden, Germany	2	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	1	-	5	11
PACOM	Osan AB, South Korea	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Yokota AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 2	Ft Drum, NY	-	-	-	-	-	-	1	-	-	1	-	-	-	1	1	-	-	-	-	-	-	-	2	-	-	-	-	2	8
	JB McGuire-Dix-Lakehurst, NJ	2	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	5
	USMA - West Point, NY	1	2	-	1	-	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	-	-	-	4	11
Region 3	Dover AFB, DE	-	2	-	-	-	-	-	-	-	1	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	2	7
	JB Andrews, MD	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	JB Langley-Eustis, VA	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
Region 4	Hurlburt Field, FL	-	7	-	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	2	-	1	12
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Moody AFB, GA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Robins AFB, GA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Shaw AFB, SC	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Tyndall AFB, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1

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 52 & 1

Cont'd from page 2

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & Corona	A(H3N2) & Corona	A(H3N2) & Rhino/Entero	B	B & Rhino/Entero	Adenovirus	Coronavirus	HBoV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & HBoV & Rhino/Entero	Adeno & Para	Adeno & Para & Rhino/Entero	Adeno & RSV	Adeno & RSV & Rhino/Entero	Corona & HBoV	Corona & RSV	Corona & Rhino/Entero	HBoV & RSV & Rhino/Entero	hMPV	hMPV & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
Region 5	Scott AFB, IL	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Wright-Patterson AFB, OH	2	59	-	1	3	1	9	1	1	15	-	1	1	8	3	1	1	-	-	-	-	-	2	-	-	2	-	-	38	149
Region 6	Altus AFB, OK	-	3	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	10
	Cannon AFB, NM	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Kirtland AFB, NM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Laughlin AFB, TX	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Little Rock AFB, AR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Sheppard AFB, TX	-	1	-	-	-	-	-	-	-	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	1	-	-	-	6
	Tinker AFB, OK	3	6	-	-	-	-	1	-	-	-	-	-	-	1	2	-	-	-	-	-	-	-	-	-	1	2	-	-	5	21
	Vance AFB, OK	-	2	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	7
Region 7	McConnell AFB, KS	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4
	Offutt AFB, NE	-	4	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	6
Region 8	Ellsworth AFB, SD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	FE Warren AFB, WY	-	2	-	-	-	-	-	-	-	2	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	2	8
	Hill AFB, UT	-	3	-	-	-	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	7
	Malmstrom AFB, MT	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Peterson AFB, CO	-	4	-	-	-	-	-	-	-	1	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	9
	USAF Academy, CO	-	2	-	-	-	-	1	-	-	1	-	-	1	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	8
Region 9	Davis-Monthan AFB, AZ	-	5	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	3	10
	Luke AFB, AZ	-	4	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	8
	Nellis AFB, NV	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Travis AFB, CA	-	2	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5
Region 10	CGS North Bend, OR	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	-	5	-	-	-	-	2	-	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	-	-	5	15
Total		10	123	2	3	4	4	22	1	4	35	1	1	2	23	16	1	1	1	1	1	1	1	4	1	1	10	1	1	105	381

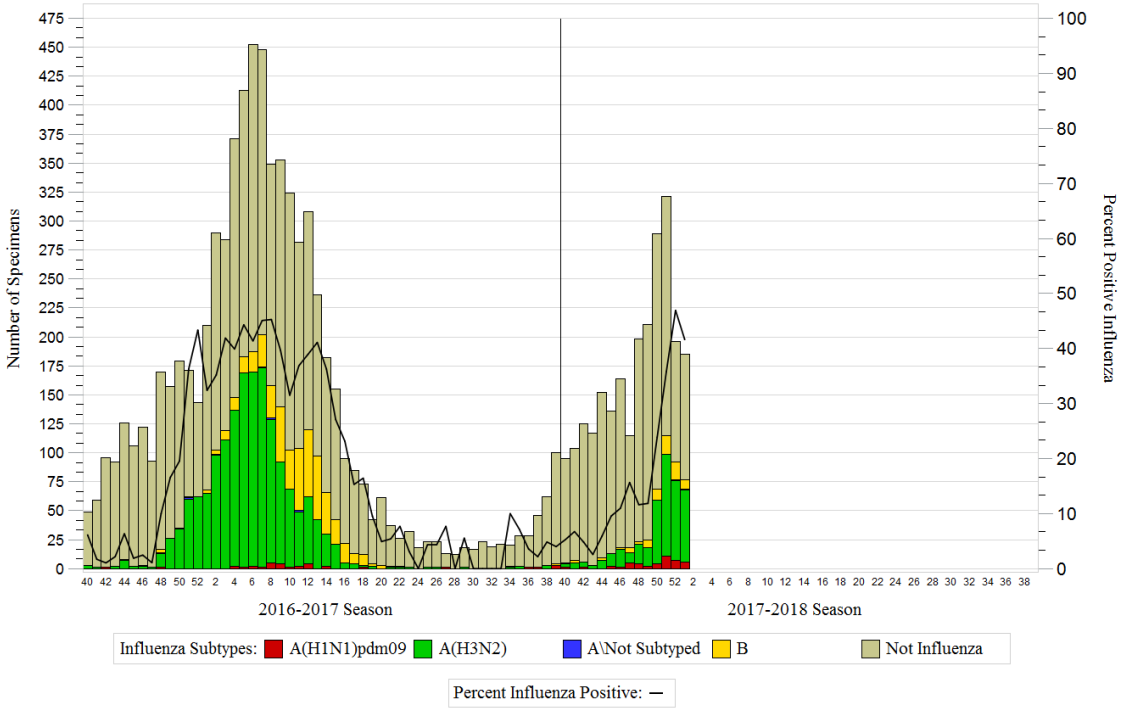
**CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.*

DoD Global Respiratory Pathogen Surveillance Program

Cumulative Laboratory Results

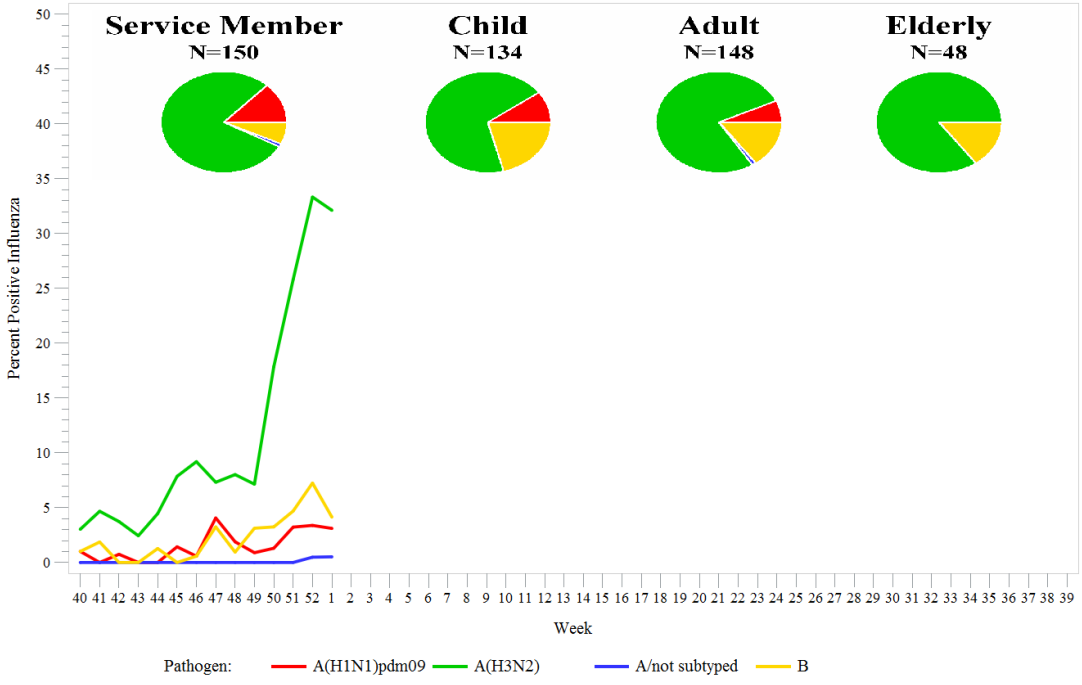
Link to cumulative results by region and location:

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



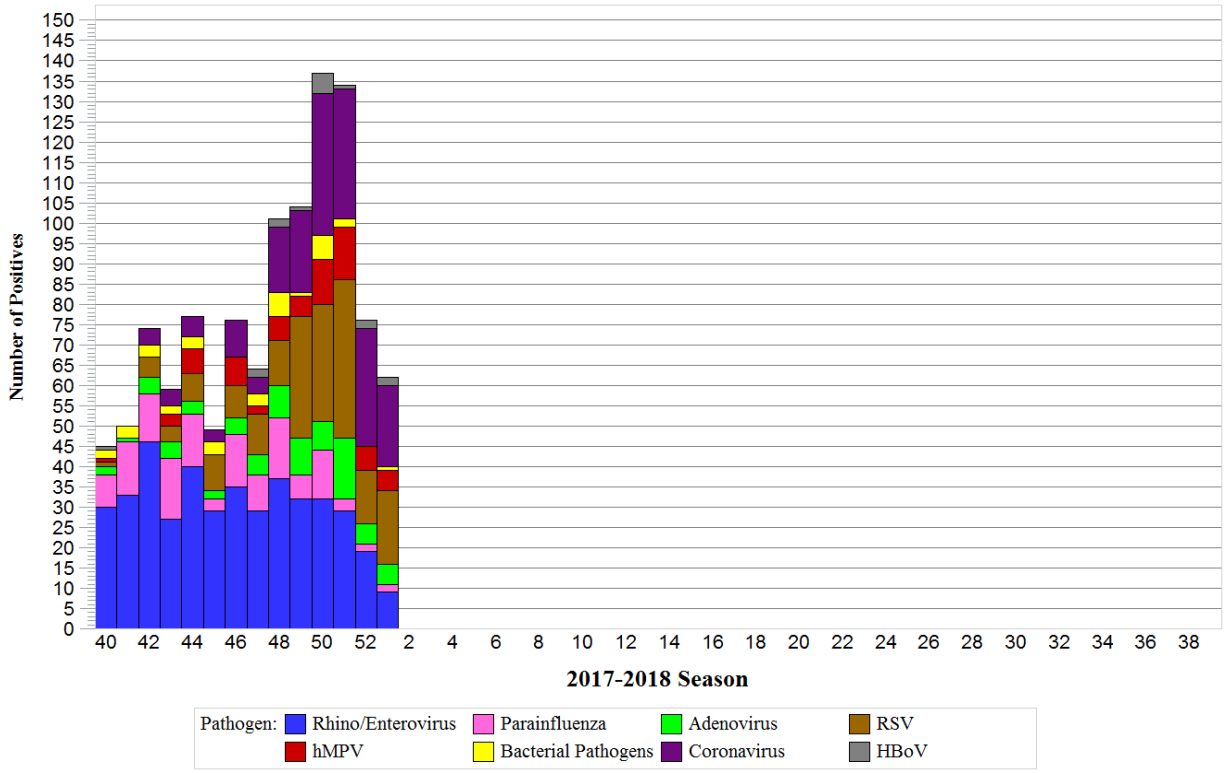
Note: Dual influenza coinfections are excluded from this graph.

Graph 2. Percent positive for influenza through ILI trends by subtype and beneficiary status through Week 1 of the 2017-2018 surveillance year

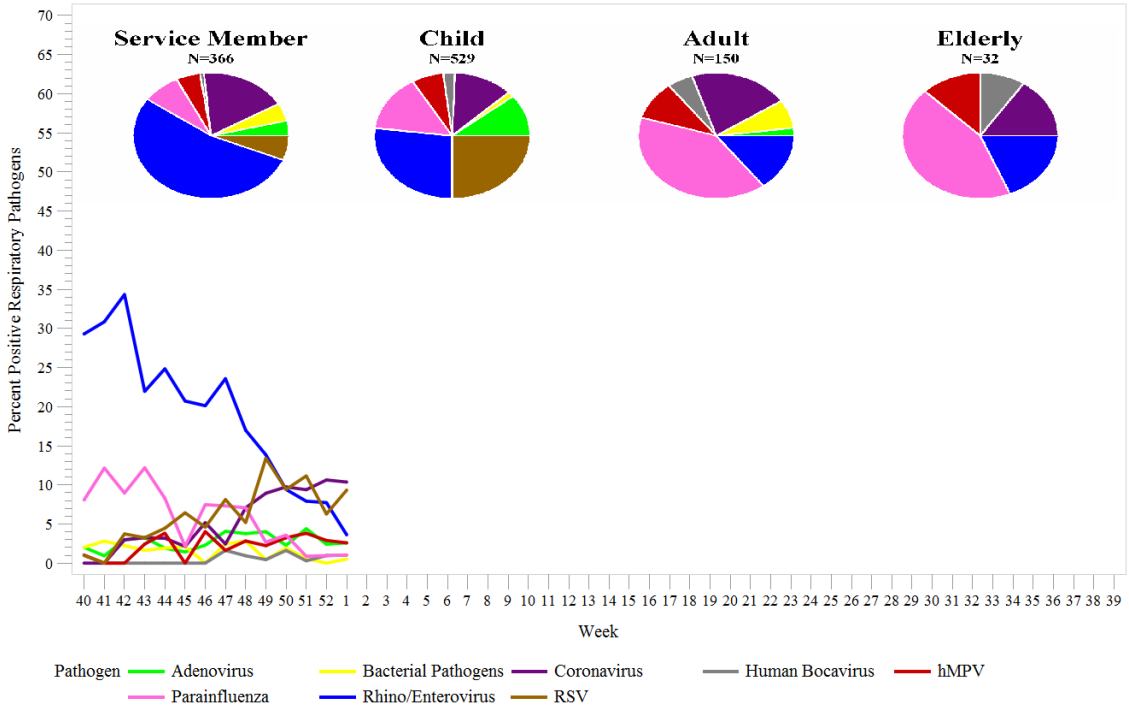


88ABW-2015-5508 and PA email guidance dated 10 November 2015.

Graph 3. Other positive respiratory pathogens for the 2017-2018 surveillance year through Week 1



Graph 4. Percent positive for respiratory pathogens through ILI trends by week and beneficiary status through Week 1 of the 2017-2018 surveillance year



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

Graph 5. Vaccination status by beneficiary type for the 2017-2018 surveillance year through Week 1 (excluding 'Other' beneficiary type)

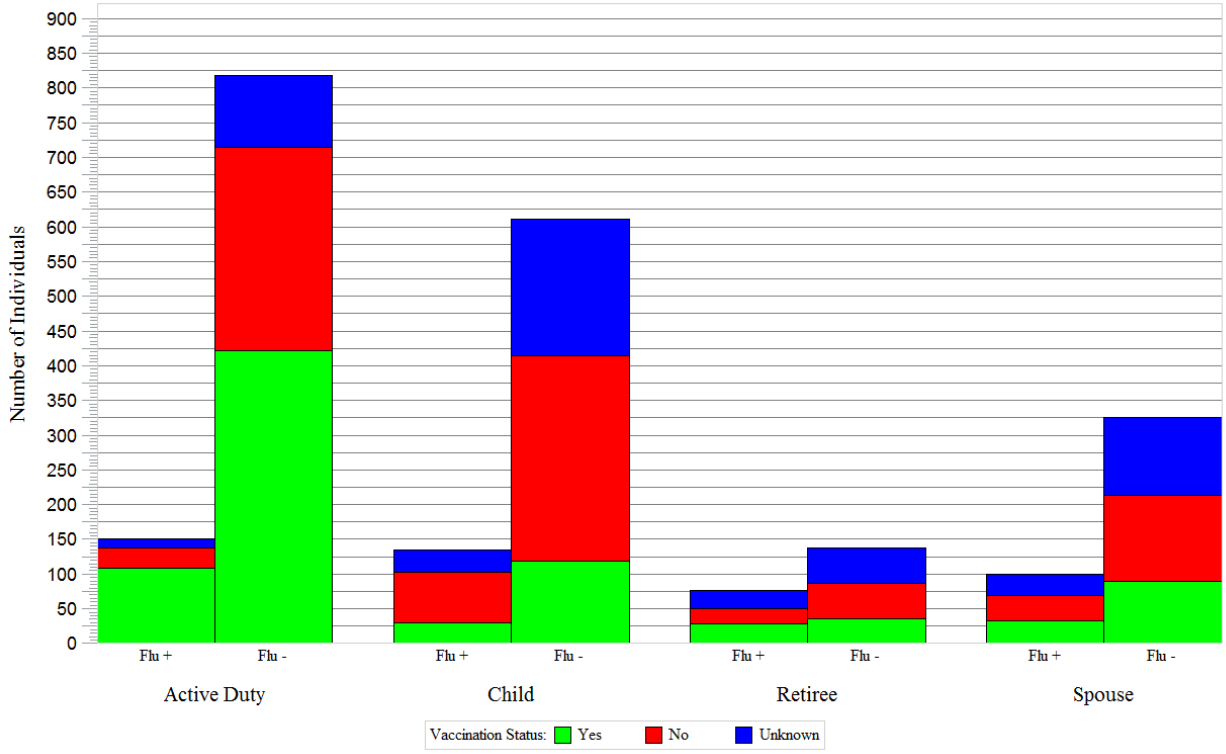
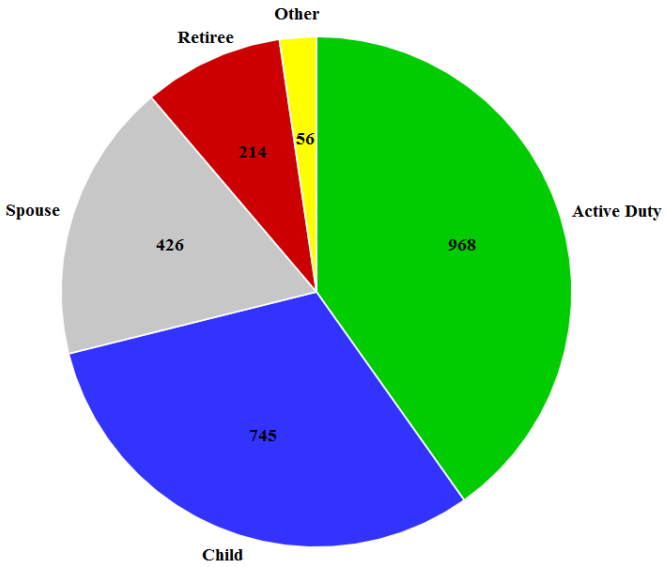


Table 2. ILI by age group for the 2017-2018 surveillance year through Week 1

Age Group	Frequency	Percent
0-5	464	19.26
6-9	130	5.40
10-17	172	7.14
18-24	375	15.57
25-44	817	33.91
45-64	294	12.20
65+	157	6.52

Graph 6. ILI by beneficiary status for the 2017-2018 surveillance year through Week 1

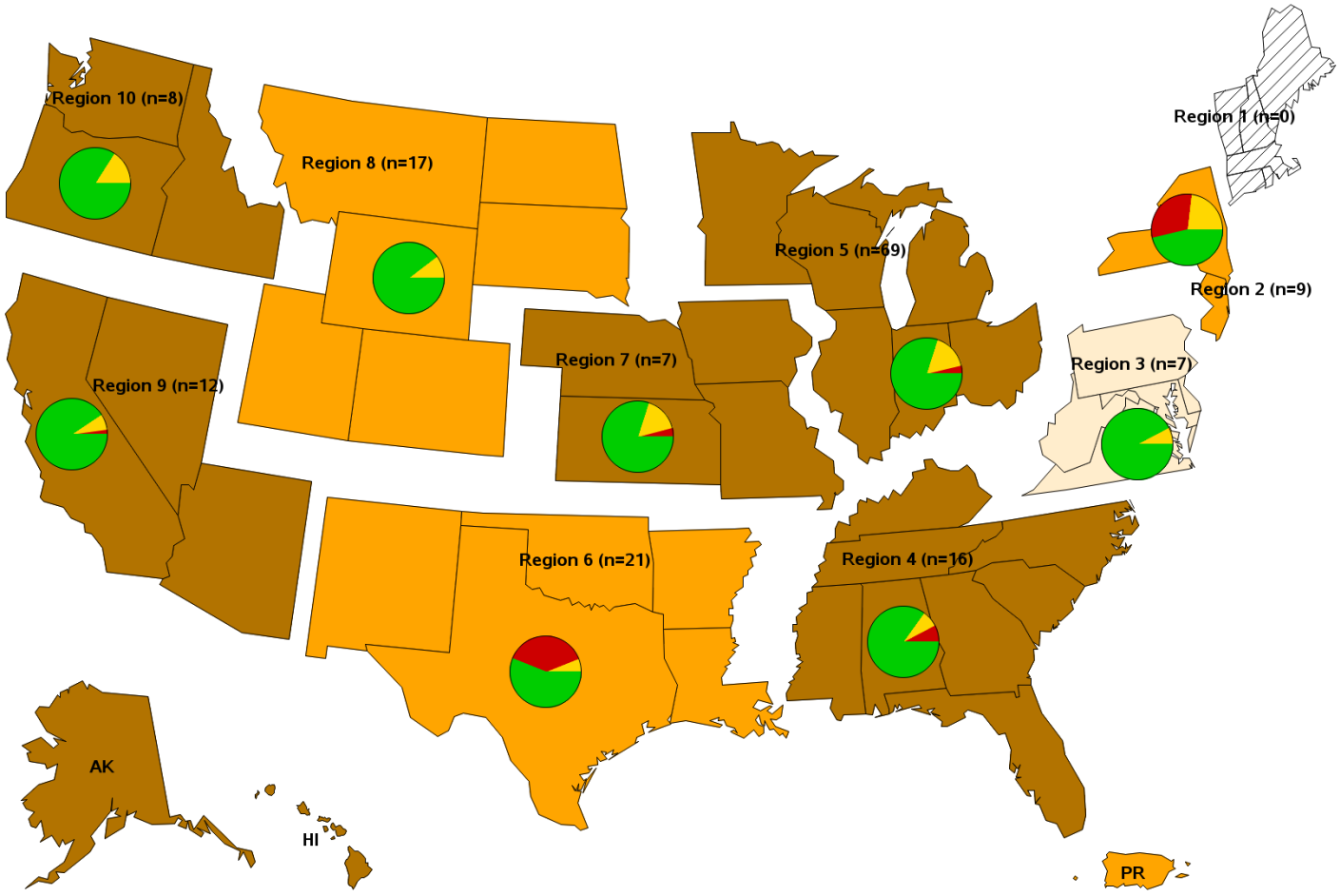


Demographic Summary

Of 2,409 ILI cases, 968 are service members (40.2%), 745 are children (30.9%), 426 are spouses (17.7%), and 270 are retirees and other beneficiaries (11.2%). The median age of ILI cases with known age (n=2,409) is 26 (range 0, 98).

DoD Global Respiratory Pathogen Surveillance Program

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



HI - Region 9

AK - Region 10

PR - Region 2

Legend

Influenza Activity - Past 2 weeks

(n = # of submissions)

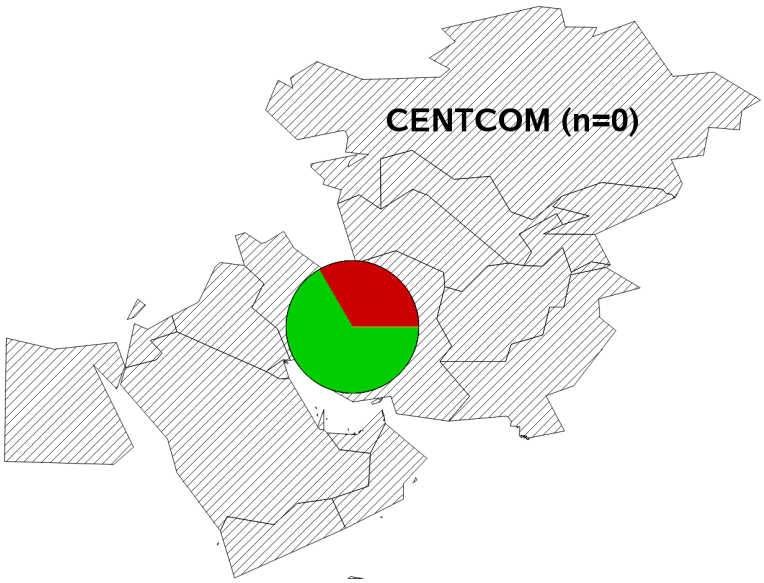
- No activity (0% +) or no submissions
- Low (<25% +)
- Moderate (25-49% +)
- High (>50% +)

Influenza Results - Cumulative

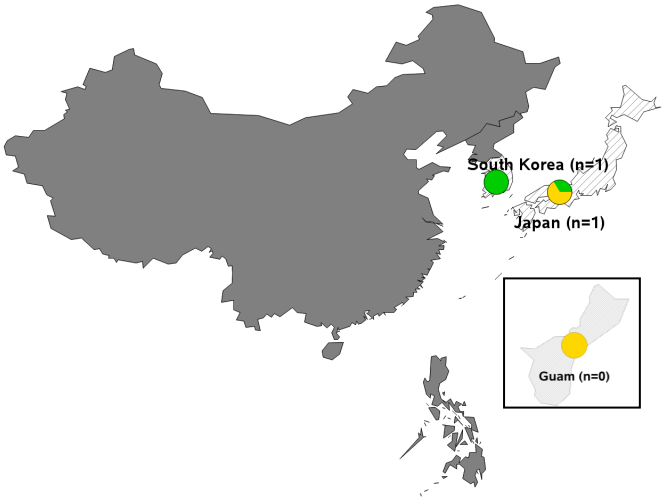
- Influenza A(H3N2)
- Influenza A(H1N1)pdm09
- Influenza B
- Influenza A/not subtyped

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

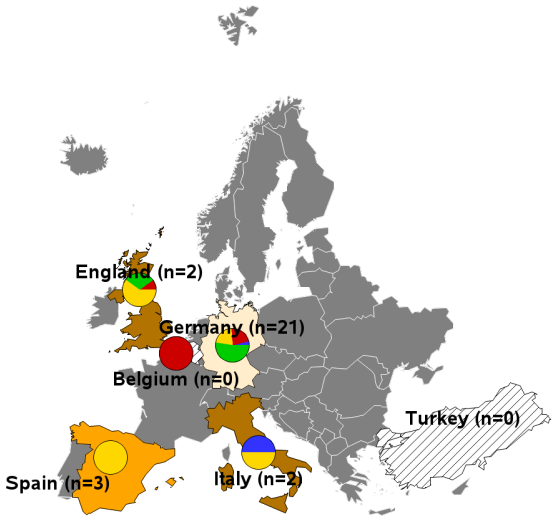
Map 2. Influenza subtypes and activity level for CENTCOM for the 2017-2018 surveillance year through Week 1



Map 3. Influenza subtypes and activity level by country for the 2017-2018 surveillance year through Week 1 (Pacific)



Map 4. Influenza subtypes and activity level by country for the 2017-2018 surveillance year through Week 1 (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

Molecular Sequence Analysis Report #2

This is the second USAFSAM influenza sequence surveillance report for the 2017-2018 influenza season and includes a total of 60 influenza specimens collected between 22 Aug 2017 and 5 December 2017, with 53 specimens sequenced at USAFSAM, and 7 hemagglutinin (HA) sequences provided by the United States Army Medical Research Unit in Kenya (USAMRD-K) [**Table 1**].

Table 1: Report 2 influenza HA sequences by subtype/lineage contributed by each DoD partner laboratory.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
USAFSAM	11	33	1	8	53
USAMRD-K	3			4	7
Total	14	33	1	12	60

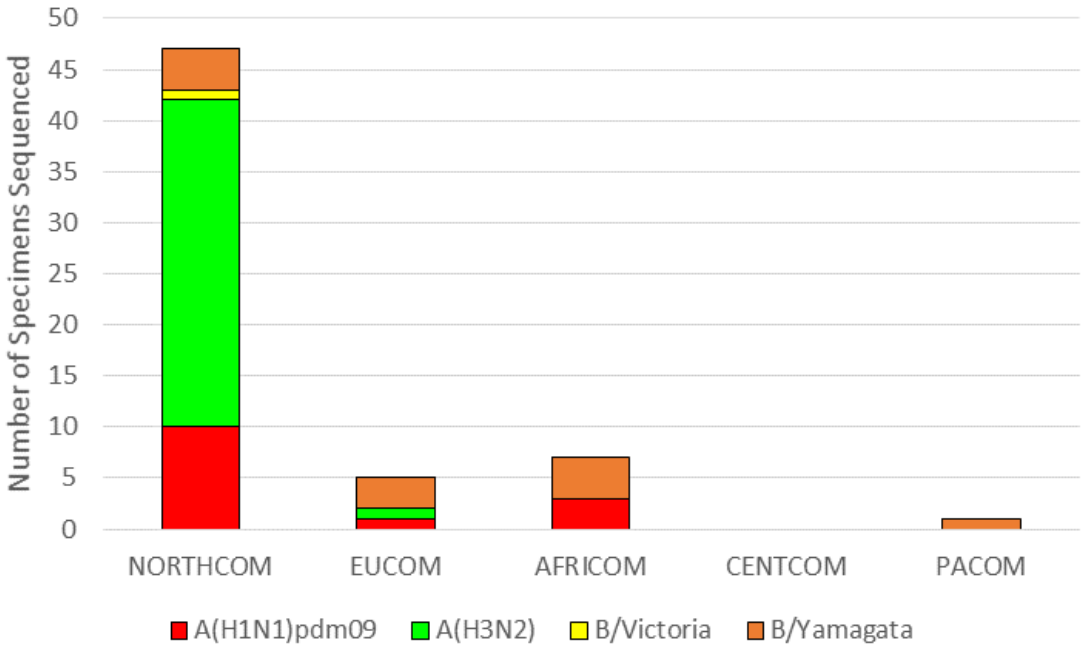


Figure 1: Total influenza sequences from each of the United States Combatant Commands analyzed for this report.

Table 2: 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					
California					
Travis AFB		2			2
Colorado					
Peterson AFB		3			3
USAF Academy		2			2
Florida					
Eglin AFB				1	1
Hurlburt Field	2				2
Georgia					
Robins AFB		1			1
Idaho					
Mt Home AFB		1			1
Illinois					
Scott AFB	1				1
Kansas					
McConnell AFB		4			4
Maryland					
JB Andrews		1			1
NCRM - Walter Reed NMMC		2			2
US Naval Academy		1			1
Nevada					
Nellis AFB		1			1
North Carolina					
Ft Bragg	2				2
Ohio					
Wright-Patterson AFB		4		3	7
Oklahoma					
Tinker AFB	3				3
South Carolina					
Shaw AFB	1				1
Texas					
SAMMC	1	2			3
Washington					
NH Bremerton		5			5
Wyoming					
FE Warren AFB		1			1
OCONUS					
Alaska					
Eielson AFB		1			1
JB Elmendorf-Richardson		1	1		2
Germany					
Landstuhl RMC	1	1		3	5
Guam					
JR Marianas - Andersen AFB				1	1
Kenya					
USAMRD-K	3			4	7
Total	**14**	**33**	**1**	**12**	**60**

The HA gene from select influenza positive specimens 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, World Health Organization and contribute to the seasonal Northern and Southern hemisphere vaccine component selections.

Table 3: Cumulative protein homologies (percent amino acid match) of 2017-2018 influenza strains relative to vaccine strains. The influenza A(H1N1)pdm09 vaccine strain was recently 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	98.5%	99.5%	99.0%
A(H3N2)	2016-2018	A/Hong Kong/4801/2014-like	97.1%	98.9%	98.3%
B/Victoria	2009-2012 and 2013-2018	B/Brisbane/60/2008-like*	98.8%	99.5%	99.3%
B/Yamagata	2015-2018	B/Phuket/3073/2013-like**	98.9%	99.5%	99.4%

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

Influenza A(H1N1)pdm09

- Among the 47 influenza A isolates, 14 (29.8%) 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 HA sequences characterized in the 2017-2018 season have exhibited an overall protein homology of 98.5-99.5% (average 99.0%) compared to the 2017-2018 influenza vaccine component, A/Michigan/45/2015-like virus [**Table 3**].
- 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 isolates, 12 occurred at predicted antigenic sites (none at site A, two at site B, three at site C, four at site D, and three at site E) and one occurred at the receptor binding site.[4,5]

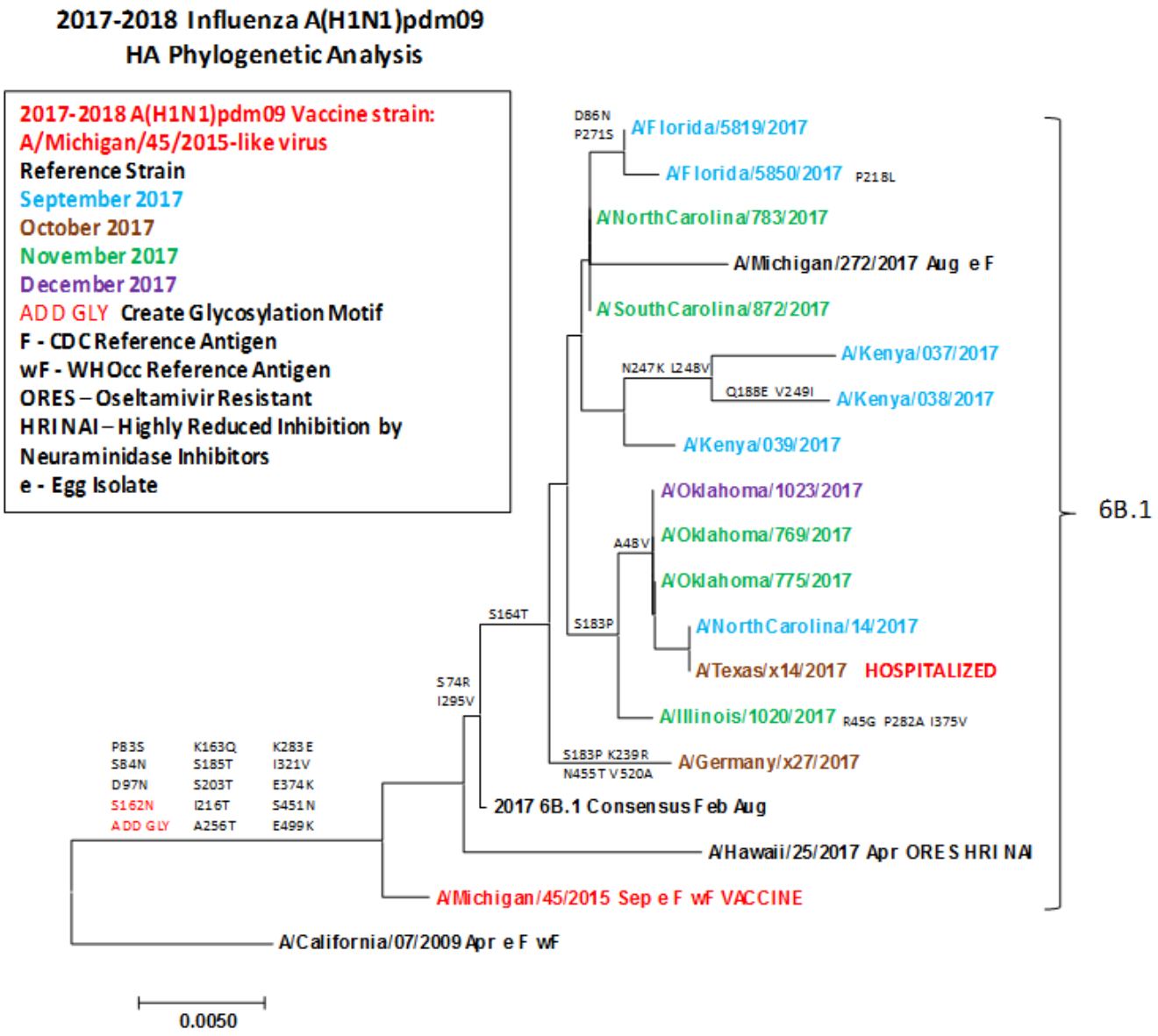


Figure 2: 2017-2018 USAFSAM Report 2 influenza A(H1N1)pdm09 HA phylogenetic analysis. Fourteen influenza A(H1N1) pdm09 isolates collected between September 2017 and December 2017 were sequenced and all resided in clade 6B.1, with one shared addition of a glycosylation motif. The influenza vaccine A(H1N1)pdm09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

Influenza A(H3N2)

- Among the 47 influenza A HA sequences, 33 (70.2%) 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) HA sequences characterized in the 2017-2018 season have exhibited an overall protein homology of 97.1 – 98.9% (average 98.3%) compared to the 2017-2018 influenza vaccine component, A/Hong Kong/4801/2014-like virus [**Table 3**].
- All of the influenza A(H3N2) viruses sequenced for this report were in clade 3C with 29 (87.9%) in clade 3C.2a and 4 (12.1%) in subclade 3C.2a1. No isolates were identified as clade 3C.3a. The mutation N121K was present in all four (100.0%) of the 3C.2a1 isolates and five (15.2%) of the total influenza A(H3N2) isolates. The mutation T135K was present in 5 isolates (100.0% of 3C.2a1 and 15.2% of total).
- Among the influenza A(H3N2) HA sequences characterized in this report, five mutations; N122D (asparagine to aspartic acid), T128A (threonine to alanine), T135K (threonine to lysine), N144S (asparagine to serine), and T160K were observed that caused the loss of a glycosylation motif. Two other mutations, N128T (asparagine to threonine) and K160T (lysine to threonine), were observed that caused the gain of a glycosylation motif.
- Of the 49 mutations present in the influenza A(H3N2) specimens, 20 occurred at predicted antigenic sites (six at site A, six at site B, none at site C, three at site D, and five at site E) and four occurred at the receptor binding site.[4,5]

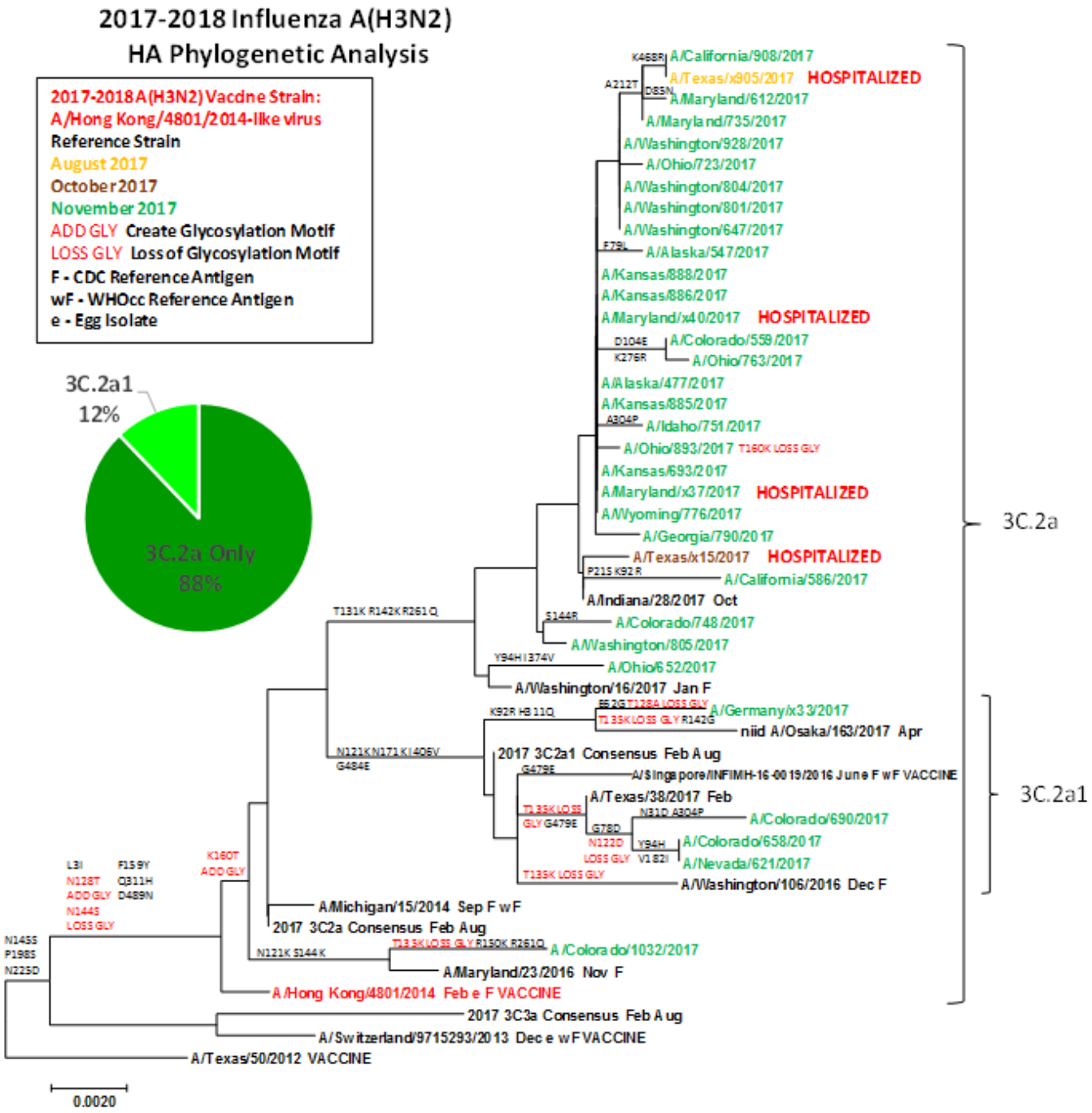


Figure 3: 2017-2018 USAFSAM Report 2 influenza A(H3N2) HA phylogenetic analysis. Thirty-three influenza A(H3N2) isolates collected between August 2017 and November 2017 were sequenced, of which the majority resided in clade 3C.2a (85%), with the rest being in subclade 3C.2a1 (15%). Five mutations caused the loss of glycosylation motifs while two mutations caused the gain of glycosylation motifs.

Influenza B

- The influenza B HA sequences are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains and are rooted from the current vaccine strain B/Brisbane/60/2008 for the B/Victoria isolates [**Figure 4**] and from the previous vaccine strain B/Massachusetts/02/2012 for the B/Yamagata isolates [**Figure 5**].
- 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] One (7.7%) of the 13 influenza B isolates characterized in this report fell into the B/Victoria lineage and 12 (92.3%) fell into the B/Yamagata lineage.
- The influenza B/Victoria HA sequences characterized in the 2017-2018 season have exhibited a protein homology from 98.8 – 99.5% (average 99.3%) when compared to the 2017-2018 B/Victoria vaccine component, B/Brisbane/60/2008-like virus [**Table 3**].
- The influenza B/Yamagata HA sequences characterized in the 2017-2018 season have 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 [**Table 3**].
- All of the influenza B/Victoria HA sequences fell into clade V1A and all of the B/Yamagata isolates fell into clade Y3. For the B/Victoria, one mutation, S197N (serine to asparagine), adds a glycosylation motif. For the B/Yamagata, one mutation, D196N (aspartic acid to asparagine) adds a glycosylation motif.

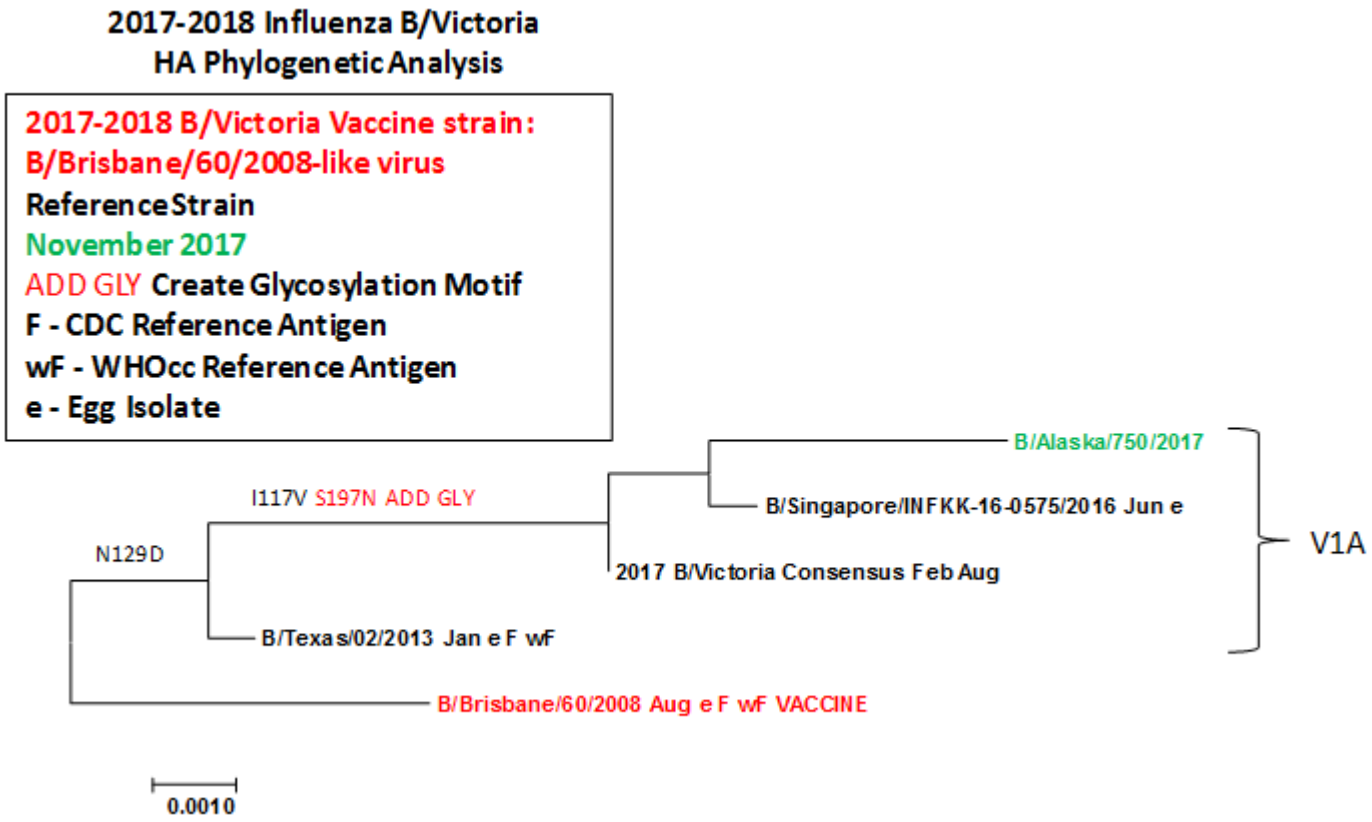


Figure 4: 2017-2018 USAFSAM Report 2 influenza B/Victoria HA phylogenetic analysis. One influenza B/Victoria isolate was collected and sequenced in November 2017 and resided in clade V1A, with one addition of a glycosylation motif.

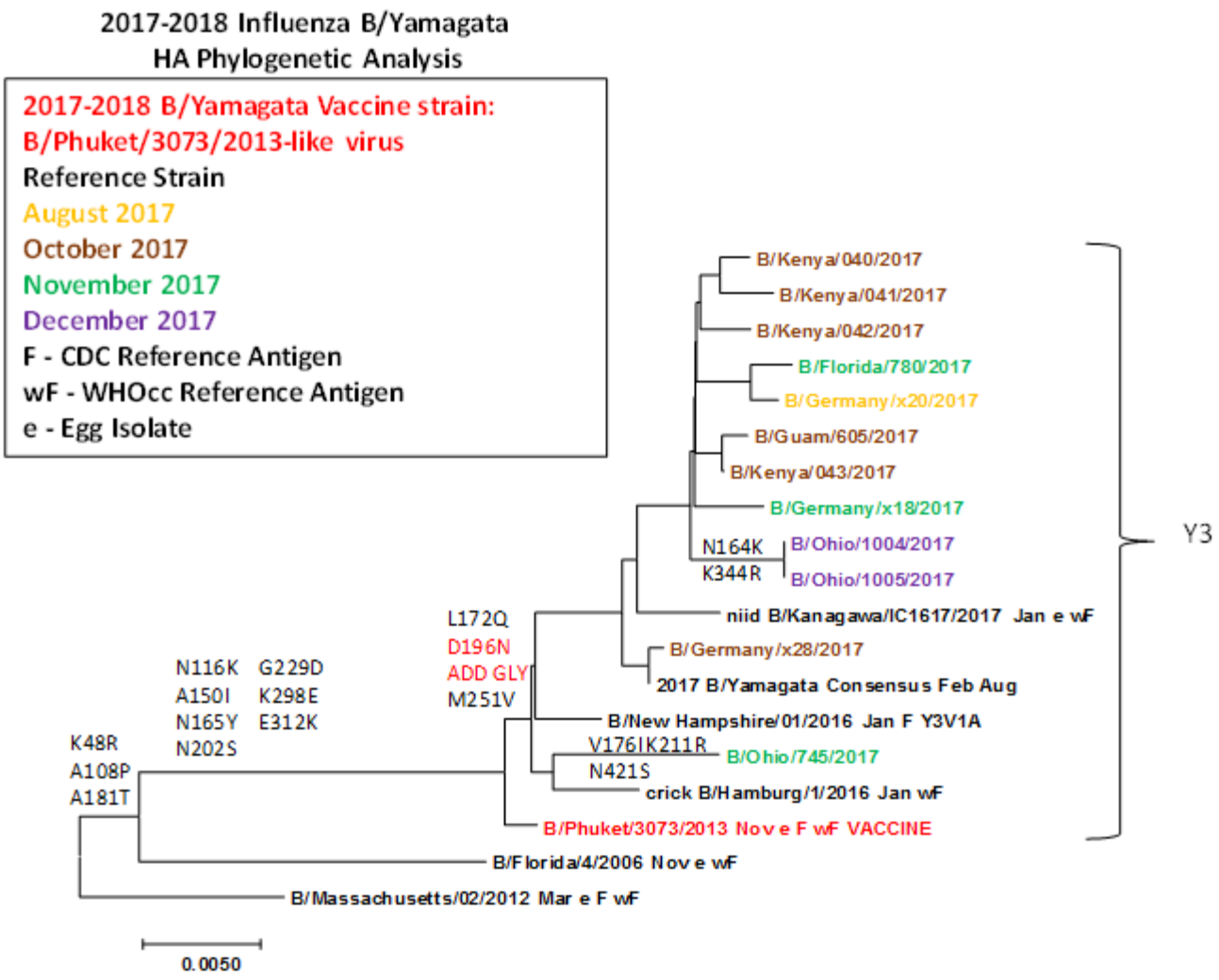


Figure 5: 2017-2018 USAFSAM Report 2 influenza B/Yamagata phylogenetic analysis. Thirteen influenza B/Yamagata isolates collected between August 2017 and December 2017 were sequenced and all resided in clade Y3, with one addition of a glycosylation motif.

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.
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4. 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.
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.

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.

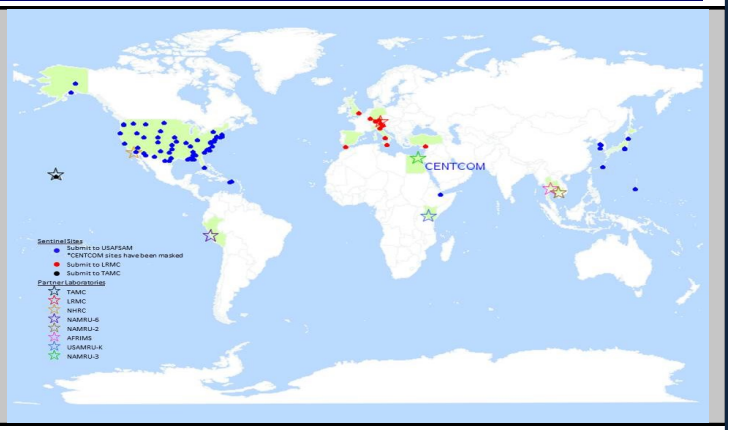
Available on our website (listed below) is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and a dashboard containing respiratory data for our sentinel sites.

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.