Cumulative Results

Locations	80
Collected	5,016
Tested	4,950

Influenza A	**1,362**
A(H1N1)pdm09	23
A(H1N1)pdm09 & Influenza B	1
A(H3N2)	1,331
A(H3N2) & Influenza B	3
A(H3N2) & Coronavirus & RSV	1
A(H3N2) & RSV	1
A/not subtyped	1
A/not subtyped & Rhino/Enterovirus	1

Influenza B*	**412**
B	411
B & Human Metapneumovirus & Rhino/Enterovirus	1

Other Respiratory Pathogens	**1,048**
Adenovirus	66
Bordetella pertussis	0
Chlamydophila pneumoniae	5
Coronavirus	118
Human Metapneumovirus	89
Mycoplasma pneumoniae	37
Parainfluenza	170
RSV	171
Rhinovirus/Enterovirus	259
Non-influenza Viral Coinfections	125
Non-influenza Bacterial Coinfections	8
-M. pneumo coinfections *(8)*	

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

Respiratory Highlights
9 - 22 April 2017 (Surveillance Weeks 15 & 16)

- During 9 - 22 April 2017, a total of 192 specimens were collected and received from 38 locations. Results were finalized for 181 specimens from 37 locations. During Week 15, 20 influenza A(H3N2), one influenza A(H3N2) & coronavirus & RSV coinfection, and 20 influenza B viruses were identified. During Week 16, two influenza A(H3N2) and 11 influenza B viruses were identified. Approximately 31% of specimens tested positive for influenza during Week 15. Approximately 23% of specimens tested positive for influenza during Week 16. The influenza percent positive for the season is currently 36%.

- According to CDC FluView, during Week 15 influenza activity decreased in the United States. The proportion of outpatient visits for influenza-like illness was below the national baseline for the first time since peak season. Five influenza pediatric deaths were reported in Week 15. (CDC, Flu View Report Week 15, cited 25 April 2017).

- A recent study found that host defense peptides from the skin of South Indian frogs contain "urumin", which was found to specifically target the conserved stalk region of H1 hemagglutinin and was effective against drug-resistant H1 influenza viruses. Current antiviral drugs are susceptible to drug resistance, and developing antivirals are essential, especially during pandemics when there is insufficient time to produce vaccines. This study showed the peptide physically destroyed the influenza virions and also protected naïve mice from lethal influenza infection. Urumin therefore has the potential to contribute to first-line antiviral treatments during influenza outbreaks. ("An Amphibian Host Defense Peptide is Virucidal for Human H1 Hemagglutinin-Bearing Influenza Viruses", Holthausen et al., 2017, Immunity 46, 587-595 April 18, 2017. http://dx.doi.org/10.1016/j.immuni.2017.03.018)

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

**Table 1.** Finalized results by region and location for specimens collected during Weeks 15 & 16

Region*		A(H3N2)	A(H3N2) & Corona & RSV	B	Adenovirus	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Rhino/Entero	Corona & Rhino/Entero	Para & Rhino/Entero	No Pathogen	Total
PACOM	CFA Okinawa, Japan	1	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Eielson AFB, AK	1	-	-	-	-	-	-	-	-	-	1	-	-	-	2
	Yokota AB, Japan	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
Region 2	Ft Drum, NY	2	-	6	-	1	2	-	2	-	4	-	-	-	9	26
	USMA - West Point, NY	-	-	2	-	-	1	-	-	1	1	1	-	-	8	14
Region 3	Dover AFB, DE	1	-	1	-	-	-	-	-	-	1	-	-	-	2	5
	JB Andrews, MD	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	JB Langley-Eustis, VA	-	-	4	-	-	-	-	-	-	2	-	-	-	3	9
Region 4	Columbus AFB, MS	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Eglin AFB, FL	-	-	-	-	-	1	-	-	-	1	-	-	-	2	4
	Ft Bragg, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Hurlburt Field, FL	1	-	-	-	-	-	-	-	-	1	-	-	-	3	5
	Keesler AFB, MS	1	1	-	-	-	1	-	-	-	-	-	-	-	1	4
	Maxwell AFB, AL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Moody AFB, GA	4	-	2	-	-	1	1	2	-	2	-	-	-	4	16
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	1	-	1	-	-	-	-	-	-	1	-	-	-	-	3
	Seymour Johnson AFB, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Shaw AFB, SC	3	-	2	-	1	-	-	1	-	4	-	1	-	9	21
	Tyndall AFB, FL	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 5	Wright-Patterson AFB, OH	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
Region 6	Altus AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Cannon AFB, NM	-	-	-	-	-	-	-	1	-	-	-	-	-	2	3
	Sheppard AFB, TX	-	-	-	-	-	1	1	-	-	-	-	-	-	1	3
	Tinker AFB, OK	-	-	2	-	-	-	-	-	-	1	-	-	-	1	4
Region 7	McConnell AFB, KS	-	-	1	-	-	-	-	1	-	3	-	-	-	1	6
	Offutt AFB, NE	-	-	1	-	1	1	-	-	-	-	-	-	-	1	4
Region 8	Ellsworth AFB, SD	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	FE Warren AFB, WY	-	-	3	-	-	-	-	-	-	-	-	-	-	-	3
	Hill AFB, UT	1	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	Minot AFB, ND	2	-	1	-	1	1	-	-	1	1	-	-	-	6	13
	Peterson AFB, CO	-	-	1	-	-	-	-	-	-	-	-	-	-	1	2
Region 9	Davis-Monthan AFB, AZ	-	-	1	-	-	2	-	-	-	-	-	-	-	2	5
	Luke AFB, AZ	-	-	1	-	-	-	-	-	-	-	-	-	-	1	2
	Travis AFB, CA	1	-	1	1	-	-	-	-	-	-	-	2	-	1	7
Region 10	Fairchild AFB, WA	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Total		22	1	31	1	4	12	2	7	2	24	2	1	1	71	181

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

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

Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2015-2016 surveillance year and through Week 16 of the 2016-2017 surveillance year

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

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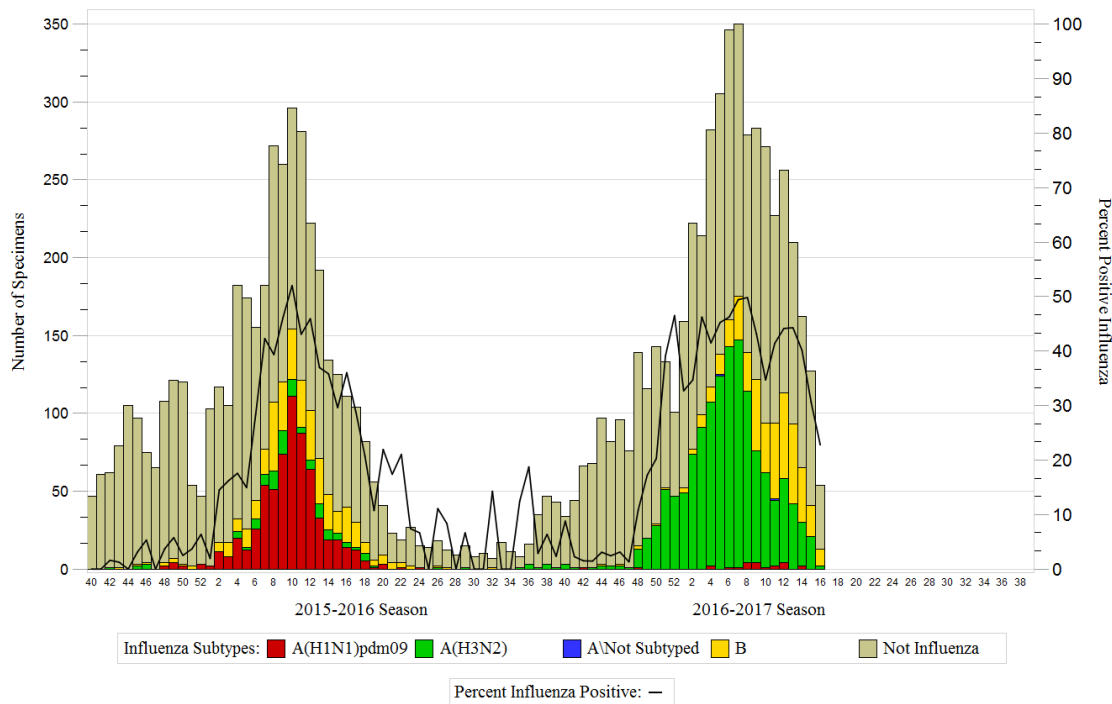
Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

Table 2. ILI by age group for the 2016-2017 surveillance year through Week 16

Age Group	Frequency	Percent
0-5	1121	22.65
6-9	464	9.37
10-17	603	12.18
18-24	670	13.54
25-44	1510	30.50
45-64	481	9.72
65+	101	2.04

Demographic Summary

Of 4,950 ILI cases, 1,714 are service members (34.7%), 2,181 are children (44.1%), 692 are spouses (13.9%), and 363 (7.3%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=4,950) is 21 (range 0, 96).

Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 16

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

3
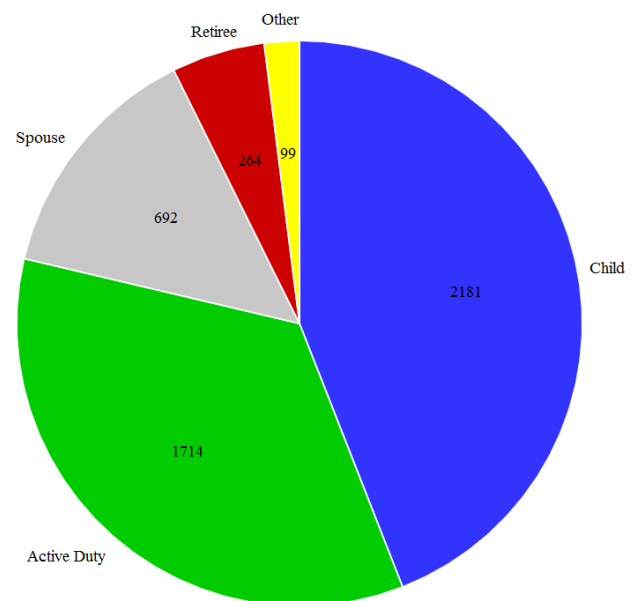
Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 16
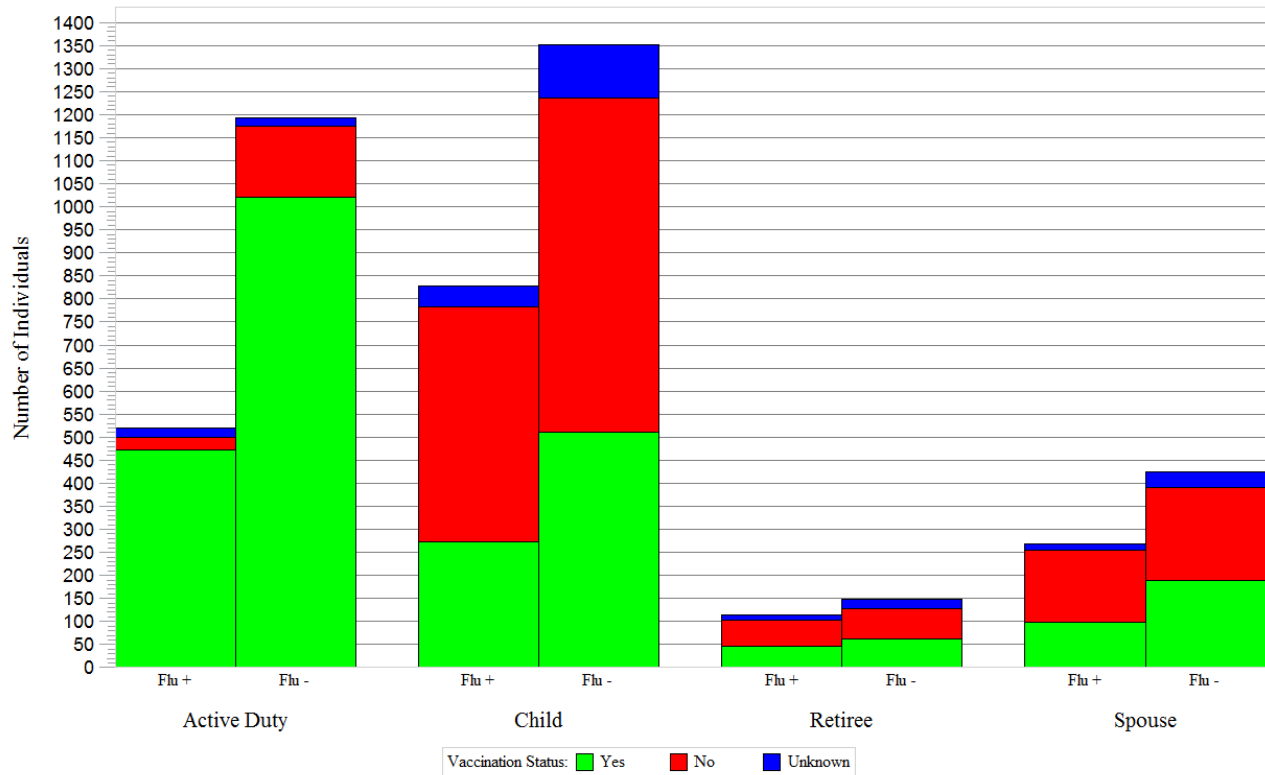
Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 16

HI - Region 9

PR - Region 2

AK - Region 10
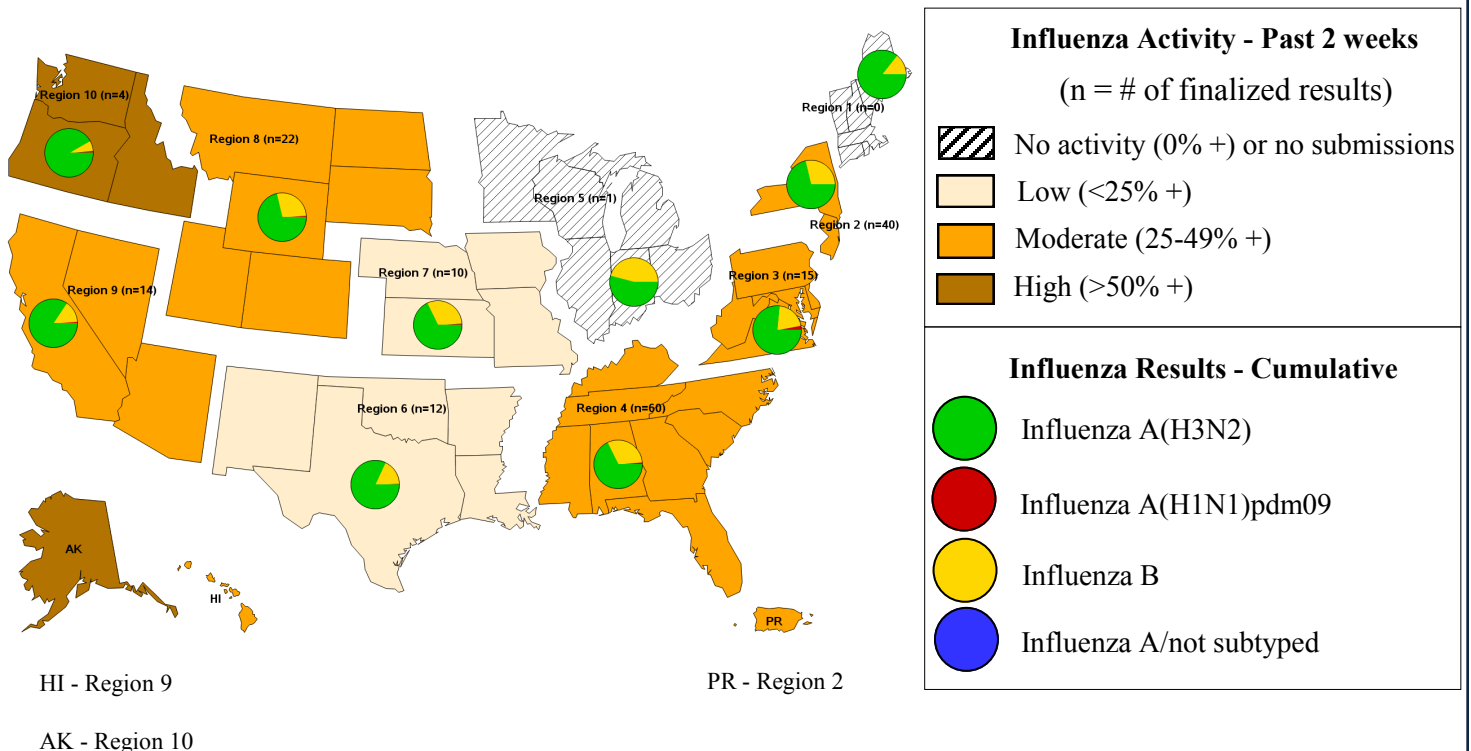
Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 16 (Pacific)
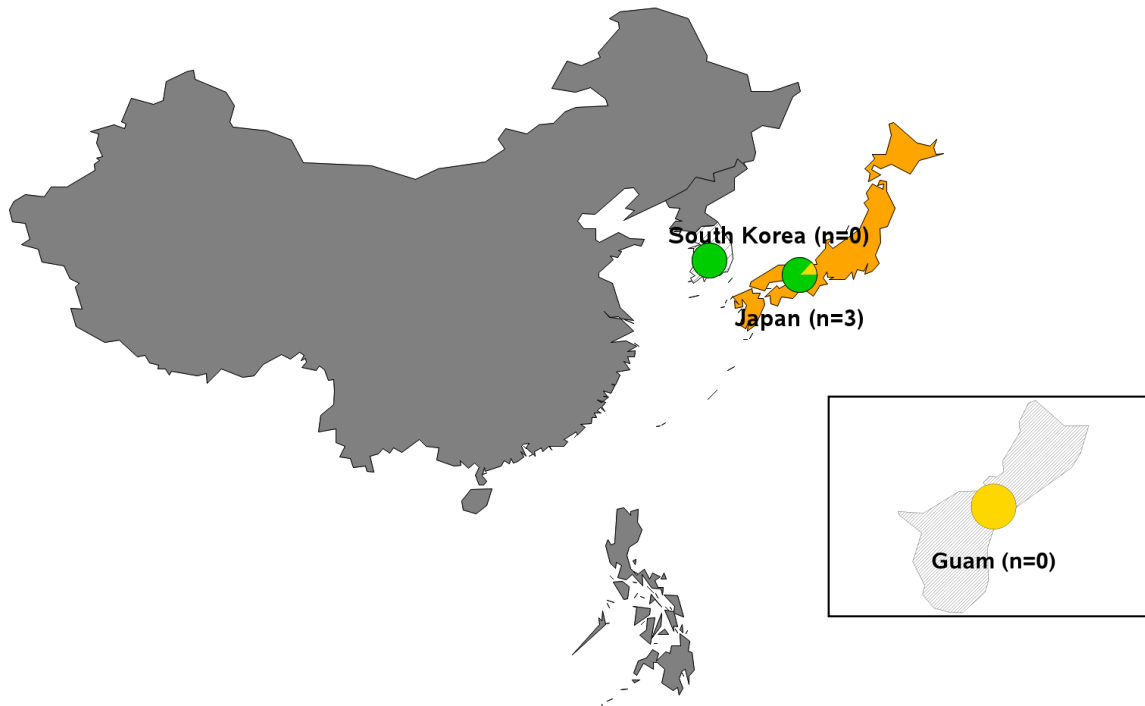
Note - Countries shaded in gray do not contain sentinel sites and are only displayed for geographical perspective.

Map 3. Influenza subtypes and activity level for CENTCOM for the 2016-2017 surveillance year through Week 16

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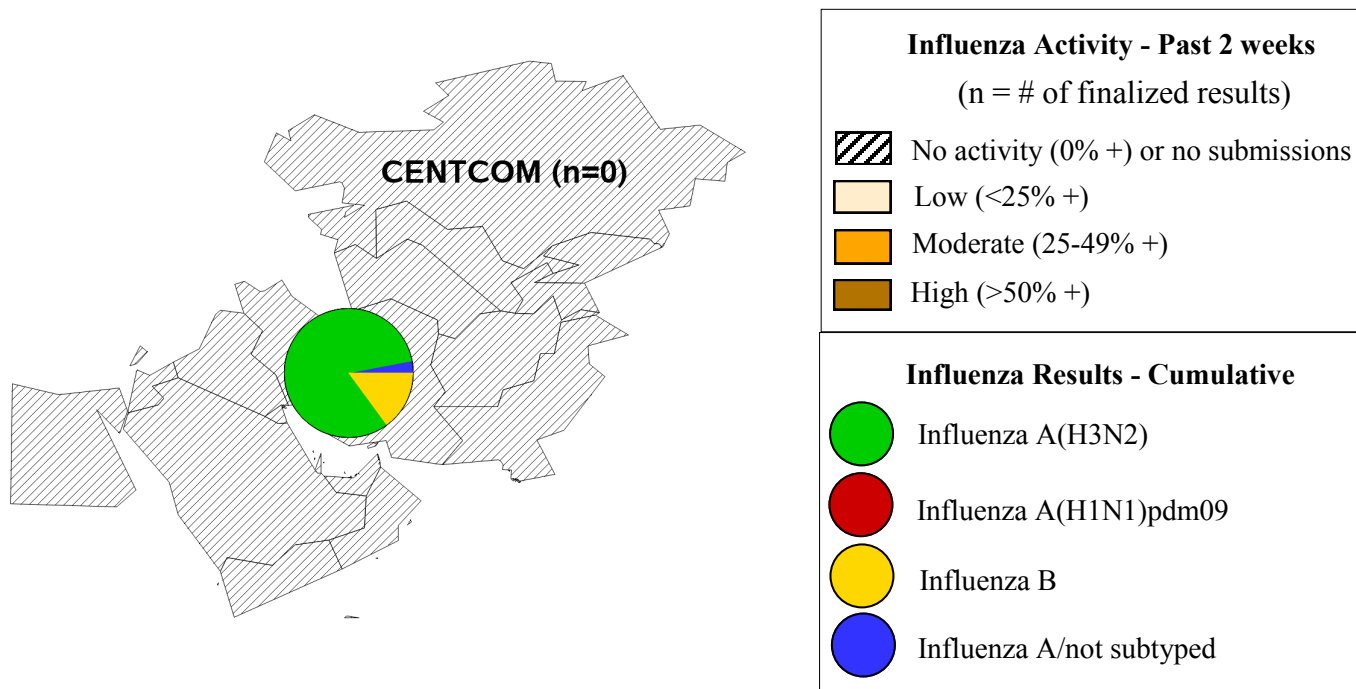
Note - Specimens for CENTCOM were tested at USAFSAM or Landstuhl Regional Medical Center (LRMC).

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

Laboratory Results—Through Current Surveillance Week 16

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/not subtyped & Rhino/Entero	A(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	B	B & hMNV & Rhino/Entero	Adenovirus	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	-	-	3	5
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-	4	6
	Kadena AB, Japan	-	4	-	-	-	-	-	-	-	-	-	-	1	-	-	3	2	-	1	1	23	35
	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	-	35	-	-	-	-	-	-	6	-	1	-	3	2	2	2	2	9	4	-	63	129
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	-	-	60	-	5	1	5	10	1	9	8	6	5	-	88	249
	JB McGuire-Dix-Lakehurst, NJ	-	54	-	-	-	-	-	-	1	-	3	-	6	9	2	9	6	12	5	-	80	187
	USMA - West Point, NY	-	86	-	-	-	-	-	-	15	-	11	-	5	7	2	10	13	9	6	-	145	309
Region 3	Dover AFB, DE	-	18	-	-	-	-	-	-	10	-	2	-	1	1	1	-	1	3	-	-	47	84
	JB Anacostia-Bolling, DC	-	14	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	1	-	-	-	19
	JB Andrews, MD	2	23	-	-	-	-	-	-	12	-	-	-	2	1	-	3	2	1	2	-	40	88
	JB Langley-Eustis, VA	6	149	-	-	1	1	-	-	30	-	1	-	3	10	2	11	20	35	10	-	256	535
	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	-	-	17	26
	Eglin AFB, FL	1	15	-	-	-	-	-	-	4	-	7	-	2	1	2	1	5	10	6	-	39	93
	Ft Bragg, NC	1	8	-	-	-	-	-	-	5	-	-	-	1	1	1	3	2	6	4	3	36	71
	Ft Campbell, KY	1	15	-	-	-	-	-	-	9	-	1	2	1	-	-	3	-	-	4	-	17	53
	Hurlburt Field, FL	-	18	-	-	-	-	-	-	5	-	1	-	1	-	1	1	2	2	-	-	26	57
	JB Charleston (AF), SC	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	17
	Keesler AFB, MS	-	2	-	-	-	1	-	-	-	-	-	-	1	-	1	2	2	2	-	-	15	26
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	6	7
	Maxwell AFB, AL	-	10	-	-	-	-	-	-	2	-	-	-	1	-	-	2	-	1	-	-	14	30
	Moody AFB, GA	-	32	-	-	-	-	-	-	36	-	1	-	2	7	1	11	7	12	14	1	76	200
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	NH Camp Lejeune, NC	-	2	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	1	-	8	13
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	24	-	-	-	-	-	-	8	-	-	-	-	-	2	-	3	2	-	-	22	61
	Seymour Johnson AFB, NC	3	16	-	-	-	-	-	-	1	-	2	-	-	1	1	2	1	-	-	-	19	46
	Shaw AFB, SC	-	69	-	-	-	-	-	-	34	-	1	1	7	5	1	4	1	10	2	-	58	193
	Tyndall AFB, FL	-	11	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	16

(Cont'd on page 7)

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

Laboratory Results—Through Current Surveillance Week 16

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

(Cont'd from page 6)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A/not subtyped & Rhino/Entero	A(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	B	B & hMNV & Rhino/Entero	Adenovirus	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	7	20
	Wright-Patterson AFB, OH	-	10	-	-	-	-	-	-	8	-	-	-	1	1	1	1	-	2	2	-	35	61
Region 6	Altus AFB, OK	-	7	-	-	-	-	-	-	1	-	1	-	1	1	-	1	5	7	4	-	39	67
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	2	-	1	-	-	8	12
	Cannon AFB, NM	-	13	-	-	-	-	-	-	4	-	-	-	2	-	1	2	-	4	1	-	37	64
	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	4	1	6	2	8	-	-	82	182
	Tinker AFB, OK	1	97	-	-	-	-	-	1	25	-	2	-	9	3	1	9	6	10	6	-	135	305
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	12
Region 7	McConnell AFB, KS	-	25	-	-	-	-	-	-	18	-	1	-	4	-	1	4	5	9	3	-	35	105
	Offutt AFB, NE	1	32	-	-	-	-	-	-	8	-	1	-	6	2	-	1	1	7	1	-	55	115
Region 8	Ellsworth AFB, SD	-	14	-	-	-	-	-	-	13	-	-	-	3	-	-	3	1	3	-	-	35	72
	FE Warren AFB, WY	-	35	-	-	-	-	-	-	5	-	3	-	4	-	2	4	6	4	-	-	50	113
	Hill AFB, UT	-	30	-	-	-	-	-	-	2	-	-	-	3	1	-	5	4	4	2	-	41	92
	Malmstrom AFB, MT	-	7	-	-	-	-	-	-	3	-	-	-	-	-	1	-	-	1	-	-	8	20
	Minot AFB, ND	1	24	-	-	-	-	-	-	15	-	-	-	3	2	1	1	6	5	3	-	46	107
	Peterson AFB, CO	1	19	-	-	-	-	-	-	12	-	-	-	3	-	-	3	9	3	4	-	26	80
	USAF Academy, CO	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	1	-	-	2	6
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	-	14	-	-	-	-	-	-	3	-	-	-	-	2	-	5	1	6	5	-	33	69
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	-	-	4	-	1	-	2	-	-	3	1	1	-	-	15	27
	Nellis AFB, NV	1	3	-	-	-	-	-	-	3	-	3	-	1	-	-	4	4	5	7	-	32	63
	Travis AFB, CA	-	58	-	-	-	-	-	-	4	-	1	1	6	7	-	6	13	15	5	-	39	155
	Vandenberg AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Fairchild AFB, WA	2	16	-	-	-	-	-	-	2	-	3	-	3	-	-	5	2	4	-	-	46	83
	JB Lewis-McChord, WA	-	2	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	3
	Mt Home AFB, ID	-	23	-	-	-	-	-	-	1	-	1	1	1	-	1	23	12	12	5	-	74	154
	NH Bremerton, WA	-	67	-	-	-	-	-	-	5	-	8	1	3	1	2	8	7	7	4	-	27	140
Total		23	1331	1	1	1	3	1	1	411	1	66	5	118	89	37	170	171	259	125	8	2128	4950

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

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

Molecular Sequence Analysis Report #8

This is the eighth USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 61 influenza specimens collected between 25 December 2016 and 10 February 2017. Fifty-six of these specimens were influenza A(H3N2) and five were influenza B/Yamagata lineage. All influenza positive specimens were sequenced at USAFSAM. Figure 1 shows the distribution of A(H3N2) and B/Yamagata specimens by US Combatant Command. The number of sequences in this report are shown for each sentinel site in Table 1. Figures 2 and 3 display the phylogenetic relationships among HA sequences for the influenza A(H3N2) and B/Yamagata specimens, respectively.

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

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

8
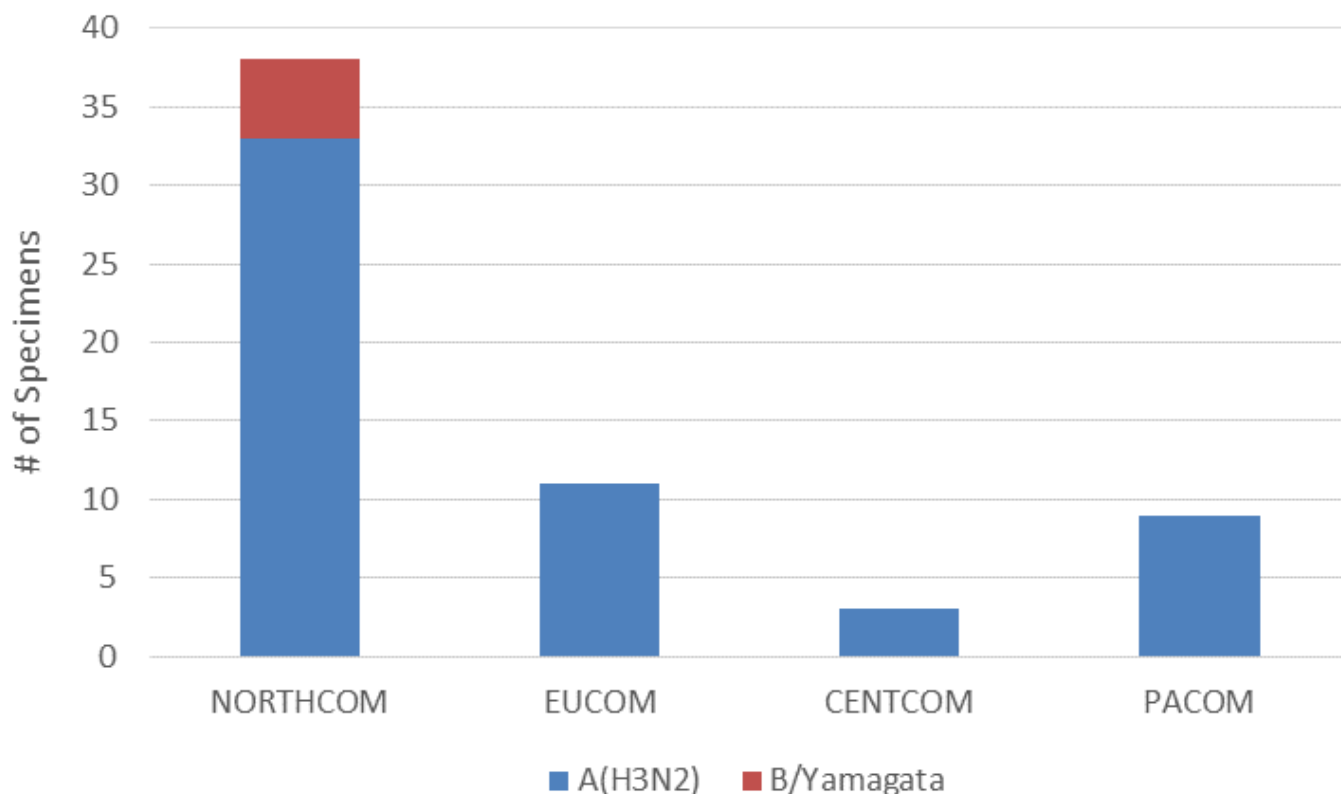
Table 1: Distribution of CONUS and OCONUS sentinel sites that contributed influenza A(H3N2) and B/Yamagata specimens for this report.

	A(H3N2)	B/Yamagata
CONUS		
Alabama		
Maxwell AFB	1	
California		
Travis AFB	1	
Colorado		
Peterson AFB	2	1
Connecticut		
USCG Academy	1	
Florida		
Eglin AFB	1	
Georgia		
Robins AFB	3	
Moody AFB		1
Kansas		
McConnell AFB	1	
Kentucky		
Ft Campbell	1	
Louisiana		
Ft Polk	1	
Maryland		
JB Andrews	1	
Montana		
Malmstrom AFB	1	
Nebraska		
Offutt AFB	2	
New York		
USMA - West Point	1	
Ft Drum	1	1
North Carolina		
Seymour Johnson AFB	1	1
North Dakota		
Minot AFB	2	1
Ohio		
Wright-Patterson AFB	1	
Oklahoma		
Tinker AFB	4	

	A(H3N2)	B/Yamagata
South Carolina		
JB Charleston (AF)	1	
South Dakota		
Ellsworth AFB	1	
Texas		
Sheppard AFB	2	
Utah		
Hill AFB	2	
Virginia		
JB Langley-Eustis	1	
OCONUS		
Country 1		
Location B	1	
Country 2		
Location A	2	
Germany		
Landstuhl RMC	6	
Hawaii		
Tripler AMC	9	
Italy		
NSA Naples	1	
USAG Vicenza	4	
Grand Total	**56**	**5**

The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously published experimental evidence.[1,3,4] Sequence data was constructed and analyzed using multiple software programs. Genetic and predicted antigenic information that resulted from this analysis is shared with United States Centers for Disease Control and Prevention (CDC), World Health Organization (WHO) and contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

Influenza A(H3N2**)**

- Among the 56 influenza A isolates, all 56 (100.0%) 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 2).

- The A(H3N2) isolates characterized for this report exhibited an overall protein homology of 97.1-98.9% (average 98.4%) 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 three (5.4%) in subclade 3C.3a and 53 (94.6%) in subclade 3C.2a. Twenty-nine of the 53 3C.2a (54.7%) 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 28 (96.6%) of the 3C.2a1 isolates and 40 (71.4%) of the total A(H3N2) isolates. The mutation T135K was present in 11 isolates (37.9% of 3C.2a1 and 19.6% of total) and the combination of mutations R142G and I242V were present in one isolate (3.4% of 3C.2a1 and 1.8% of total).

- Among the influenza A(H3N2) isolates characterized in this report, six mutations; N122D (asparagine to aspartic acid), T135K (threonine to lysine), N144K (asparagine to lysine), N144S (asparagine to serine), T160K (threonine to lysine), and N246S (asparagine to serine) were observed that could cause the loss of a glycosylation motif. Three other mutations, N128T (asparagine to threonine), S144N (serine to asparagine), and K160T (lysine to threonine), were observed that could cause the gain of a glycosylation motif.

- Of the 53 mutations present in the A(H3N2) specimens, 19 occurred at predicted antigenic sites (five at site A, four at site B, two at site C, two at site D, and six at site E) and three occurred at the receptor binding site.[2,5]

- One specimen, A/California/1207/2016, was collected from a hospitalized patient. This patient was unvaccinated and presented with a cough, a fever of 103.2°F, and pneumonia.
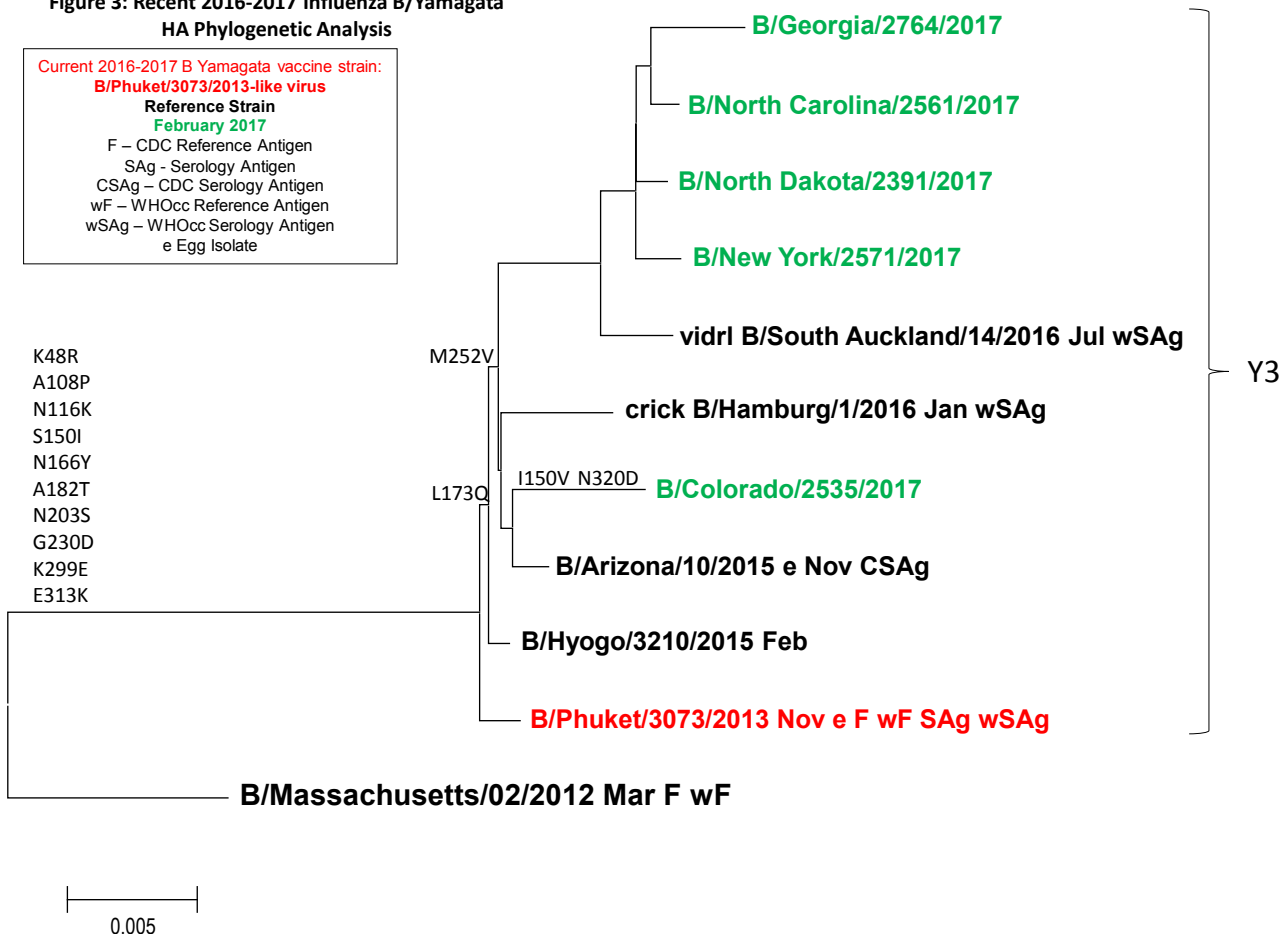
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10

**Figure 2: 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
December 2016
January 2017
February 2017
ADD GLY Create Glycosylation Motif
LOSS GLY Loss of Glycosylation Motif
F – CDC Reference Antigen
wF – WHOcc Reference Antigen
SAg - Serology Antigen
wSAg – WHOcc Serology Antigen
MNAg - Microneutralization Antigen
e Egg Isolate

A(H3N2) Clade Proportions

3C.3a 5.4%

3C.2a1 51.8%

3C.2a Only 42.9%

Influenza B

- All of the influenza B isolates fell into the Yamagata lineage and are characterized in a lineage specific, neighbor-joining phylogenetic tree with reference strains and rooted from the reference strain B/Massachusetts/02/2012-like virus (Figure 3).

- 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/Yamagata isolates fell into clade Y3. No changes in glycosylation motif states were observed.

Figure 3: Recent 2016-2017 Influenza B/Yamagata HA Phylogenetic Analysis

Current 2016-2017 B Yamagata vaccine strain:
B/Phuket/3073/2013-like virus
Reference Strain
February 2017
F – CDC Reference Antigen
SAg - Serology Antigen
CSAg – CDC Serology Antigen
wF – WHOcc Reference Antigen
wSAg – WHOcc Serology Antigen
e Egg Isolate

K48R
A108P
N116K
S150I
N166Y
A182T
N203S
G230D
K299E
E313K

M252V

L173Q

I150V N320D

B/Georgia/2764/2017

B/North Carolina/2561/2017

B/North Dakota/2391/2017

B/New York/2571/2017

vidrl B/South Auckland/14/2016 Jul wSAg

crick B/Hamburg/1/2016 Jan wSAg

B/Colorado/2535/2017

B/Arizona/10/2015 e Nov CSAg

B/Hyogo/3210/2015 Feb

B/Phuket/3073/2013 Nov e F wF SAg wSAg

B/Massachusetts/02/2012 Mar F wF

Y3

0.005

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

12

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

13

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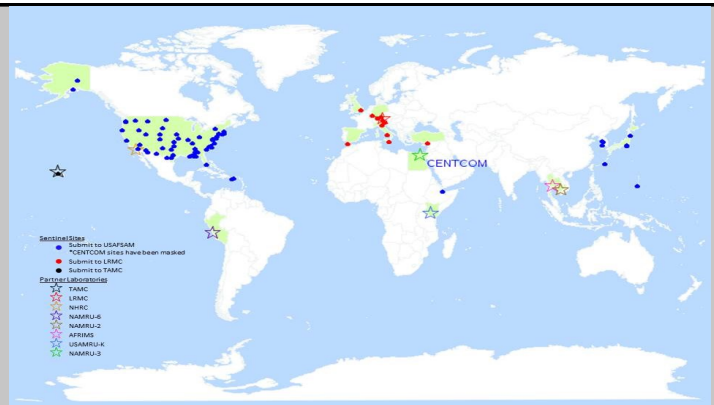
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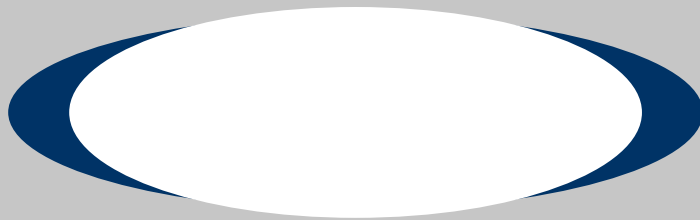
For Public Health Services
937-938-3196; DSN 798-3196

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

USAFSAM.PHRFlu@us.af.mil

Sentinel Sites
• Submit to USAFSAM
  *CENTCOM sites have been masked
• Submit to LRMC
• Submit to TAMC
Partner Laboratories
☆ TAMC
☆ LRMC
☆ NHRC
☆ NAMRU-6
☆ NAMRU-2
☆ AFRIMS
☆ USAMRU-K
☆ NAMRU-3

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.

14