Cumulative Results

Locations	80
Collected	5,331
Tested	5,267

Influenza A	**1,378**
A(H1N1)pdm09	24
A(H1N1)pdm09 & Influenza B	1
A(H3N2)	1,346
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*	**442**
B	441
B & Human Metapneumovirus & Rhino/Enterovirus	1

Other Respiratory Pathogens	**1,126**
Adenovirus	72
Bordetella pertussis	1
Chlamydophila pneumoniae	5
Coronavirus	121
Human Metapneumovirus	93
Mycoplasma pneumoniae	38
Parainfluenza	190
RSV	177
Rhinovirus/Enterovirus	290
Non-influenza Viral Coinfections	131
Non-influenza Bacterial Coinfections	8
-M. pneumo 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
28 May - 8 July 2017 (Surveillance Weeks 22 - 27)

- During 28 May - 8 July 2017 , a total of 86 specimens were collected and received from 31 locations. Results were finalized for 81 specimens from 30 locations. During Week 22, there was one influenza A(H3N2) and one influenza B identified. During Weeks 23,25, and 26, there was one influenza A(H3N2) identified during each week. There were no influenza viruses identified during Weeks 24 and 27. The highest percent positive during this time period occurred at Week 22 (11%) and showed a decreasing trend through the remaining Weeks (23-27). The influenza percent positive for the season is currently 35%.

- According to CDC FluView, during Week 26, influenza activity continued to decrease in the United States. The proportion of outpatient visits for influenza-like illness was below the national baseline. There were no influenza-associated pediatric deaths reported in Week 26. (CDC, Flu View Report Week 26, cited 13 July 2017).

- This report contains the 11th molecular sequence analysis report which includes 218 specimens collected between 11 January 2017 and 15 March 2017.

- This report contains the monthly supplemental EUCOM report for surveillance through 8 July 2017. See pages 8 and 9 for more details.

DoD Global, Laboratory-Based, Influenza Surveillance Program

**Table 1.** Finalized results by region and location for specimens collected during Weeks 22-27

Region*		A(H3N2)	B	Adenovirus	*B. pertussis*	hMNV	Parainfluenza	RSV	Rhinovirus/Enterovirus	No Pathogen	Total
PACOM	JR Marianas - Andersen AFB, Guam	-	-	2	-	-	1	-	-	1	4
	Yokota AB, Japan	-	-	-	-	-	-	-	-	1	1
Region 2	Ft Drum, NY	-	-	-	-	-	-	-	-	4	4
	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	1	-	-	-	1
	USMA - West Point, NY	-	-	-	-	-	1	-	-	1	2
Region 3	Dover AFB, DE	1	-	-	-	-	-	-	2	1	4
	JB Andrews, MD	-	-	-	-	-	-	-	-	1	1
	JB Langley-Eustis, VA	-	-	-	-	-	-	-	1	1	2
Region 4	Columbus AFB, MS	-	-	-	-	-	-	-	-	1	1
	Eglin AFB, FL	-	-	-	-	1	1	-	-	1	3
	JB Charleston (AF), SC	-	-	-	-	-	-	-	-	1	1
	Keesler AFB, MS	-	-	-	-	-	-	1	1	1	3
	Moody AFB, GA	-	-	-	-	-	1	1	1	4	7
	Robins AFB, GA	1	-	-	-	-	-	-	-	1	2
	Seymour Johnson AFB, NC	1	-	-	-	-	-	-	-	1	2
	Shaw AFB, SC	-	-	-	-	-	-	-	-	2	2
Region 5	Wright-Patterson AFB, OH	-	-	-	-	-	-	-	-	1	1
Region 6	Cannon AFB, NM	-	-	-	-	-	-	-	-	1	1
	Sheppard AFB, TX	-	-	-	-	-	-	-	-	1	1
	Tinker AFB, OK	-	-	-	-	-	-	-	-	6	6
Region 7	McConnell AFB, KS	-	-	-	-	-	-	-	-	1	1
	Offutt AFB, NE	-	-	-	-	-	-	-	2	2	4
Region 8	FE Warren AFB, WY	-	-	-	-	-	-	-	-	1	1
	Hill AFB, UT	-	-	-	-	-	2	-	-	3	5
	Minot AFB, ND	1	-	-	-	-	-	-	-	-	1
	Peterson AFB, CO	-	-	-	1	-	-	-	-	5	6
Region 9	Davis-Monthan AFB, AZ	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	1	-	-	-	-	-	1	3	5
	Travis AFB, CA	-	-	-	-	1	-	-	1	3	5
Region 10	Mt Home AFB, ID	-	-	-	-	-	-	-	-	2	2
Total		4	1	2	1	2	7	2	9	53	81

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 27 of the 2016-2017 surveillance year

Influenza Subtypes: ■ A(H1N1)pdm09 ■ A(H3N2) ■ A\Not Subtyped ■ B ■ Not Influenza

Percent Influenza Positive: —
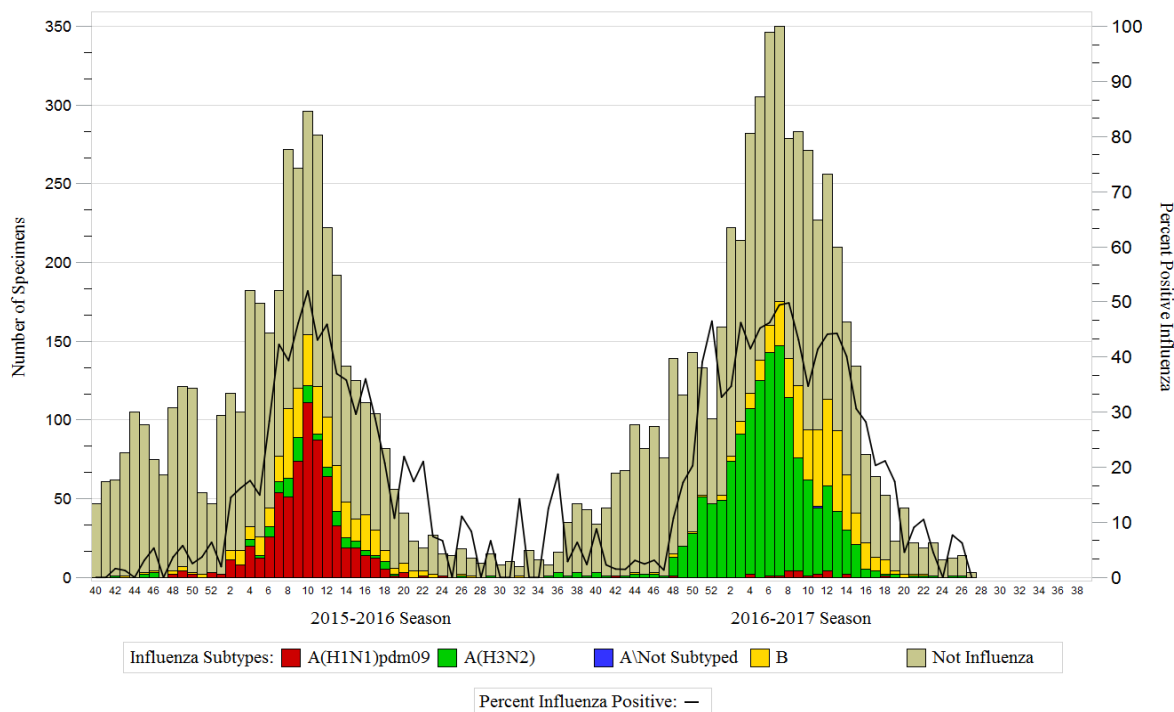
Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

Table 2. ILI by age group for the 2016-2017 surveillance year through Week 27

Age Group	Frequency	Percent
0-5	1198	22.75
6-9	483	9.17
10-17	626	11.89
18-24	712	13.52
25-44	1623	30.81
45-64	514	9.76
65+	111	2.11

Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 27

Demographic Summary

Of 5,267 ILI cases, 1,829 are service members (34.7%), 2,300 are children (43.7%), 753 are spouses (14.3%), and 385 (7.3%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=5,267) is 21 (range 0, 96).
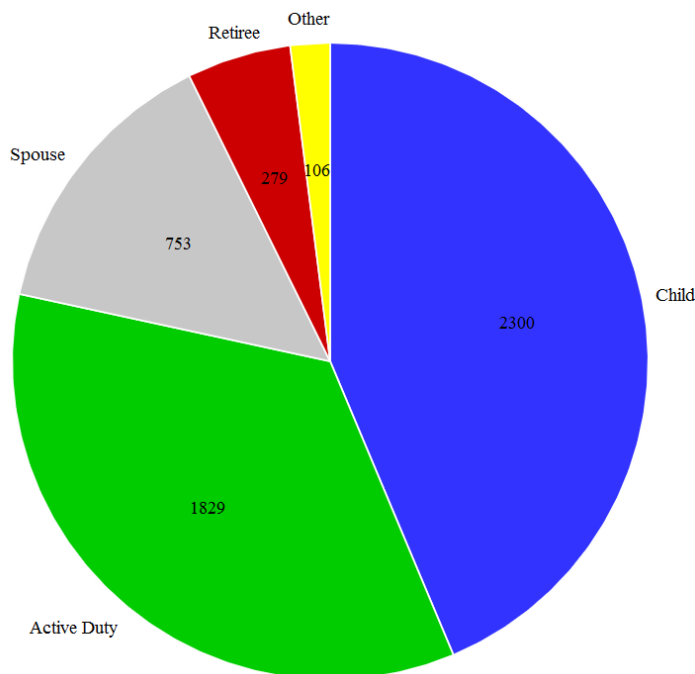
Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 25
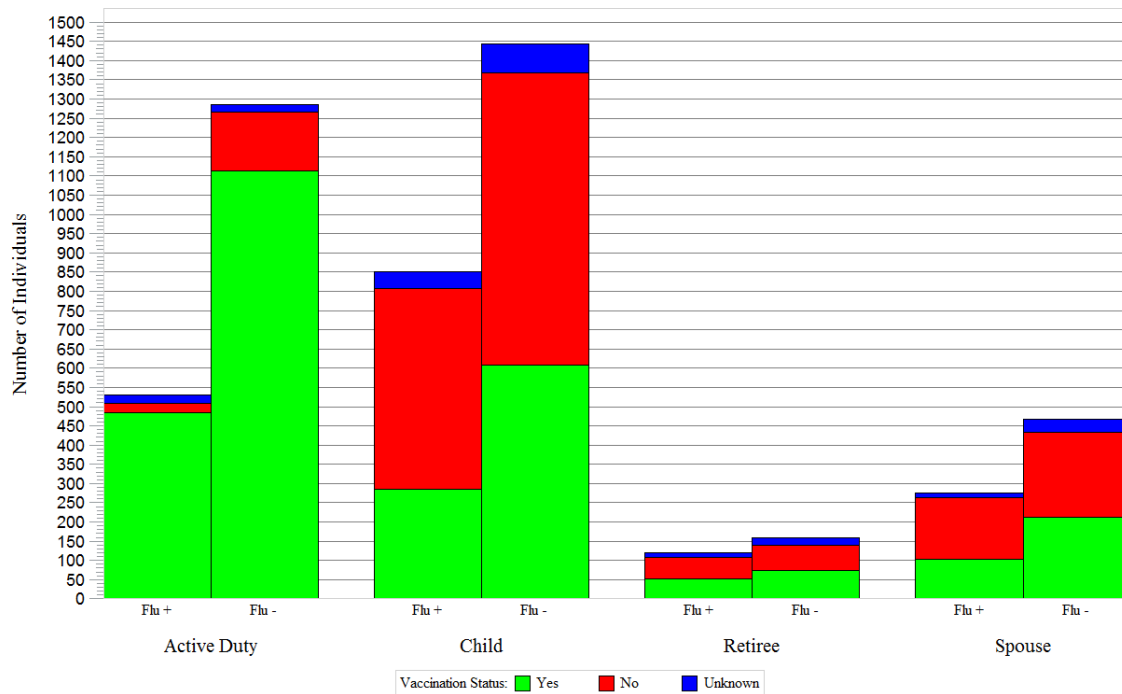
*Vaccine data is only available through Week 25.

Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 27

HI - Region 9

AK - Region 10

PR - Region 2

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 27 (Pacific)

South Korea (n=0)

Japan (n=0)

Guam (n=1)
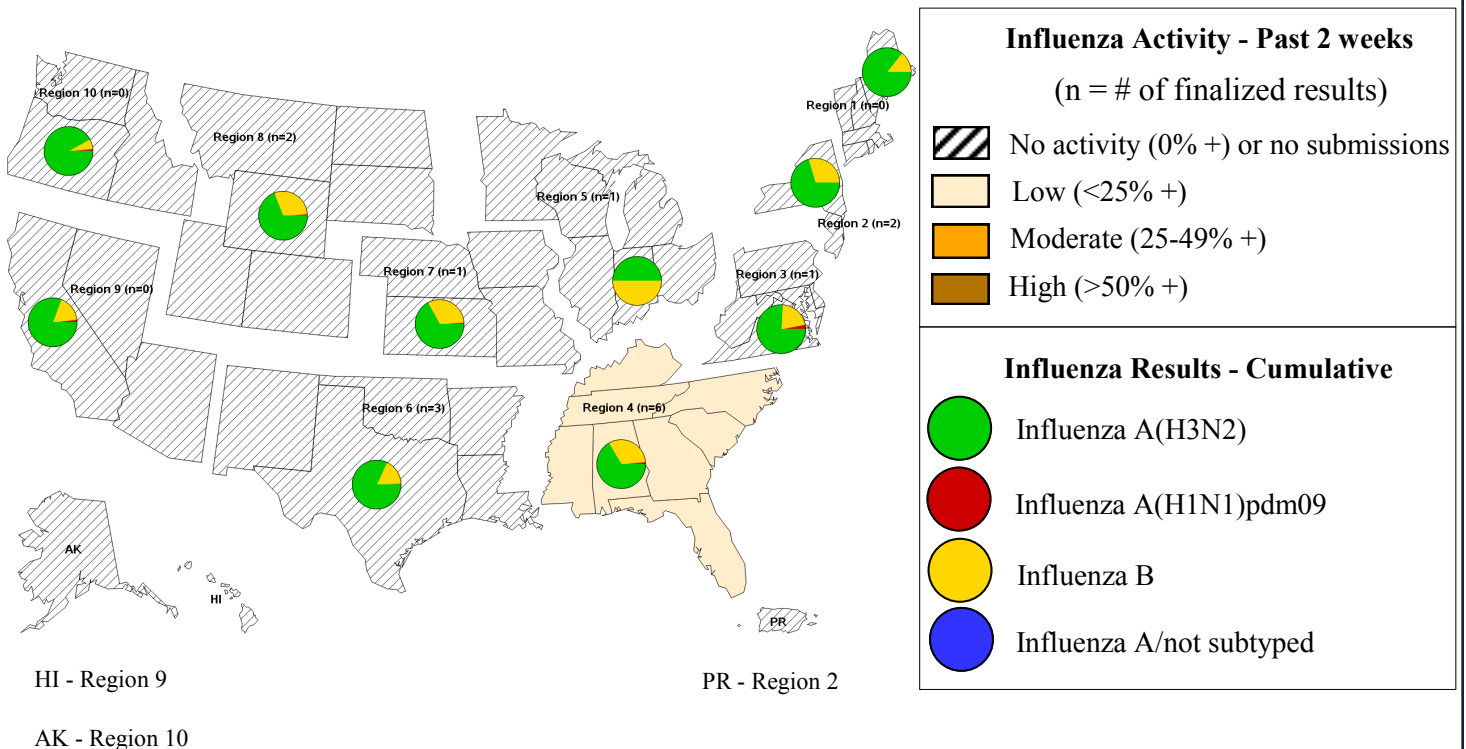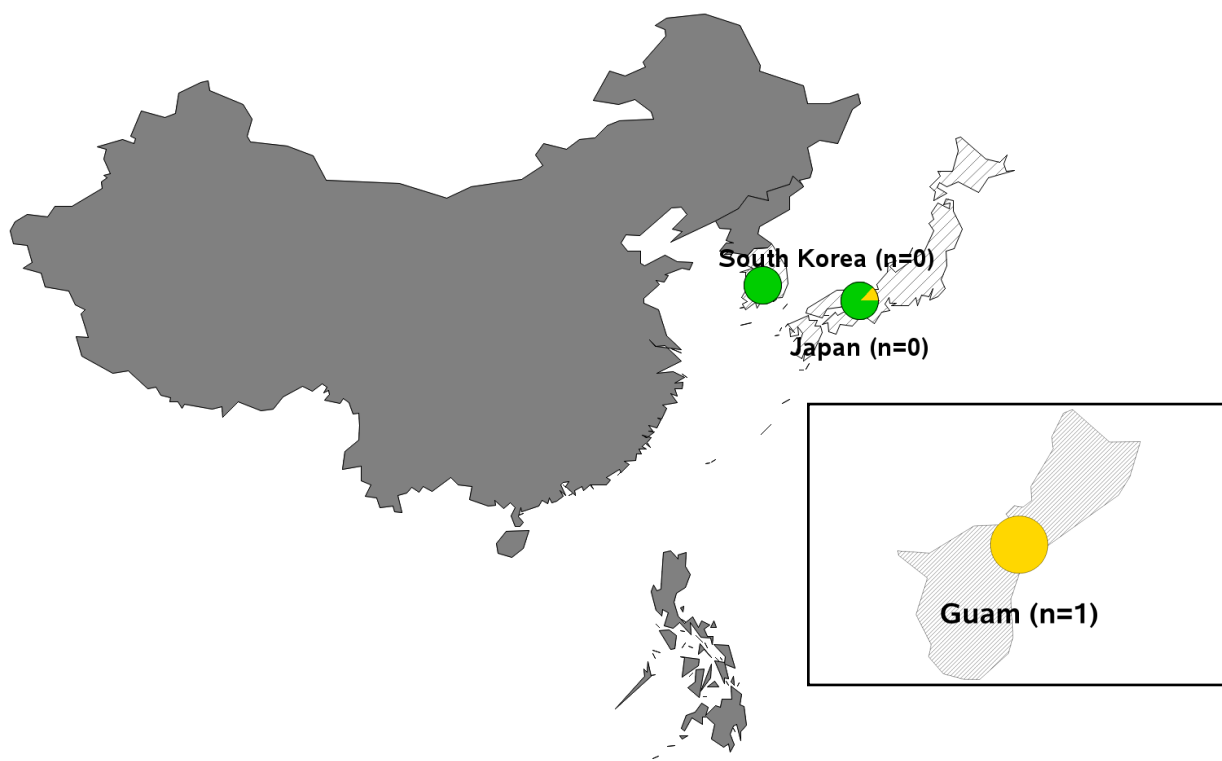
Note - Countries shaded in gray do not contain sentinel sites and are only displayed for geographical perspective.

Map 3. Influenza subtypes and activity level for CENTCOM for the 2016-2017 surveillance year through Week 27

CENTCOM (n=0)
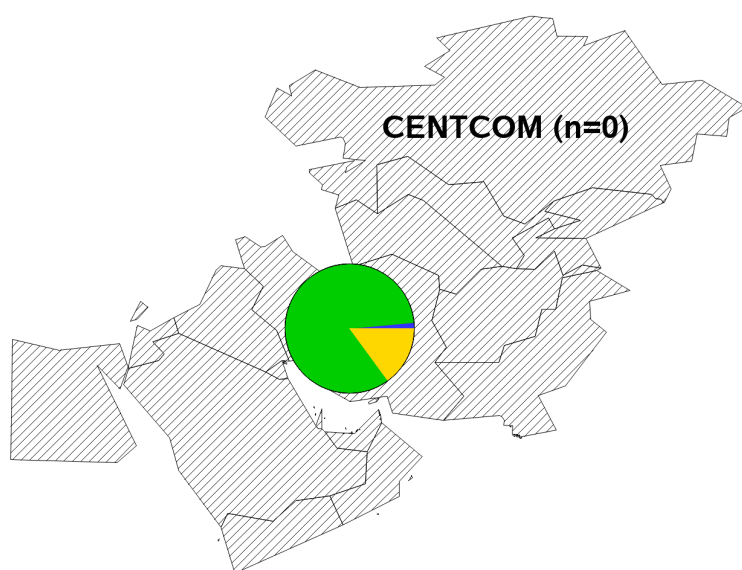
Influenza Activity - Past 2 weeks
(n = # of finalized results)

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

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

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

5

Laboratory Results—Through Current Surveillance Week 27

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

Region*	Location	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
PACOM	CFA Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Eielson AFB, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	2	-	-	5	10
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	4	6
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	1	-	2	-	-	-	1	1	-	-	-	-	-	7	12
	Kadena AB, Japan	-	4	-	-	-	-	-	-	-	-	-	-	-	-	1	-	3	-	2	1	1	25	37
	Kunsan AB, South Korea	-	2	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	5
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Osan AB, South Korea	-	4	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	7	12
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	36	-	-	-	-	-	-	6	-	1	-	-	3	1	2	3	2	9	5	-	70	138
Region 1	Hanscom AFB, MA	-	3	-	-	-	-	-	-	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	-	6	-	1	5	10	1	9	8	7	5	-	96	261
	JB McGuire-Dix-Lakehurst, NJ	-	54	-	-	-	-	-	-	2	-	3	-	-	6	9	2	10	6	12	5	-	84	193
	USMA - West Point, NY	-	86	-	-	-	-	-	-	15	-	12	-	-	5	7	2	11	13	10	8	-	156	325
Region 3	Dover AFB, DE	-	19	-	-	-	-	-	-	11	-	2	-	-	2	1	1	-	1	6	-	-	51	94
	JB Anacostia-Bolling, DC	-	14	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	1	-	-	-	19
	JB Andrews, MD	2	23	-	-	-	-	-	-	12	-	-	-	-	2	1	-	3	2	1	2	-	43	91
	JB Langley-Eustis, VA	6	149	-	1	1	-	-	-	31	-	1	-	-	4	10	2	12	20	38	11	-	262	548
	NCRM - Walter Reed NMMC, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 4	CGS Mobile, AL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
	Columbus AFB, MS	-	5	-	-	-	-	-	-	1	-	-	-	-	2	-	-	-	1	-	-	-	19	28
	Eglin AFB, FL	1	15	-	-	-	-	-	-	5	-	7	-	-	2	2	2	2	5	12	6	-	45	104
	Ft Bragg, NC	1	8	-	-	-	-	-	-	6	-	-	-	-	1	1	1	3	2	7	4	3	39	76
	Ft Campbell, KY	1	15	-	-	-	-	-	-	9	1	2	-	-	1	-	-	-	3	-	4	-	17	53
	Hurlburt Field, FL	-	18	-	-	-	-	-	-	6	-	2	-	-	1	-	1	1	2	4	1	-	28	64
	JB Charleston (AF), SC	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	18
	Keesler AFB, MS	-	2	-	-	1	-	-	-	-	-	-	-	-	1	-	-	2	3	5	3	-	16	33
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	-	6	8
	Maxwell AFB, AL	-	10	-	-	-	-	-	-	2	-	-	-	-	1	-	-	2	-	1	-	-	14	30
	Moody AFB, GA	-	36	-	-	-	-	-	-	44	-	1	-	-	2	7	1	14	9	17	14	1	95	241
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	NH Camp Lejeune, NC	-	2	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	11	16
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	25	-	-	-	-	-	-	8	-	-	-	-	-	-	-	2	1	3	2	-	30	71
	Seymour Johnson AFB, NC	3	17	-	-	-	-	-	-	1	-	2	-	-	-	-	-	1	1	2	1	-	21	49
	Shaw AFB, SC	-	71	-	-	-	-	-	-	34	-	1	-	1	7	5	1	5	1	13	2	-	72	213
	Tyndall AFB, FL	-	11	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	16

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

Laboratory Results—Through Current Surveillance Week 27

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

(Cont'd from page 6)

Region*	Location	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
Region 5	Scott AFB, IL	-	3	-	-	-	-	-	-	3	-	-	-	-	-	-	1	3	1	1	-	1	9	22
	Wright-Patterson AFB, OH	-	10	-	-	-	-	-	-	10	-	-	-	-	1	1	1	1	-	2	2	-	40	68
Region 6	Altus AFB, OK	-	7	-	-	-	-	-	-	1	-	1	-	-	1	1	-	1	5	7	4	-	40	68
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	2	-	1	-	-	8	12
	Cannon AFB, NM	-	13	-	-	-	-	-	-	4	-	-	-	-	2	-	1	3	-	4	1	-	41	69
	Ft Polk, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	3
	JBSA Lackland, TX	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1
	Laughlin AFB, TX	1	-	-	-	-	-	-	-	1	-	-	-	-	1	2	-	-	-	-	-	-	5	10
	Little Rock AFB, AR	-	12	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	12	25
	Sheppard AFB, TX	-	60	-	-	-	-	-	-	9	-	1	-	-	9	5	1	6	2	8	-	-	88	189
	Tinker AFB, OK	1	97	-	-	-	-	1	-	25	-	2	-	-	10	4	1	9	7	12	6	-	147	322
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	12
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	9	1	-	61	125
Region 8	Ellsworth AFB, SD	-	14	-	-	-	-	-	-	15	-	-	-	-	3	-	-	3	1	3	-	-	38	77
	FE Warren AFB, WY	-	36	-	-	-	-	-	-	7	-	3	-	-	4	1	2	4	6	4	-	-	53	120
	Hill AFB, UT	-	30	-	-	-	-	-	-	5	-	-	-	-	3	1	1	8	4	4	2	-	48	106
	Malmstrom AFB, MT	-	7	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	1	-	-	9	21
	Minot AFB, ND	1	25	-	-	-	-	-	-	15	-	-	-	-	3	2	1	1	6	5	3	-	47	109
	Peterson AFB, CO	1	19	-	-	-	-	-	-	12	-	-	1	-	3	-	-	3	11	4	4	-	32	90
	USAF Academy, CO	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	1	-	2	6
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	1	16	-	-	-	-	-	-	4	-	-	-	-	2	-	-	5	1	6	5	-	38	78
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	-	-	5	-	1	-	-	2	-	-	1	3	2	1	-	20	35
	Nellis AFB, NV	1	3	-	-	-	-	-	-	4	-	3	-	-	1	-	-	4	4	5	7	-	32	64
	Travis AFB, CA	-	58	-	-	-	-	-	-	5	-	1	-	1	6	8	-	7	13	16	5	-	47	167
	Vandenberg AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Fairchild AFB, WA	2	17	-	-	-	-	-	-	2	-	4	-	-	3	-	-	5	2	4	-	-	48	87
	JB Lewis-McChord, WA	-	2	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	3
	Mt Home AFB, ID	-	23	-	-	-	-	-	-	1	-	1	-	1	1	-	1	23	12	12	5	-	78	158
	NH Bremerton, WA	-	67	-	-	-	-	-	-	5	-	8	-	1	3	1	2	8	7	7	4	-	27	140
Total		24	1346	1	1	3	1	1	1	441	1	72	1	5	121	93	38	190	177	290	131	8	2321	5267

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

Monthly EUCOM Respiratory Surveillance Supplemental Report Through 8 July 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 22-27

Region	Location	Adenovirus	hMNV	Parainfluenza	Rhinovirus/Enterovirus	Adeno & Rhino/Entero	No Pathogen	Total
EUCOM	Landstuhl RMC, Germany	-	1	1	3	1	7	13
	NAVSTA Rota, Spain	-	-	-	1	-	1	2
	NSA Naples, Italy	-	1	-	1	-	5	7
	RAF Lakenheath, England	-	-	-	1	-	1	2
	Ramstein AB, Germany	1	-	-	-	-	4	5
	USAG Stuttgart, Germany	-	-	-	3	-	2	5
Total		1	2	1	9	1	20	34

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

Region	Location	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	-	-	-	-	-	-	-	-	17	26
EUCOM	Aviano AB, Italy	-	-	-	-	-	-	-	2	-	-	-	-	-	2	-	-	-	-	-	-	-	-	11	15
	Landstuhl RMC, Germany	1	58	-	-	-	2	1	6	-	2	12	10	17	43	1	-	2	-	1	1	-	3	165	325
	NAS Sigonella, Italy	-	6	-	-	-	-	-	-	-	-	1	-	3	4	-	-	-	-	-	-	-	-	5	19
	NAVSTA Rota, Spain	-	2	1	-	-	-	-	-	-	-	2	4	5	10	-	-	-	-	-	-	-	-	32	56
	NSA Naples, Italy	-	10	-	-	-	-	1	-	-	-	2	3	4	9	-	-	-	-	-	-	-	-	31	60
	RAF Lakenheath, England	-	24	-	-	-	-	-	2	1	3	9	4	14	28	-	1	1	-	1	-	-	2	88	178
	Ramstein AB, Germany	-	24	1	-	-	-	-	2	-	1	8	3	12	21	-	-	1	-	-	-	1	-	53	127
	Spangdahlem AB, Germany	-	1	-	-	-	-	1	-	-	-	-	-	1	2	-	-	-	-	-	-	-	-	6	11
	USAG Stuttgart, Germany	-	17	-	-	-	-	1	1	-	-	5	3	7	17	-	-	-	-	-	-	-	-	31	82
	USAG Vicenza, Italy	-	14	1	2	-	-	-	-	-	-	3	-	2	2	-	-	-	-	-	-	-	-	27	51
	Vilseck AHC, Germany	-	40	-	-	1	-	-	4	-	1	14	16	31	30	-	-	1	1	-	2	3	-	93	237
Total		1	199	3	2	1	2	6	17	1	7	56	43	96	172	1	1	5	1	2	3	4	5	561	1189

Graph 4. Percent influenza positive by week: 2015-2016 surveillance year and through Week 27 of the 2016-2017 surveillance year (EUCOM)
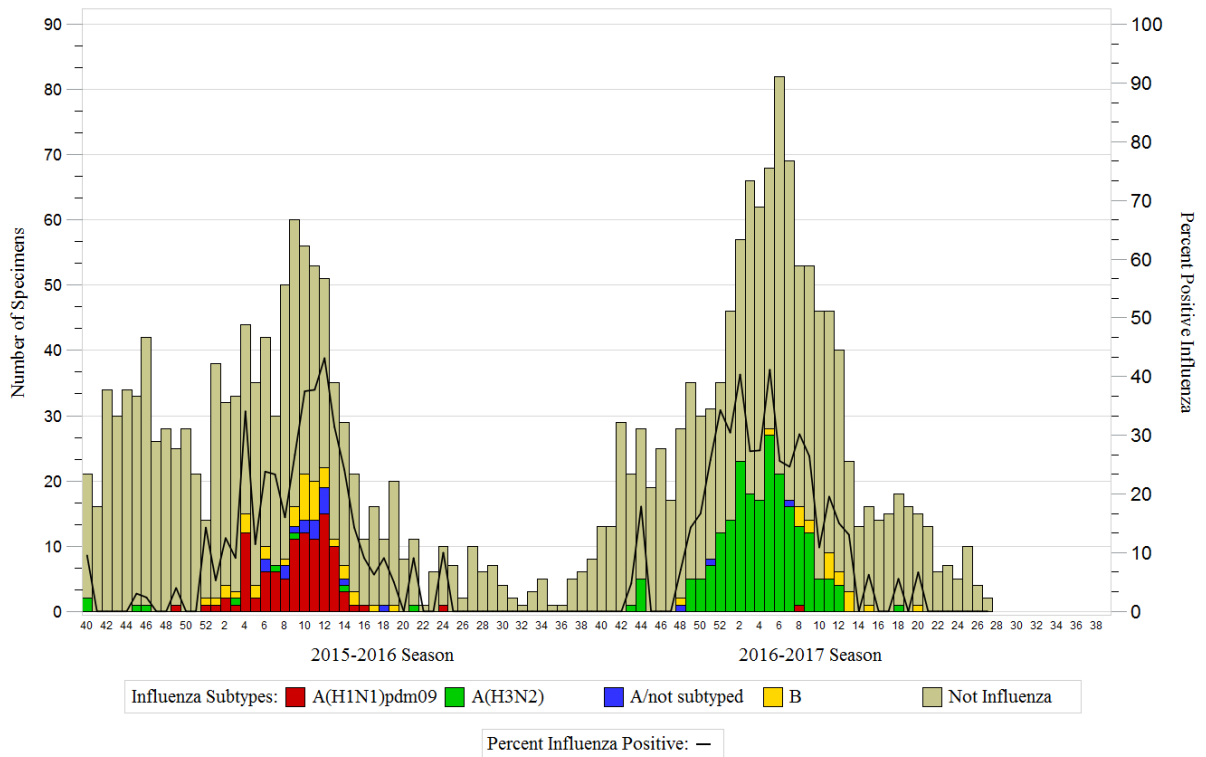
Note: Dual influenza co-infections have been excluded from the graph.

Map 4. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 27(Europe)

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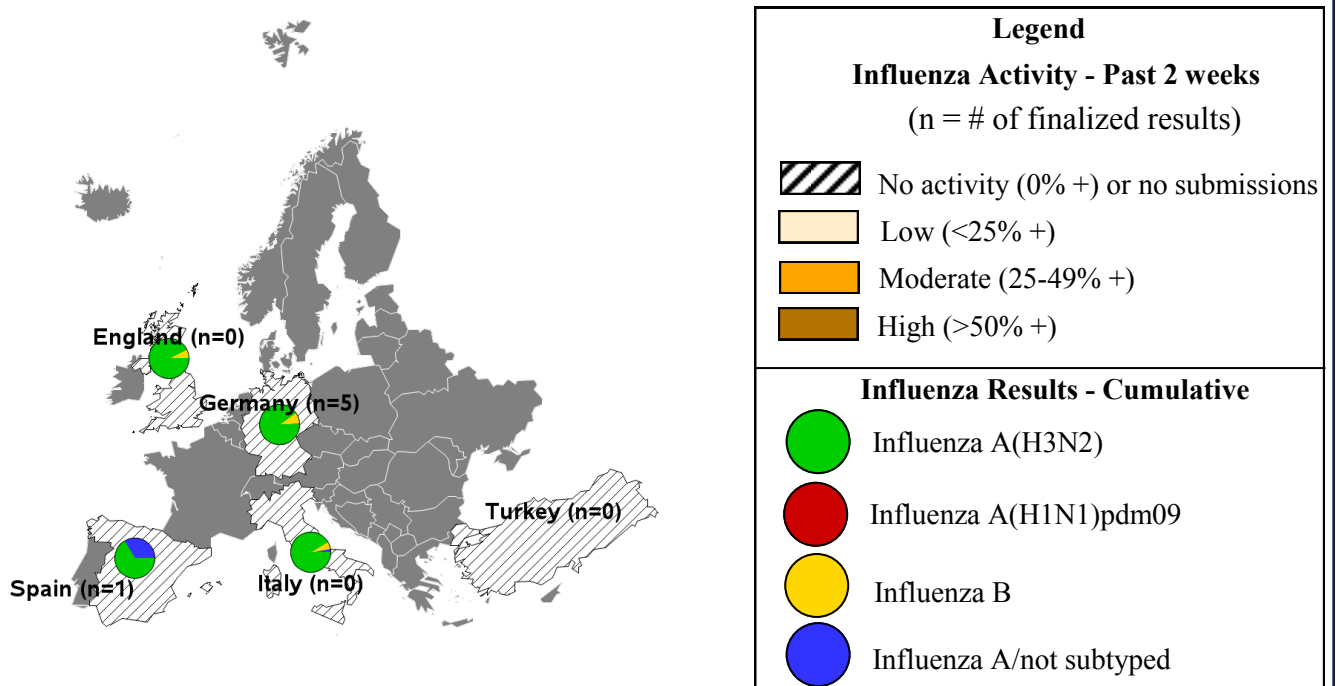
Molecular Sequence Analysis Report #11

This is the 11th USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 218 influenza specimens collected between 11 January 2017 and 15 March 2017. Ten (4.6%) of these specimens were influenza A(H1N1)pdm09, 131 (60.1%) were influenza A (H3N2), 14 (6.4%) were influenza B/Victoria lineage, and 63 (28.9%) were influenza B/Yamagata lineage. All influenza positive specimens were sequenced at USAFSAM. Figure 1 shows the distribution of all specimens by US Combatant Command. The number of sequences in this report are 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, respectively.
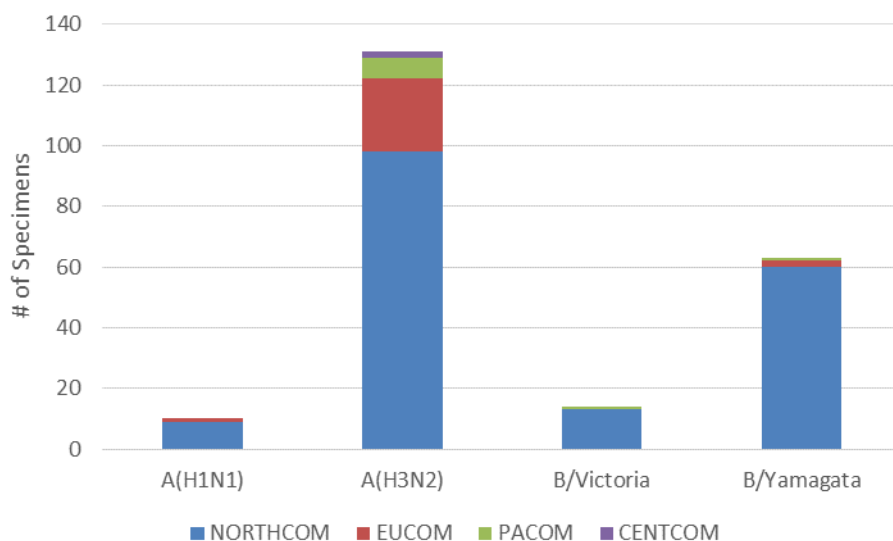

Figure 1: The total HA sequences of influenza A(H1N1), A(H3N2), B/Victoria, and B/Yamagata from each of the United States Combatant Commands listed in this report.

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

	A(H1N1) pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
CONUS					
Alabama					
Maxwell AFB		3			3
Arizona					
Davis-Monthan AFB		3	1		4
Arkansas					
Little Rock AFB		4			4
California					
Travis AFB		2			2
Vandenburg AFB		1			1
Colorado					
Peterson AFB		3	1	3	7
District of Columbia					
JB Anacostia-Bolling		1		1	2
Delaware					
Dover AFB				1	1
Florida					
Eglin AFB				1	1
Hurlburt Field			1		1
Tyndall AFB		2		1	3
Georgia					
Moody AFB		2	6	1	9
Robins AFB		2		2	4
Idaho					
Mt Home AFB		1			1
Illinois					
Scott AFB		1			1
Kansas					
McConnell AFB		1		2	3
Maryland					
JB Andrews	2	1			3
NCRM - Walter Reed NMMC		1			1
Massachusetts					
Hanscom AFB		1			1
Mississippi					
Columbus AFB		1			1

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	A(H1N1) pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
Keesler AFB		1		2	3
Montana					
Malmstrom AFB				2	2
New Jersey					
JB McGuire-Dix-Lakehurst		4			4
New Mexico					
Cannon AFB		2	1		3
New York					
Ft Drum	1	4		9	14
USMA - West Point		3		2	5
North Carolina					
NH Camp Lejeune		1		1	2
Seymour Johnson AFB		1			1
North Dakota					
Minot AFB		2		3	5
Ohio					
Wright-Patterson AFB		5		5	10
Oklahoma					
Altus AFB		1			1
Tinker AFB	1	6		6	13
South Carolina					
Shaw AFB		2	2	2	6
JB Charleston (AF)		4			4
South Dakota					
Ellsworth AFB				1	1
Texas					
Ft Bliss		2			2
Laughlin AFB				1	1
SAMMC	5	9		8	22
Sheppard AFB		4		5	9
Utah					
Hill AFB		2		1	3
Virginia					
JB Langley-Eustis		5	1		6
Washington					
Fairchild AFB		1			1
NH Bremerton		5			5
Wyoming					
FE Warren AFB		4			4

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(Cont'd from page 12)

	A(H1N1) pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
OCONUS					
Belgium					
Shape AHC		1			1
Country 6					
Location A		2			2
Germany					
Landstuhl RMC	1	3		1	5
Ramstein AB		3			3
USAG Baumholder		1		1	2
USAG Grafenwoehr		2			2
USAG Stuttgart		2			2
USAG Wiesbaden		2			2
Vilseck AHC		2			2
Guam					
JR Marianas - Andersen AFB			1		1
Hawaii					
Tripler AMC		2			2
Italy					
NAS Sigonella		2			2
USAG Vicenza		6			6
Japan					
Yokota AB		4		1	5
South Korea					
Osan AB		1			1
Total	10	131	14	63	218

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.

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Influenza A(H1N1)pdm09

- Among the 141 influenza A isolates, 10 (7.1%) 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 current vaccine strain, A/California/07/2009-like virus (Figure 2).

- The A(H1N1)pdm09 isolates characterized for this report exhibited an overall protein homology of 96.2 – 97.1% (average 96.9%) compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus. In addition, overall protein homology of 98.9 – 99.8% (average 99.6%) was observed between the A(H1N1)pdm09 isolates and the 2017-2018 influenza vaccine component, A/Michigan/45/2015-like virus.

- 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 (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 mutations present in the A(H1N1)pdm09 isolates, six occurred at predicted antigenic sites (one at site A, one at site B, none at site C, two at site D, and two at site E) and two occurred at the receptor binding site.[2,5]

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

Current 2016-2017 A(H1N1)pdm09 Vaccine strain:
A/California/07/2009-like virus
2017-2018 A(H1N1) vaccine strain:
A/Michigan/45/2015-like virus
Reference Strain
January 2017
February 2017
March 2017
ADD GLY Create Glycosylation Motif
F – CDC Reference Antigen
wF – WHOcc Reference Antigen
SAg - Serology Antigen
wSAg – WHOcc Serology Antigen
e Egg Isolate

A/Texas/x544/2017 E258K
A/Texas/x551/2017 H126Y
A/Texas/x435/2017
A/Germany/x507/2017
A/Texas/x539/2017
A/Texas/x540/2017
A/NewYork/3651/2017
cnic A/Guangdong-Luohu/SWL1294/2016 Apr e wSAg
sing A/Singapore/GP1908/2015 Nov wSAg
2016 6B.1 Consensus Feb-Sep
A/Maryland/3721/2017 T474A
A/Valparaiso/43870/2016 Jun F
A/Maryland/3743/2017
G39E E235K
A/Oklahoma/3646/2017
A/Michigan/45/2015 Sep e wF F SAg wSAg
2016 6B.2 Consensus Feb-Sep
A/California/07/2009 Apr e F SAg wSAg

6B.1

P83S   K283E
D97N   I321V
K163Q E374K
S185T S451N
S203T E499K
A256T

S84N S162N ADD GLY I216T

R205K

S183P   I166V

0.0020

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Influenza A(H3N2)

- Among the 141 influenza A isolates, 131 (92.9%) 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 A(H3N2) isolates characterized for this report exhibited an overall protein homology of 97.1 – 99.1% (average 98.3%) compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014-like virus.

- All of the influenza A(H3N2) isolates sequenced for this report were in clade 3C with 17 (13.0%) in subclade 3C.3a and 114 (87.0%) in subclade 3C.2a. Seventy-three of the 114 3C.2a (64.0%) further classified as the newly distinguished subclade within 3C.2a, 3C.2a1 (determined by the mutations N171K, I406V, and G484E). The mutation N121K was present in 67 (91.8%) of the 3C.2a1 isolates and 76 (58.0%) of the total A(H3N2) isolates. The mutation T135K was present in 33 isolates (45.2% of 3C.2a1 and 41.8% of total).

- Among the influenza A(H3N2) isolates characterized in this report, nine mutations; T10M (threonine to methionine), N122D (asparagine to aspartic acid), T135K (threonine to lysine), N144K (asparagine to lysine), N144S (asparagine to serine), N158K (asparagine to lysine), T160K (threonine to lysine), T160A (threonine to alanine), and N246S (asparagine to serine) 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 78 mutations present in the A(H3N2) specimens, 25 occurred at predicted antigenic sites (six at site A, five at site B, three at site C, four at site D, and seven at site E) and three occurred at the receptor binding site.[2,5]

- Four of the sequenced A(H3N2) specimens were from hospitalized patients. Additionally, one specimen was isolated from an individual infected with both influenza A(H3N2) and influenza B/ Yamagata lineage (see B/Yamagata tree).

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

Current 2016-2017 A(H3N2) Vaccine strain:
A/Hong Kong/4801/2014-like virus
Reference Strain
January 2017
February 2017
March 2017
ADD GLY Create Glycosylation Motif
LOSS GLY Loss of Glycosylation Motif
F – CDC Reference Antigen
wF – WHOcc Reference Antigen
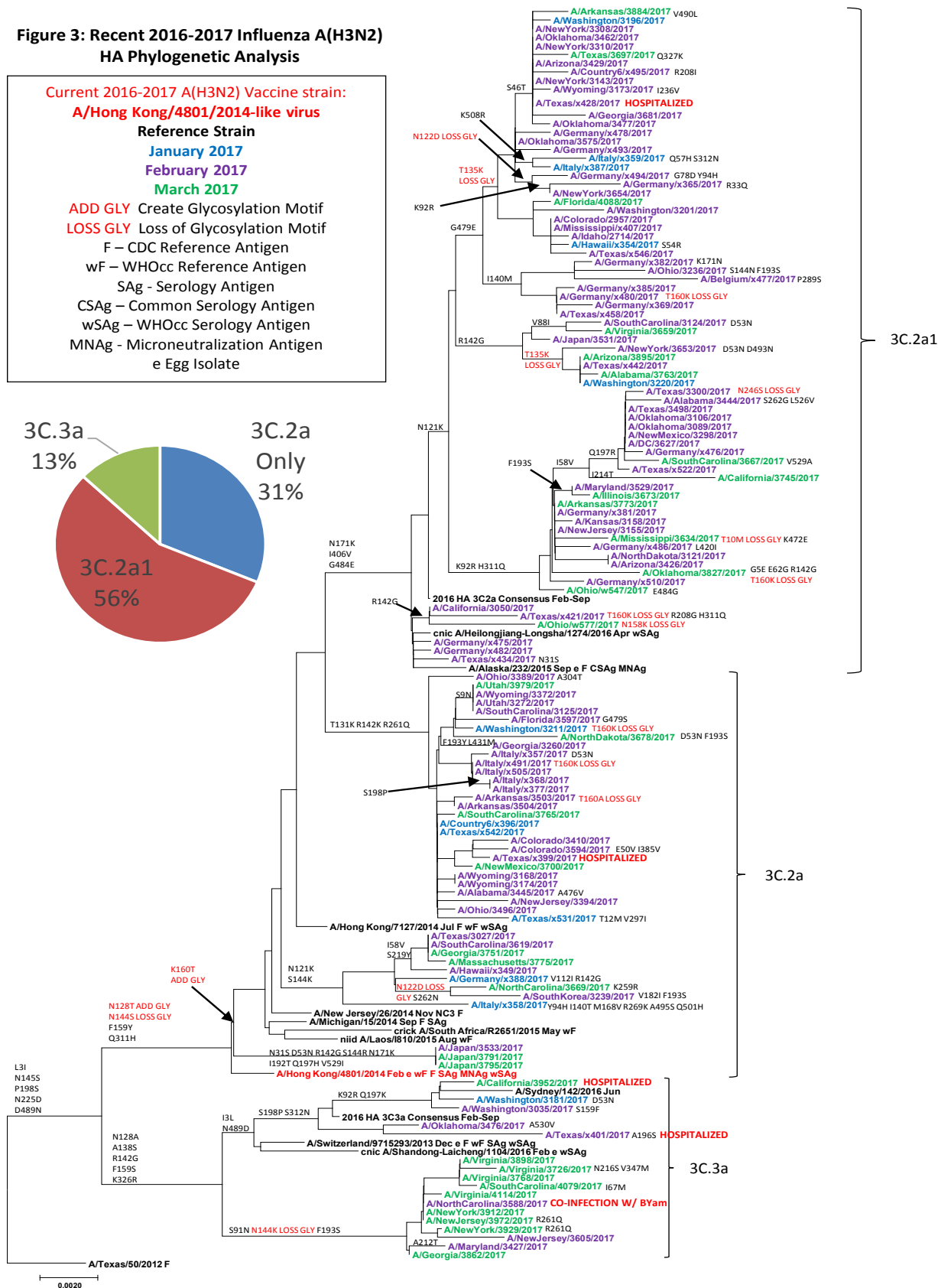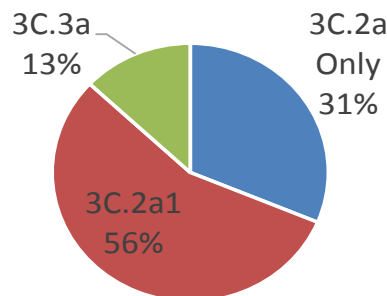SAg - Serology Antigen
CSAg – Common Serology Antigen
wSAg – WHOcc Serology Antigen
MNAg - Microneutralization Antigen
e Egg Isolate

3C.3a 13%
3C.2a Only 31%
3C.2a1 56%

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Influenza B

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains and are rooted from the reference strain B/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] Fourteen (18.2%) of the influenza B isolates characterized in this report fell into the B/Victoria lineage and 63 (81.8%) fell into the B/Yamagata lineage.

- Of interest, seven of the influenza B/Victoria isolate sequences contained a six base pair deletion causing a double amino acid deletion (positions 162-163), which fall in the same region as the single amino acid deletion at 162 observed in Yamagata lineage specimens.

- The influenza B/Victoria isolates characterized for this report exhibited a protein homology from 98.6 – 99.5% (average 99.0%) 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 98.9 – 99.3% (average 99.2%) 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 and for B/Yamagata, one mutation, D197N (aspartic acid to asparagine), adds a glycosylation motif.

- One specimen was isolated from an individual infected with both influenza A(H3N2) and influenza B/Yamagata lineage (see A(H3N2) tree).

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

Current 2016-2017 B/Victoria vaccine strain:
B/Brisbane/60/2008-like virus
Reference Strain
February 2017
March 2017
ADD GLY Create Glycosylation Motif
F – CDC Reference Antigen
SAg - Serology Antigen
wF – WHOcc Reference Antigen
wSAg – WHOcc Serology Antigen
e Egg Isolate
LR – Low Reactor to:
B/Brisbane/60/2008 (≥ 8 fold)

D129G
K162 Del
N163 Del

D527N

I180V
R498K

B/Georgia/3880/2017
B/Georgia/3871/2017
B/Georgia/3864/2017
B/Georgia/3456/2017
B/Georgia/3878/2017
B/Florida/3631/2017
B/Colorado/4086/2017   V117A
K162 Del
N163 Del
B/SouthCarolina/4075/2017

crick B/Ireland/3154/2016 Jan wF wSAg

V559I   B/Georgia/3879/2017
2016 B/Victoria HA Consensus Feb Sep
B/NewMexico/4106/2017
B/SouthCarolina/3622/2017

K48E   N165K
N75K   S172P   I117V
E80R   I190V
K129D   A199T ADD GLY
V146I   I555V

B/Virginia/4032/2017
K345R   B/Guam/3544/2017
D129G   B/Arizona/4053/2017
A202E
B/Zhejiang-Dinghai/1466/2016 Jun
B/Florida/78/2015 Nov F SAg
B/Indiana/25/2015 Apr F

V1A

B/Brisbane/60/2008 Aug e F

B/Ohio/01/2005 Feb e LR F

0.0050

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**Figure 5: Recent 2016-2017 Influenza B/Yamagata
HA Phylogenetic Analysis**

Current 2016-2017 B/Yamagata Vaccine strain:
B/Phuket/3073/2013-like virus
Reference Strain
January 2017
February 2017
March 2017
ADD GLY Create Glycosylation Motif
F – CDC Reference Antigen
wF – WHOcc Reference Antigen
SAg - Serology Antigen
wSAg – WHOcc Serology Antigen
e Egg Isolate

D126N
R279K

B/Oklahoma/3649/2017
B/SouthCarolina/3885/2017
B/Texas/4074/2017
B/Oklahoma/3854/2017
B/Texas/x519/2017
B/Texas/x518/2017
B/Oklahoma/3472/2017
B/NorthDakota/3814/2017
B/NorthDakota/3480/2017
B/NewYork/3437/2017
B/Texas/x543/2017

G184E

B/Texas/3738/2017
B/Texas/3794/2017
B/NewYork/3642/2017
B/NewYork/3937/2017
B/NewYork/3349/2017
B/NewYork/3938/2017   G184E
B/NewYork/3637/2017
B/NewYork/3639/2017
B/NewYork/3661/2017
B/NewYork/3679/2017   I150L
B/NewYork/3931/2017
B/Utah/4115/2017
B/Georgia/3866/2017   G256E
B/Kansas/4043/2017
B/Oklahoma/3573/2017
B/Ohio/w497/2017
B/Ohio/3540/2017
B/DC/3401/2017

L269F

B/Germany/x476/2017   A541V
B/NorthCarolina/3588/2017   CO-INFECTION W/ H3N2
B/Ohio/w503/2017
B/NorthDakota/3997/2017   G256E
B/Florida/3563/2017   HOSPITALIZED
B/Texas/x523/2017
B/Texas/x533/2017
B/Texas/x425/2017
B/SouthDakota/3692/2017
B/Kansas/3629/2017   A276V
B/Montana/3764/2017
B/Mississippi/x410/2017
B/Oklahoma/3808/2017
B/Montana/3590/2017
B/Texas/3512/2017
B/Ohio/3551/2017
B/Ohio/w533/2017
B/Japan/4062/2017
vidrl B/South Auckland/14/2016 Jul wSAg
B/Colorado/4084/2017
B/Colorado/3593/2017
B/Colorado/3965/2017
B/Delaware/3797/2017
B/NewYork/3440/2017

N505D

B/Texas/3954/2017
B/Texas/4040/2017
B/Texas/x520/2017
B/Georgia/3264/2017
B/Georgia/3583/2017
B/Germany/x509/2017   I150T P339A
B/Mississippi/x417/2017

L173Q
D197N
ADD GLY
M252V

2016 B/Yamagata HA Consensus Feb Sep
B/Florida/3468/2017
B/California/12/2015 Feb F
B/Texas/x521/2017

K48R
A108P
S150I
N166Y
A182T
N203S
G230D

N116K
K299E
E313K

V177I K212R

B/Oklahoma/3856/2017
B/SouthCarolina/3323/2017
B/Phuket/3073/2013 Nov e F wF SAg wSAg
B/Wisconsin/01/2010 Feb e F wF

B/Massachusetts/02/2012 Mar e F wF

Y3

0.0050

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DoD Global, Laboratory-Based, Influenza 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 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.
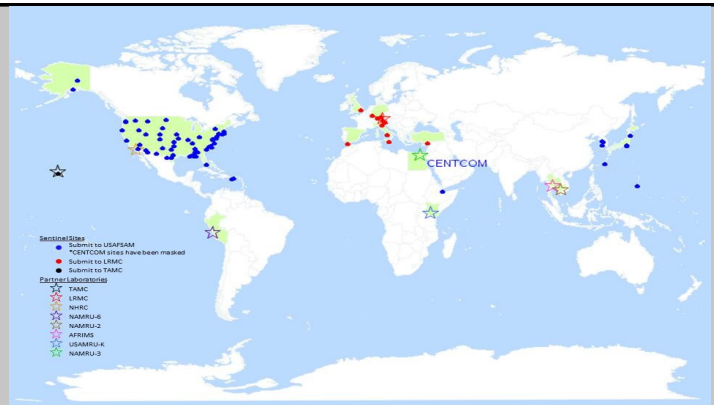
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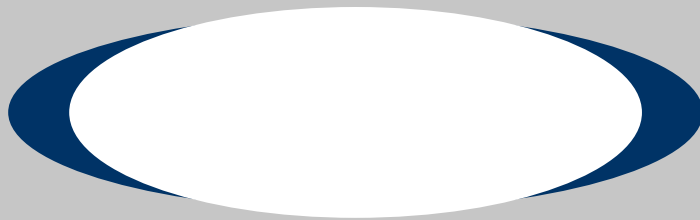
For Public Health Services
937-938-3196; DSN 798-3196

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.

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