



**Cumulative Results**

Locations	92
Collected	3,997
Tested	3,630

**Influenza A 905**

A(H1N1)pdm09	125
A(H1N1)pdm09 Coinfection	11
A(H1N1)pdm09 & A(H3N2)	1
A(H3N2)	708
A(H3N2) Coinfection	51
A(H3N2) & B	4
A/not subtyped	4
A/not subtyped Coinfection	1

**Influenza B\* 182**

B	167
B & Coinfection	15

**Other Respiratory Pathogens 1,225**

Adenovirus	48
<i>Chlamydomphila pneumoniae</i>	7
Coronavirus	211
Human Bocavirus	8
Human Metapneumovirus	72
<i>Mycoplasma pneumoniae</i>	27
Parainfluenza	108
RSV	198
Rhinovirus/Enterovirus	392
Non-influenza Viral Coinfections	147
Non-influenza Bacterial Coinfections	7
-C. pneumo coinfections (2)	
-M. pneumo coinfections (5)	

**No Pathogen Detected 1,318**

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**

**7 - 20 January 2018 (Surveillance Weeks 2 & 3)**

- During 7 - 20 January 2018, a total of 998 specimens were collected and received from 61 locations. Results were finalized for 768 specimens from 56 locations. The percent influenza positive for Week 2 and 3 were 46% and 48%, respectively. The influenza percent positive for the season is 30%..

Surveillance Week	A(H1N1)pdm09	A(H1N1)pdm09 & Corona	A(H1N1)pdm09 & RSV	A(H1N1)pdm09 & hMPV	A(H3N2)	A(H3N2) & B	A(H3N2) & Corona	A(H3N2) & Corona & Rhino/Entero	A(H3N2) & HBoV	A(H3N2) & Para	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	A(H3N2) & hMPV	A/not subtyped	B	B & Adeno	B & Corona	B & Corona & Rhino/Entero	B & RSV	B & Rhino/Entero	B & hMPV	Total	
Week 2	31	1	1	0	138	3	3	2	1	1	2	5	0	3	52	1	1	0	1	0	1	0	247
Week 3	26	1	0	1	50	0	3	0	0	1	0	2	1	0	23	0	1	1	0	1	0	1	111
Total	57	2	1	1	188	3	6	2	1	2	2	7	1	3	75	1	2	1	1	1	1	1	358

- According to the CDC FluView, influenza activity increased during Week 3 in the U.S. with influenza A(H3N2) remaining the predominant virus subtype reported by public health laboratories. The influenza percent positive for respiratory specimens in clinical laboratories slightly increased. “The proportion of deaths attributed to pneumonia and influenza (P&I) was above the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System”. “There were seven influenza-associated pediatric deaths”. The cumulative laboratory-confirmed influenza-associated hospitalization rate was 41.9 per 100,000 population, which is more than double the cumulative rate of 19.9 per 100,000 population from Week 3 of last season. The proportion of outpatient Influenza-like Illness (ILI) visits was 6.6%, 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, Puerto Rico, and 39 states experienced high ILI activity.” Forty-nine states and Puerto Rico reported widespread influenza activity, with regional activity reported in Guam. (CDC, [FluView Report Week 3](#), cited 26 January 2018).

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# DoD Global Respiratory Pathogen Surveillance Program

**Table 1.** Finalized results by region and location for specimens collected during Weeks 2 & 3

Region*	A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & Corona	A(H1N1)pdm09 & hMPV	A(H1N1)pdm09 & RSV	A(H3N2) & B	A(H3N2) & Corona	A(H3N2) & Corona & Rhino/Entero	A(H3N2) & HBoV	A(H3N2) & hMPV	A(H3N2) & Para	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & Adeno	B & Corona	B & Corona & Rhino/Entero	B & hMPV	B & RSV	B & Rhino/Entero	Adenovirus	C. pneumoniae	Coronavirus	HBoV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & hMPV	Corona & HBoV	Corona & hMPV	Corona & Para	Corona & RSV	Corona & Rhino/Entero	HBoV & hMPV	HBoV & RSV	HBoV & RSV & Rhino/Entero	HBoV & Rhino/Entero	hMPV	hMPV & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total			
EUCOM	Landsstuhl RMC, Germany	4	2	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	1	-	1	-	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	1	10	26				
	NAVSTA Rota, Spain	-	2	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	6		
	NSA Naples, Italy	2	1	-	-	-	-	-	1	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	8	
	RAF Lakenheath, England	3	4	1	-	-	-	1	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	1	1	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	14	32	
	Ramstein AB, Germany	2	1	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	1	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	5	16		
	SHAPE, Belgium	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4		
	Spangdahlem AB, Germany	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4		
	USAG Grafenwoehr, Germany	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	5			
	USAG Stuttgart, Germany	-	1	-	-	-	-	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	2	-	-	-	1	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	2	10		
	USAG Vicenza, Italy	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	6		
	USAG Wiesbaden, Germany	-	1	-	-	-	-	-	-	-	-	-	-	7	1	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	19		
	Vilseck AHC, Germany	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	5		
	PACOM	Kadena AB, Japan	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-
Osan AB, South Korea		-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	
Yokota AB, Japan		1	4	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9	-	
Region 1	USCG Academy, CT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	
Region 2	Ft Drum, NY	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	8	
	JB McGuire-Dix-Lakehurst, NJ	1	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	6	16		
	USMA - West Point, NY	2	3	1	-	1	-	-	-	-	-	-	4	-	1	-	-	1	-	1	-	1	3	-	-	-	1	3	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	23	41	
Region 3	Dover AFB, DE	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	1	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	12
	JB Andrews, MD	2	1	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	2	-	-	1	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	-
	JB Langley-Eustis, VA	-	1	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	8		
	US Naval Academy, MD	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	
	Eglin AFB, FL	3	6	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	14	
Region 4	Ft Bragg, NC	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	6	
	Ft Campbell, KY	3	4	-	-	1	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10	-	
	Hurlburt Field, FL	1	3	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	8	
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2		
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1		
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1		
	Robins AFB, GA	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	-	
	Seymour Johnson AFB, NC	1	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	8		
	Shaw AFB, SC	1	3	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	10		

Cont'd on page 3

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

# DoD Global Respiratory Pathogen Surveillance Program

**Table 1.** Finalized results by region and location for specimens collected during Weeks 2 & 3  
*Cont'd from page 2*

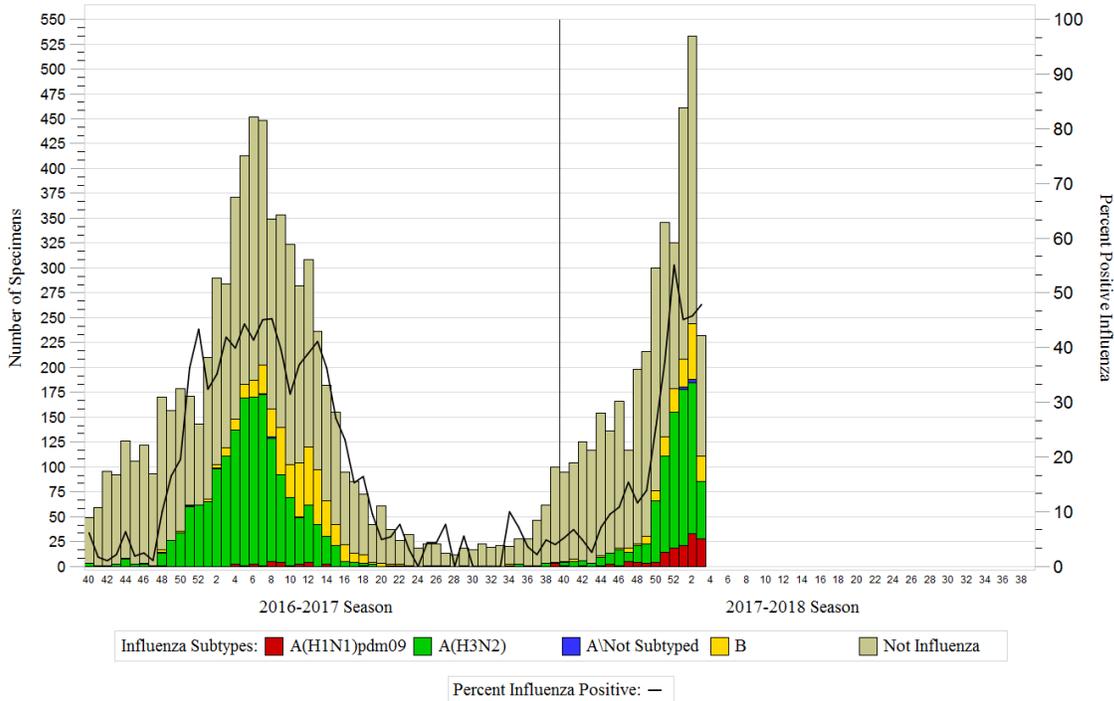
Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & Corona	A(H1N1)pdm09 & hMPV	A(H1N1)pdm09 & RSV	A(H3N2) & B	A(H3N2) & Corona	A(H3N2) & Corona & Rhino/Entero	A(H3N2) & hBoV	A(H3N2) & hMPV	A(H3N2) & Para	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & Adeno	B & Corona	B & Corona & Rhino/Entero	B & hMPV	B & RSV	B & Rhino/Entero	Adenovirus	C. pneumoniae	Coronavirus	hBoV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & hMPV	Corona & hBoV	Corona & hMPV	Corona & Para	Corona & RSV	Corona & Rhino/Entero	hBoV & hMPV	hBoV & RSV	hBoV & RSV & Rhino/Entero	hBoV & Rhino/Entero	hMPV	hMPV & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total			
Region 5	Scott AFB, IL	-	7	-	1	-	-	-	-	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	20		
	Wright-Patterson AFB, OH	15	35	-	-	-	1	-	-	-	-	-	-	3	6	-	-	-	-	-	-	-	-	-	6	-	-	10	5	-	2	1	-	1	-	-	-	-	1	-	3	-	1	45	136			
Region 6	Altus AFB, OK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	6		
	Cannon AFB, NM	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3	
	JBSA Lackland, TX	8	29	-	1	-	1	-	1	1	1	1	1	4	-	-	-	-	-	-	-	-	-	-	4	-	1	1	6	-	-	1	1	-	-	-	-	-	-	1	-	-	-	20	82			
	Laughlin AFB, TX	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3		
	Little Rock AFB, AR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4		
	Sheppard AFB, TX	1	5	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	2	-	1	2	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	12	30		
	Tinker AFB, OK	3	6	1	1	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	3	1	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	25	
	Vance AFB, OK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5		
Region 7	McConnell AFB, KS	1	5	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	1	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	3	15	
	Offutt AFB, NE	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	12	
Region 8	Ellsworth AFB, SD	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	9	
	FE Warren AFB, WY	-	4	-	-	-	-	1	-	-	-	-	1	5	-	1	-	-	-	-	-	-	-	2	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	19
	Hill AFB, UT	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	17	
	Malmstrom AFB, MT	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Minot AFB, ND	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	13
	Peterson AFB, CO	1	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	10
	USAF Academy, CO	-	7	-	-	-	-	-	-	1	-	-	3	-	3	-	-	-	-	-	-	-	-	1	3	-	1	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	8
Region 9	Davis-Monthan AFB, AZ	-	4	-	-	-	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	12
	Los Angeles AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	-	2	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4
Region 10	Fairchild AFB, WA	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
<b>Total</b>		57	188	3	2	1	1	3	6	2	1	1	2	2	7	75	1	2	1	1	1	1	7	1	47	4	1	5	37	29	1	2	3	1	3	1	3	1	1	4	1	2	15	1	4	240	768	

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

## Cumulative Laboratory Results

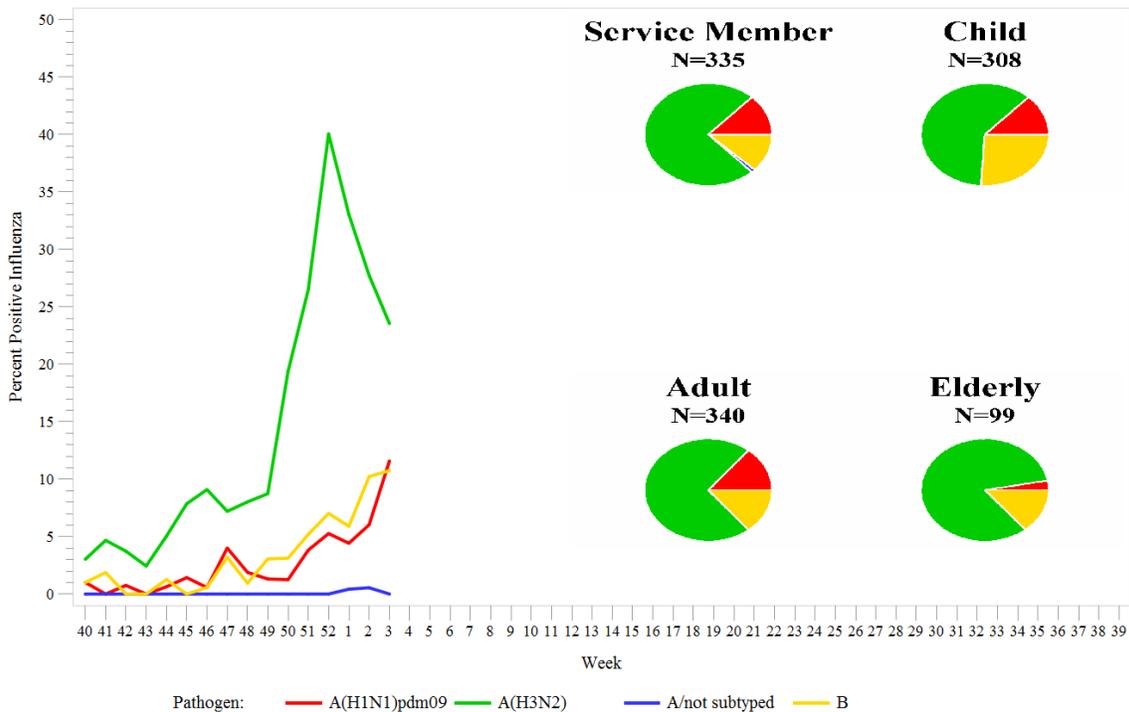
[Link to cumulative results by region and location:](#)

**Graph 1.** Percent influenza positive by week: 2016-2017 surveillance year and through Week 3 of the 2017-2018 surveillance year

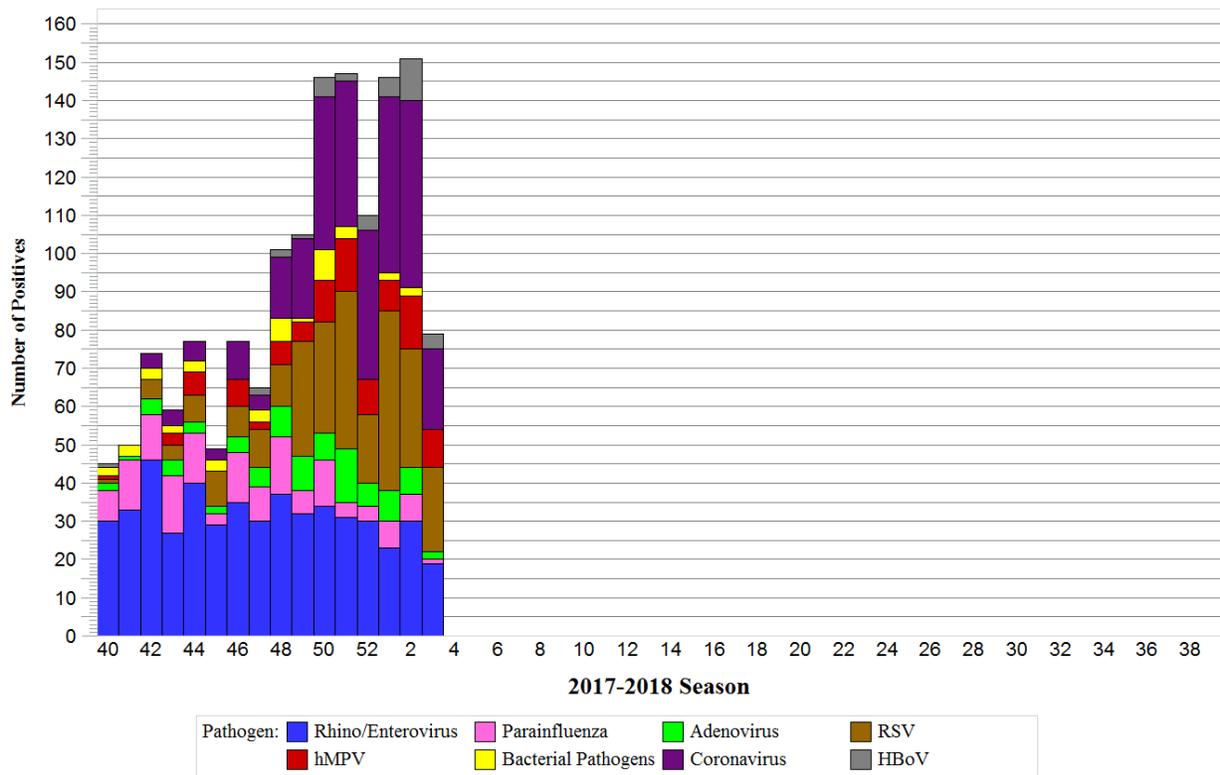


Note: Dual influenza coinfections are excluded from this graph.

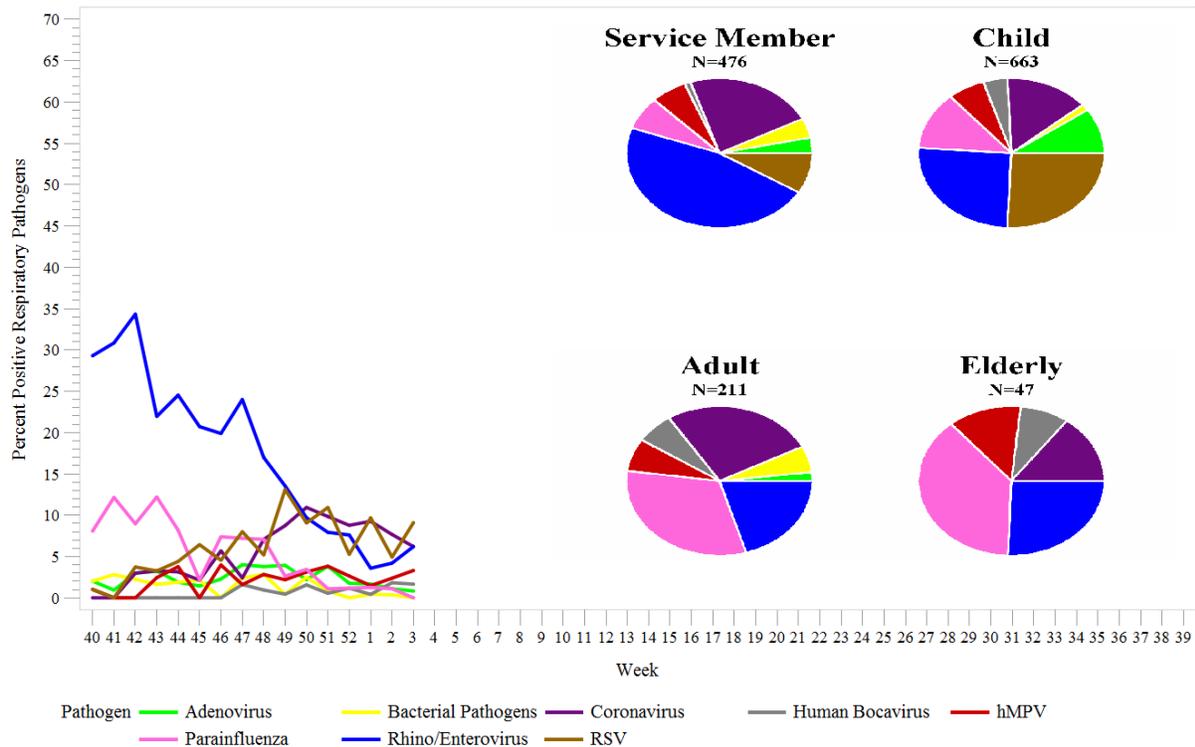
**Graph 2.** Percent positive for influenza through ILI trends by subtype and beneficiary status through



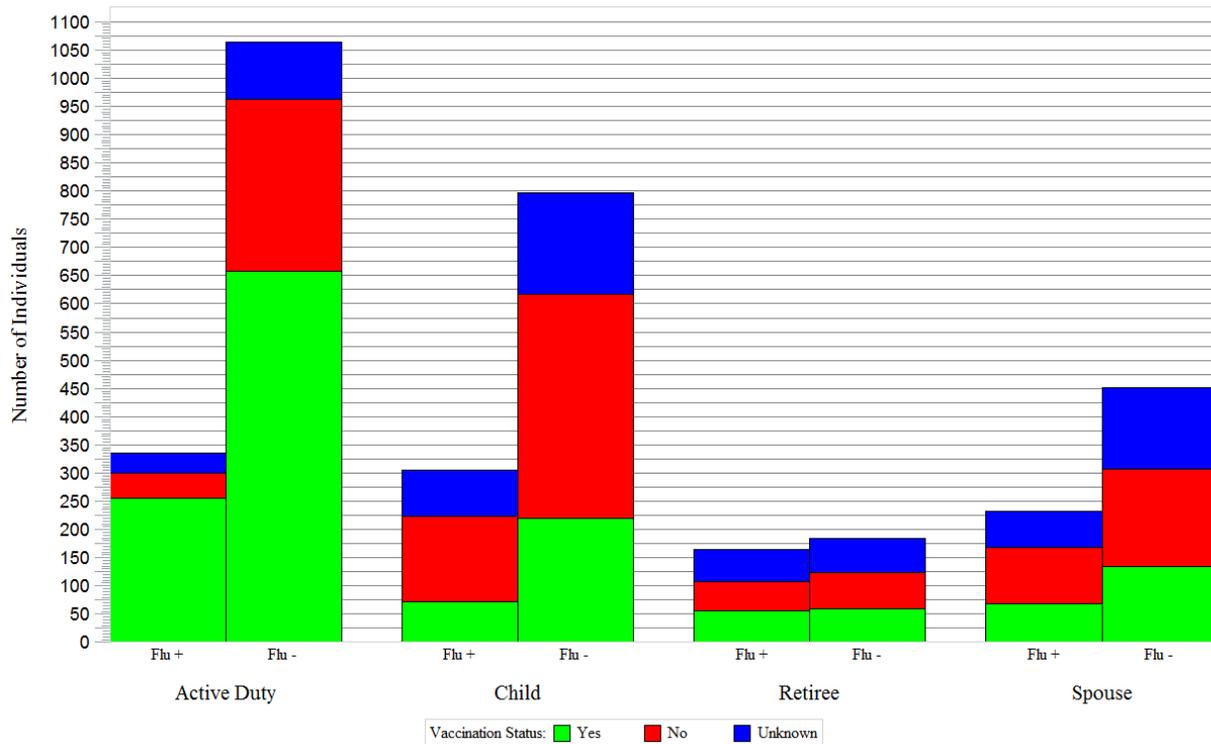
**Graph 3. Other positive respiratory pathogens through Week 3 of the 2017-2018 surveillance year**



**Graph 4. Percent positive for respiratory pathogens through ILI trends by week and beneficiary status**



**Graph 5.** Vaccination status by beneficiary type through Week 3 of the 2017-2018 surveillance year (excluding ‘Other’ beneficiary type)



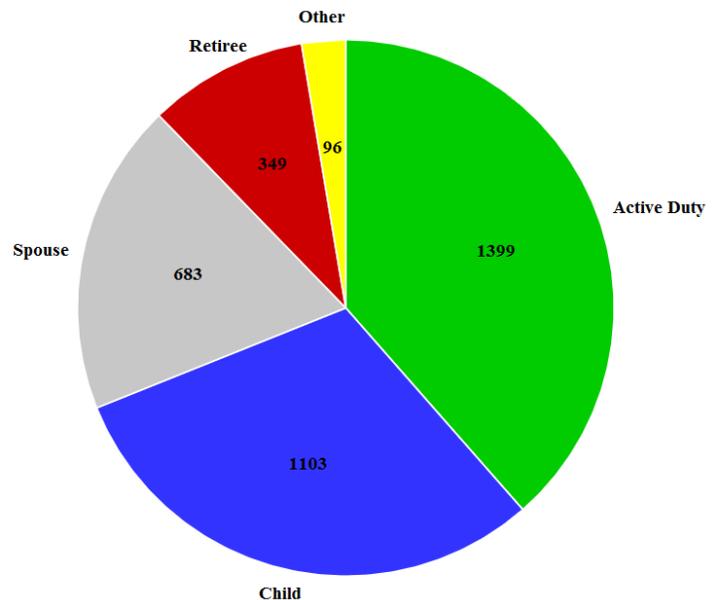
**Table 2.** ILI by age group through Week 3 of the 2017-2018 surveillance year

Age Group	Frequency	Percent
0-5	674	18.57
6-9	191	5.26
10-17	264	7.27
18-24	573	15.79
25-44	1179	32.48
45-64	489	13.47
65+	257	7.08
Unknown	3	0.08

**Demographic Summary**

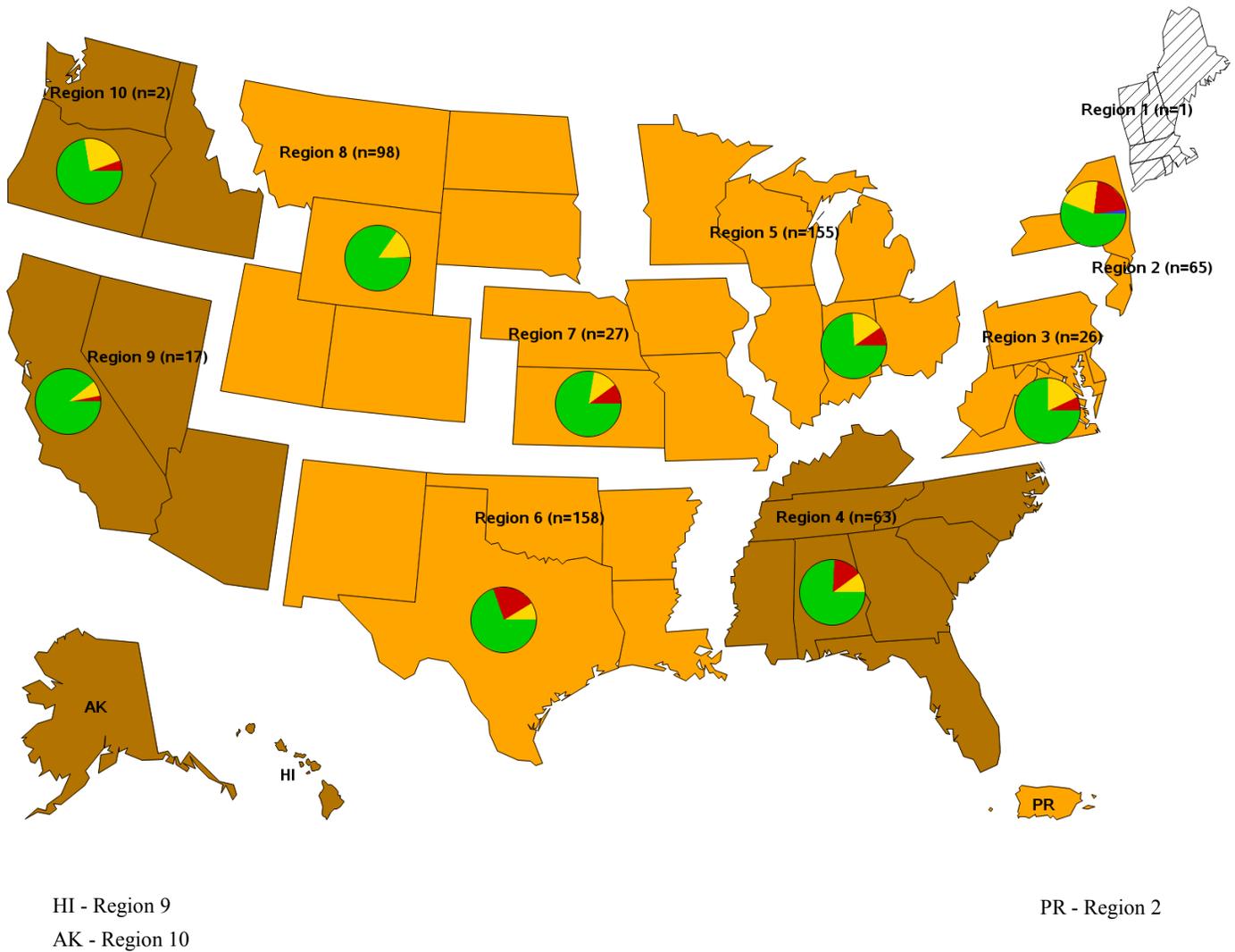
Of 3,630 ILI cases, 1,399 are service members (38.6%), 1,103 are children (30.3%), 683 are spouses (18.8%), and 445 are retirees and other beneficiaries (12.3%). The median age of ILI cases with known age (n=3,627) is 26 (range 0, 98).

**Graph 6.** ILI by beneficiary status through Week 3 of the 2017-2018 surveillance year



# DoD Global Respiratory Pathogen Surveillance Program

**Map 1.** Influenza subtypes and activity level by U.S. region through Week 3 of the 2017-2018 surveillance year



## Legend

### Influenza Activity - Past 2 weeks (n = # of submissions)

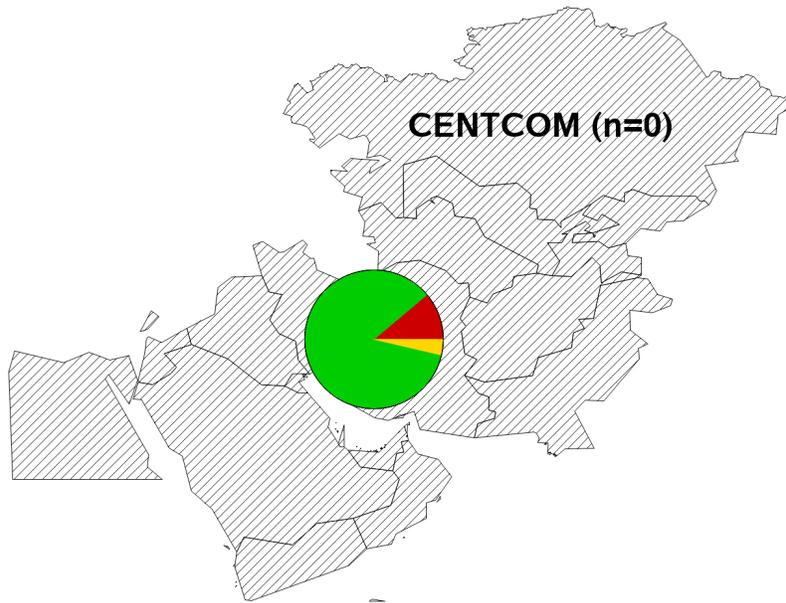
-  No activity (0%+) or no submissions
-  Low (<25%+)
-  Moderate (25-49%+)
-  High (>50%+)

### Influenza Results - Cumulative

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

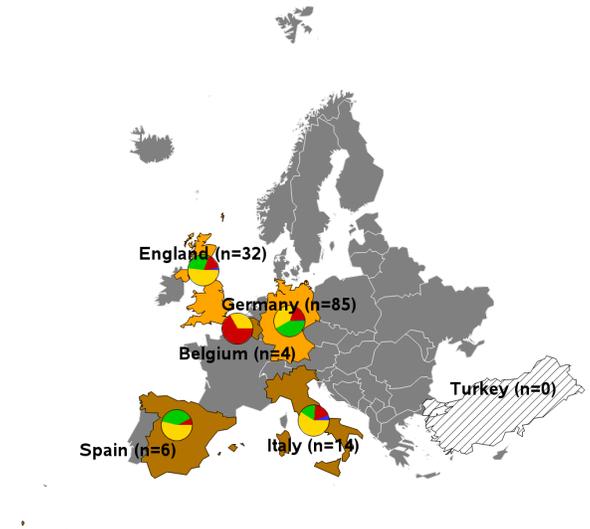
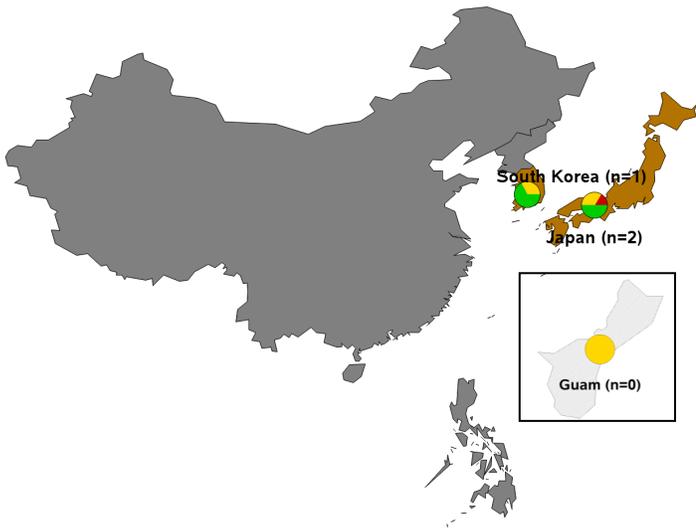
**Map 2. Influenza**

subtypes and activity



**Map 3. Influenza subtypes and activity level by country through Week 3 of the 2017-2018**

**Map 4. Influenza subtypes and activity level by country through Week 3 of the**



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**

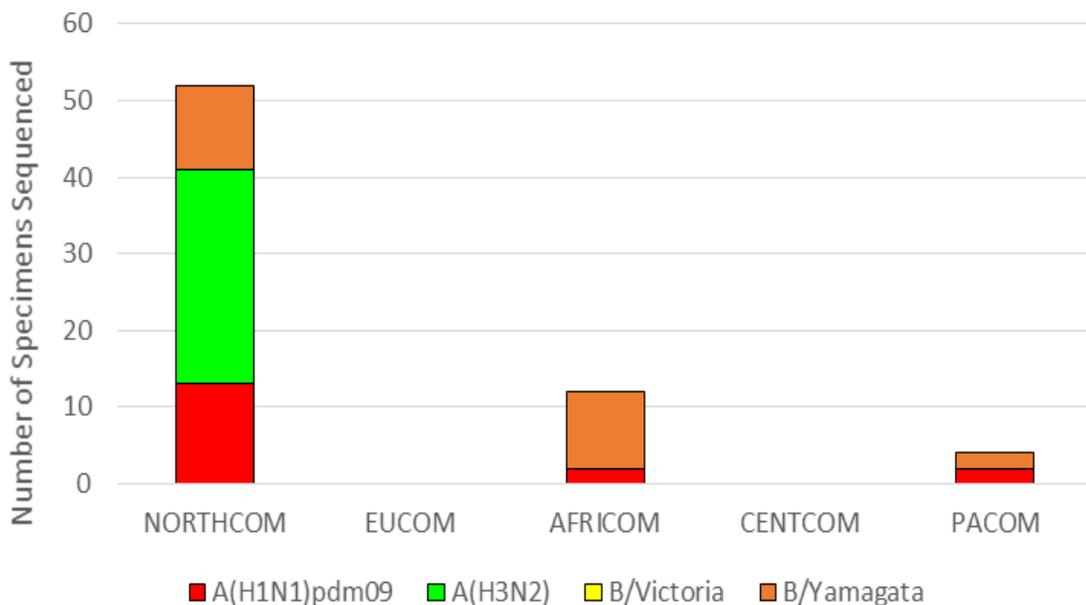
-  Influenza A(H3N2)
-  Influenza A(H1N1)pdm09
-  Influenza B
-  Influenza A/not subtyped

**Molecular Sequence Analysis Report #3**

This is the third USAFSAM influenza sequence surveillance report for the 2017-2018 influenza season and includes a total of 125 influenza specimens collected between 1 September 2017 and 19 December 2017, with 89 specimens sequenced at USAFSAM, 24 hemagglutinin (HA) sequences provided by the Naval Medical Research Unit Two (NAMRU-2) in Cambodia, and 12 HA sequences provided by the United States Army Medical Research Unit in Kenya (USAMRD-K) [Table 1].

**Table 1:** Report 3 influenza HA sequences by subtype/lineage contributed by each DoD partner laboratory.

	<b>A(H1N1)pdm09</b>	<b>A(H3N2)</b>	<b>B/Yamagata</b>	<b>Total</b>
NAMRU-2	2	20	2	24
USAFSAM	13	65	11	89
USAMRD-K	2		10	12
<b>Total</b>	<b>17</b>	<b>85</b>	<b>23</b>	<b>125</b>



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

# DoD Global Respiratory Pathogen Surveillance Program

**Table 2:** Distribution of CONUS and OCONUS sentinel sites that contributed influenza specimens or sequences for this report.

	A(H1N1)pdm09	A(H3N2)	B/Yamagata	Total
<b>CONUS</b>				
Arizona				
Luke AFB	3			3
Arkansas				
Little Rock AFB	1			1
California				
Edwards AFB	1			1
Travis AFB	2		1	3
Colorado				
Peterson AFB	9			9
USAF Academy	3			3
Florida				
Eglin AFB	3			3
Hurlburt Field	7		1	8
Georgia				
Robins AFB	1			1
Illinois				
Scott AFB	1	2		3
Kentucky				
Ft Campbell	1			1
Mississippi				
Keesler AFB	8	4	5	17
Nebraska				
Offutt AFB	6			6
Nevada				
Nellis AFB	2			2
New York				
USMA - West Point	2			2
North Dakota				
Minot AFB	3			3
Ohio				
Wright-Patterson AFB	5		3	8
Oklahoma				
Altus AFB	1			1
Tinker AFB	3	1		4
South Carolina				
Shaw AFB	1			1
Texas				
SAMMC	1			1
Sheppard AFB	1		1	2
Virginia				
JB Langley-Eustis	1			1
Washington				
NH Bremerton	1			1
Wyoming				
FE Warren AFB	1			1

**Table 2:** Distribution of CONUS and OCONUS sentinel sites that contributed influenza specimens or sequences for this report.

	A(H1N1)pdm09	A(H3N2)	B/Yamagata	Total
<b>OCONUS</b>				
Alaska				
Eielson AFB		1		1
Cambodia				
NAMRU-2	2	20	2	24
Hawaii				
Tripler AMC		1		1
Japan				
Camp Zama		1		1
Kenya				
USAMRD-K	2		10	12
<b>Total</b>	<b>17</b>	<b>85</b>	<b>23</b>	<b>125</b>

**Table 3:** Cumulative 2017-2018 protein homologies (percent amino acid match) 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	Vaccine Component	Season(s) Used	Min	Max	Average
A(H1N1)pdm09	A/Michigan/45/2015-like	2017-2018	98.4%	99.5%	99.0%
A(H3N2)	A/Hong Kong/4801/2014-like	2016-2018	97.1%	98.9%	98.3%
B Victoria	B/Brisbane/60/2008-like*	2009-2012 and 2013-2018	98.8%	99.5%	99.3%
B Yamagata	B/Phuket/3073/2013-like**	2015-2018	98.9%	99.5%	99.4%

\*Quadrivalent only during the 2013-2016 seasons

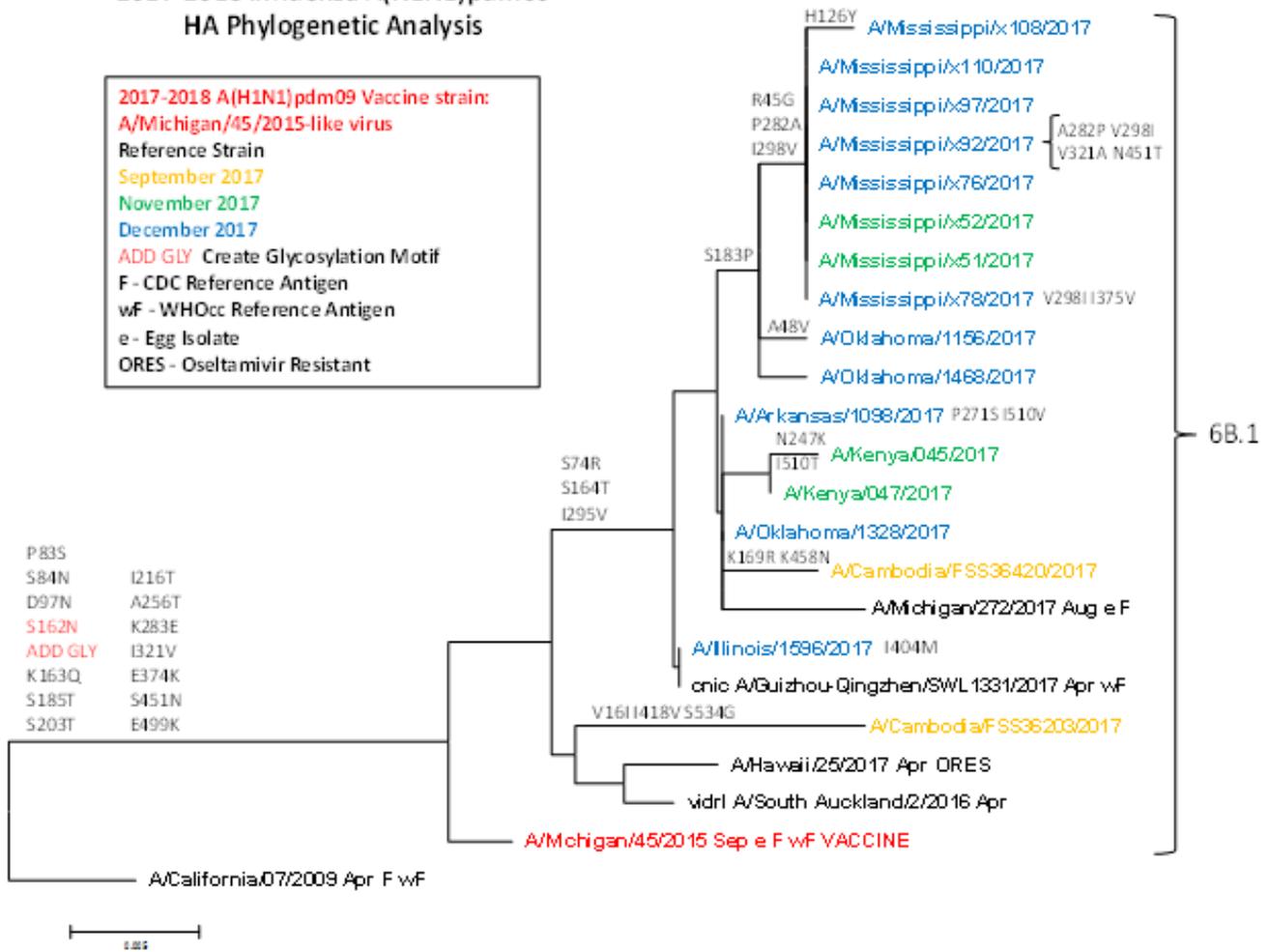
\*\* Quadrivalent only during the 2016-2018 seasons

## Influenza A(H1N1)pdm09

- Among the 102 influenza A HA sequences, 17 (16.7%) 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 98.8%) 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 99.0%) [**Table 3**]. One influenza A(H1N1)pdm09 sequence from Kenya was excluded from the protein homology analysis due to truncation. 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.
- 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.<sup>4</sup> Observations are based solely on sequence motifs. For the influenza A(H1N1)pdm09 sequences characterized in this report, one mutation, S162N (serine to asparagine), was observed that caused a gain of a glycosylation motif.
- Of the 33 mutations present in the influenza A(H1N1)pdm09 sequences, 12 occurred at predicted antigenic sites (one at site A, one at site B, four at site C, three at site D, and three at site E) and two occurred at the receptor binding site.<sup>4,5</sup>

2017-2018 Influenza A(H1N1)pdm09  
HA Phylogenetic Analysis

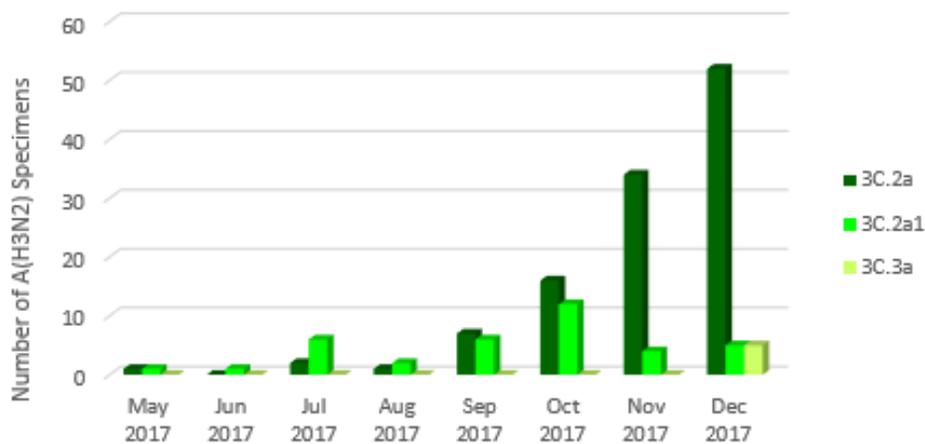
2017-2018 A(H1N1)pdm09 Vaccine strain:  
A/Michigan/45/2015-like virus  
Reference Strain  
September 2017  
November 2017  
December 2017  
ADD GLY Create Glycosylation Motif  
F - CDC Reference Antigen  
wF - WHOcc Reference Antigen  
e - Egg Isolate  
ORES - Oseltamivir Resistant



**Figure 2:** 2017-2018 USAFSAM Report 3 influenza A(H1N1)pdm09 HA phylogenetic analysis. Seventeen influenza A(H1N1)pdm09 specimens collected between September 2017 and December 2017 were sequenced for HA 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 102 influenza A HA sequences, 85 (83.3%) 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) sequences characterized for this report exhibited an overall protein homology of 97.1-98.3% (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 97.1-98.9% (average 98.3%) [Table 3].
- All of the influenza A(H3N2) specimens sequenced for this report were in clade 3C with 64 (75.3%) in clade 3C.2a, 16 (18.8%) in subclade 3C.2a1, and five (5.9%) in clade 3C.3a. The mutation N121K was present in all 16 (100.0%) of the 3C.2a1 and 20 (23.5%) of the total influenza A(H3N2) sequences. The mutation T135K was present in 16 sequences (75.0% of 3C.2a1 and 18.8% of total). Cumulative influenza A(H3N2) clade proportions since May 2017 are shown in [Figure 3].
- Among the influenza A(H3N2) sequences characterized in this report, seven mutations; T24K (threonine to lysine), N122D (asparagine to aspartic acid), T135K (threonine to lysine), N144K (asparagine to lysine), N158K (asparagine to lysine), T160K (threonine to lysine), and N246S (asparagine to serine) 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 65 mutations present in the influenza A(H3N2) specimens, 19 occurred at predicted antigenic sites (six at site A, six at site B, none at site C, three at site D, and four at site E) and four occurred at the

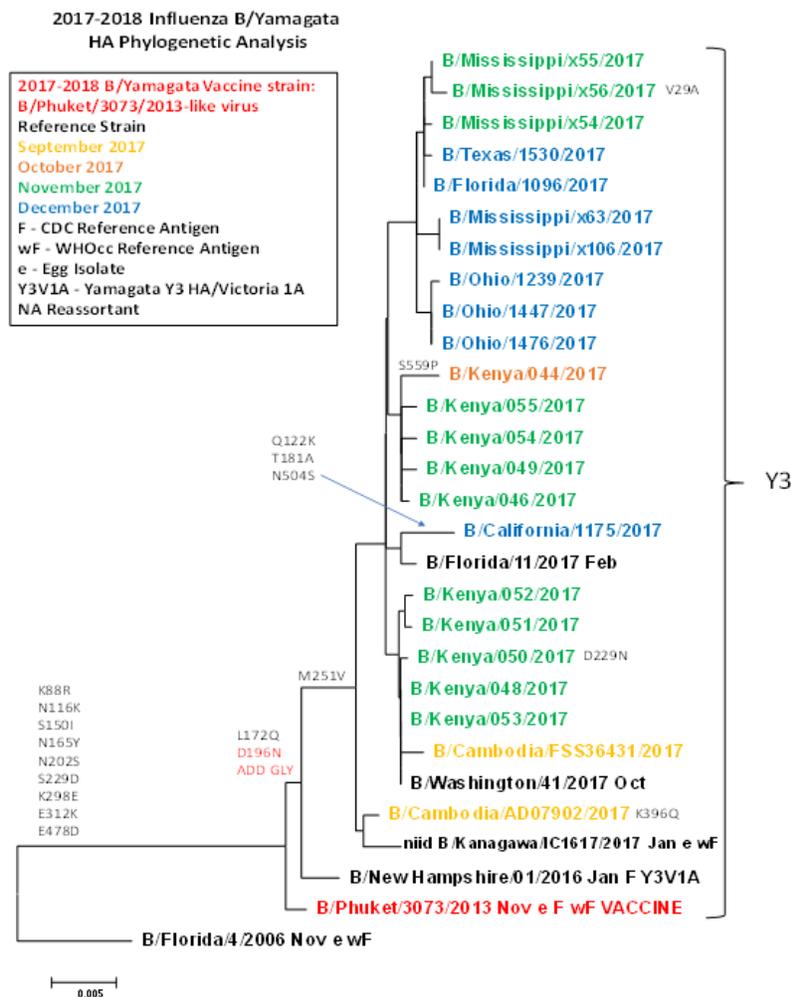


**Figure 3:** Cumulative proportion of influenza A(H3N2) clades among specimens collected from May 2017 through December 2017. Subclade 3C.2a1 was the dominant A(H3N2) genetic group throughout the 2016-2017 season but declined prior to the start of the 2017-2018 season as clade 3C.2a increased in prevalence.



## Influenza B

- All 23 of the influenza B HA sequences for this report fell into the Yamagata lineage and are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains and are rooted from the previous vaccine strain B/Florida/4/2006 [Figure 5].
- 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 98.9-99.5% (average 99.4%) [Table 3].
- All of the influenza B/Yamagata sequences fell into clade Y3 and shared one mutation, D196N (aspartic acid to aspara-



**Figure 5:** 2017-2018 USAFSAM Report 3 influenza B/Yamagata phylogenetic analysis. Twenty-three influenza B/Yamagata specimens collected between September 2017 and December 2017 were sequenced. All resided in clade Y3 and shared one addition of a glycosylation motif relative to the root strain.

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.<sup>1-3</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, World Health Organization and contribute to the seasonal Northern and Southern hemisphere vaccine component selections.

### **References:**

1. Wright, P., Neumann, G., and Kawaoka, Y. (2007). Orthomyxoviruses In: Knipe, D.M., Howley, P.M. (Eds.), *Fields Virology*. Wolters Kluwer, Lippincott Williams & Wilkins, Philadelphia, pp.1692-1740.
2. 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.
3. 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.
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.

## 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, 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. 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.

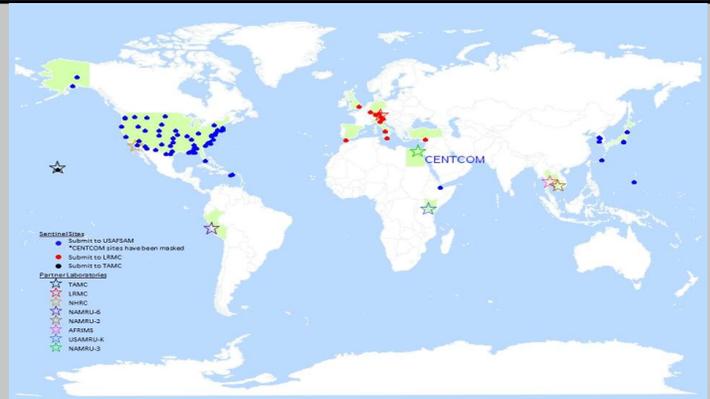
Errata:



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.

