



Cumulative Results

Locations	80
Collected	5,169
Tested	5,098

Influenza A 1,371

A(H1N1)pdm09	24
A(H1N1)pdm09 & Influenza B	1
A(H3N2)	1,339
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* 436

B	435
B & Human Metapneumovirus & Rhino/Enterovirus	1

Other Respiratory Pathogens 1,089

Adenovirus	69
<i>Bordetella pertussis</i>	0
<i>Chlamydia pneumoniae</i>	5
Coronavirus	121
Human Metapneumovirus	91
<i>Mycoplasma pneumoniae</i>	37
Parainfluenza	179
RSV	174
Rhinovirus/Enterovirus	276
Non-influenza Viral Coinfections	129
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

30 April - 13 May 2017 (Surveillance Weeks 18 & 19)

- During 30 April - 13 May 2017, a total of 67 specimens were collected and received from 25 locations. Results were finalized for 54 specimens from 21 locations. During Week 18, one influenza A(H1N1)pdm09, one influenza A(H3N2), and nine influenza B viruses were identified. No influenza viruses were detected during Week 19. Approximately 21% of specimens tested positive for influenza during Week 18 and 0% during Week 19. The influenza percent positive for the season is currently 35%.
- Included in this report is the ninth USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 73 influenza specimens collected between 01 January 2017 and 22 February 2017. Five of these specimens were influenza A(H1N1), 56 were influenza A(H3N2), three were influenza B/Victoria lineage, and nine were influenza B/Yamagata lineage. All influenza positive specimens were sequenced at USAFSAM.
- Avian influenza outbreaks continue to occur throughout Asia, with highly pathogenic H5N1 outbreaks in poultry in Vietnam and H5N8 outbreaks in Russia and South Korea. Human infection with avian strains also continues to be a concern in China, where the second case of H9N2 infection was detected in a 32-year-old man in Beijing this year. Nineteen cases of human infection with H7N9 have also been reported in Beijing this year. (CIDRAP, [News Scan for May 15, 2017](#) & [Flu Scan for May 16, 2017](#), cited 17 May 2017)
- Influenza activity in the Southern Hemisphere has started to pick up, with some countries having reached or surpassed seasonal thresholds. Chile reported increased ILI activity and Bolivia reported an increase in influenza in recent weeks with influenza A(H3N2) predominating. (WHO, [Influenza Update - 289](#), cited 17 May 2017)

Table of Contents

Respiratory Highlights	Page 1
Results by Region and Location for Specimens Collected during Weeks 18-19	Page 2
Laboratory Results - Cumulative for Season and Demographic Summary	Page 3
Vaccination Status by Beneficiary Type and Service	Page 4
Geographic Distribution of Influenza Subtype and Activity Level Maps	Pages 4 & 5
Cumulative Results by Region and Location	Pages 6 & 7
Molecular Sequence Analysis Report #9	Pages 8-16
DoD Global, Laboratory-Based, Influenza Surveillance Program Background	Page 17

DoD Global, Laboratory-Based, Influenza Surveillance Program

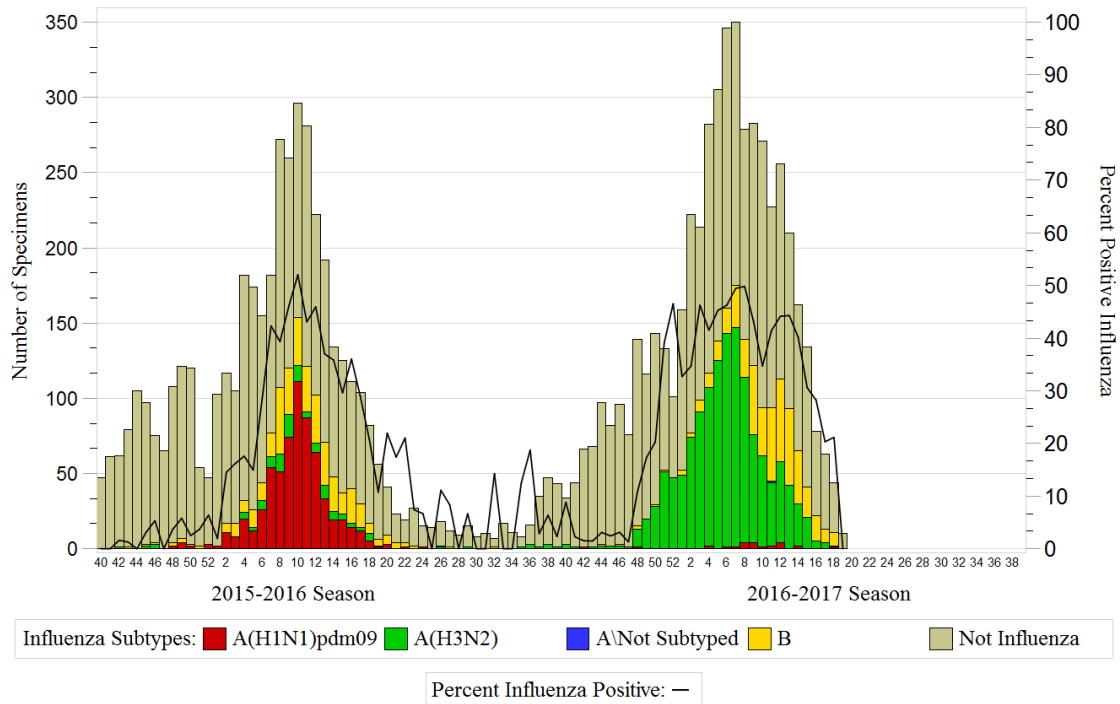
Table 1. Finalized results by region and location for specimens collected during Weeks 18 & 19

Region *		A(H1N1)pdm09	A(H3N2)	B	Adenovirus	Coronavirus	hMPV	Parainfluenza	Rhinovirus/Enterovirus	Adeno & Rhino/Entero	No Pathogen	Total
PACOM	Yokota AB, Japan	-	-	-	-	-	-	1	-	-	1	2
Region 2	Ft Drum, NY	-	-	-	-	-	-	-	1	-	2	3
	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	-	-	-	-	1	1
	USMA - West Point, NY	-	-	-	1	-	-	-	-	1	1	3
Region 3	Dover AFB, DE	-	-	-	-	1	-	-	1	-	1	3
	JB Langley-Eustis, VA	-	-	1	-	-	-	-	2	-	2	5
Region 4	Ft Bragg, NC	-	-	-	-	-	-	-	1	-	1	2
	Hurlburt Field, FL	-	-	-	1	-	-	-	-	1	-	2
	Keesler AFB, MS	-	-	-	-	-	-	-	1	-	-	1
	Moody AFB, GA	-	-	3	-	-	-	1	1	-	3	8
	Robins AFB, GA	-	-	-	-	-	-	-	-	-	1	1
	Shaw AFB, SC	-	-	-	-	-	-	-	-	-	2	2
Region 5	Wright-Patterson AFB, OH	-	-	2	-	-	-	-	-	-	1	3
Region 6	Cannon AFB, NM	-	-	-	-	-	-	1	-	-	1	2
	Sheppard AFB, TX	-	-	-	-	-	1	-	-	-	2	3
	Tinker AFB, OK	-	-	-	-	1	1	-	-	-	-	2
Region 7	Offutt AFB, NE	-	-	1	-	-	-	-	-	-	-	1
Region 8	FE Warren AFB, WY	-	-	1	-	-	1	-	-	-	1	3
Region 9	Davis-Monthan AFB, AZ	1	1	-	-	-	-	-	-	-	1	3
	Luke AFB, AZ	-	-	-	-	-	-	1	-	-	-	1
	Travis AFB, CA	-	-	1	-	-	-	-	-	-	2	3
Total		1	1	9	2	2	3	4	7	2	23	54

*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 19 of the 2016-2017 surveillance year



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.

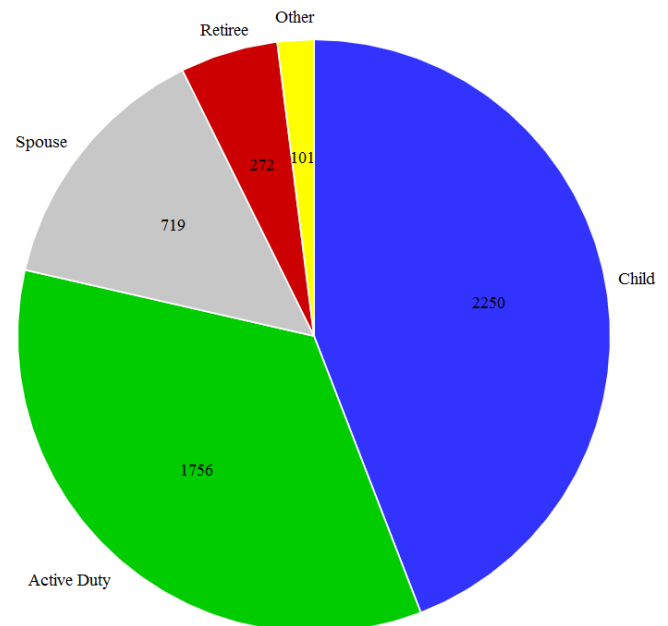
Table 2. ILI by age group for the 2016-2017 surveillance year through Week 19

Age Group	Frequency	Percent
0-5	1164	22.83
6-9	478	9.38
10-17	615	12.06
18-24	682	13.38
25-44	1553	30.46
45-64	500	9.81
65+	106	2.08

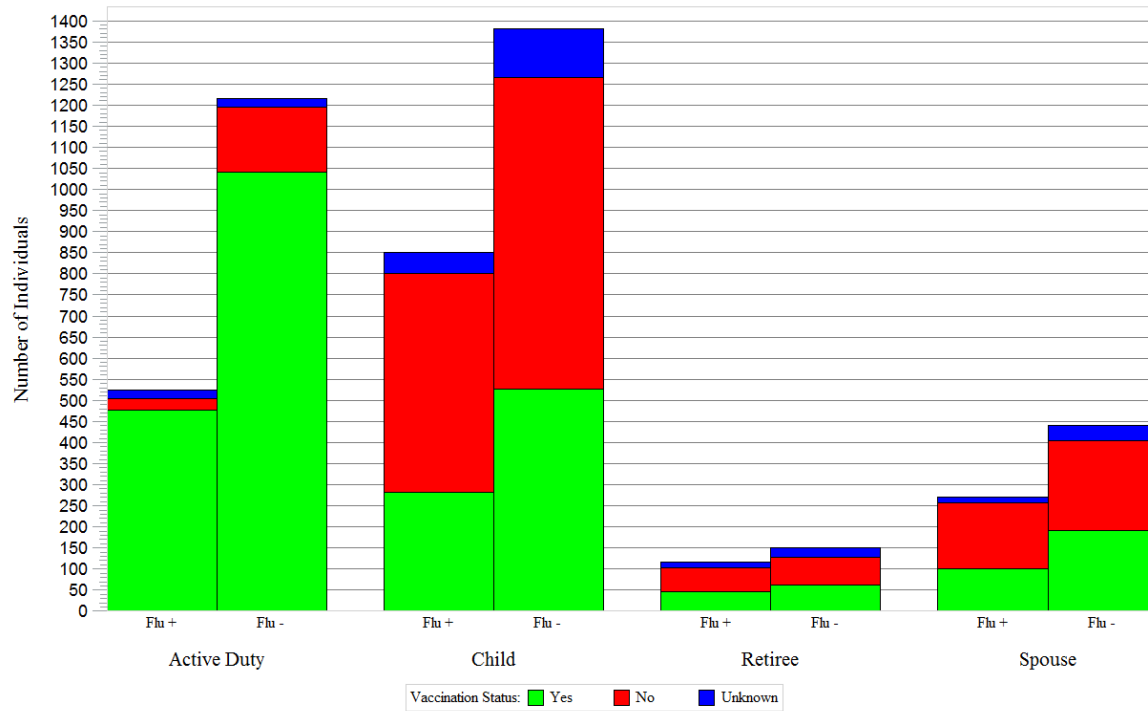
Demographic Summary

Of 5,098 ILI cases, 1,756 are service members (34.5%), 2,250 are children (44.1%), 719 are spouses (14.1%), and 373 (7.3%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=5,098) is 21 (range 0, 96).

Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 19

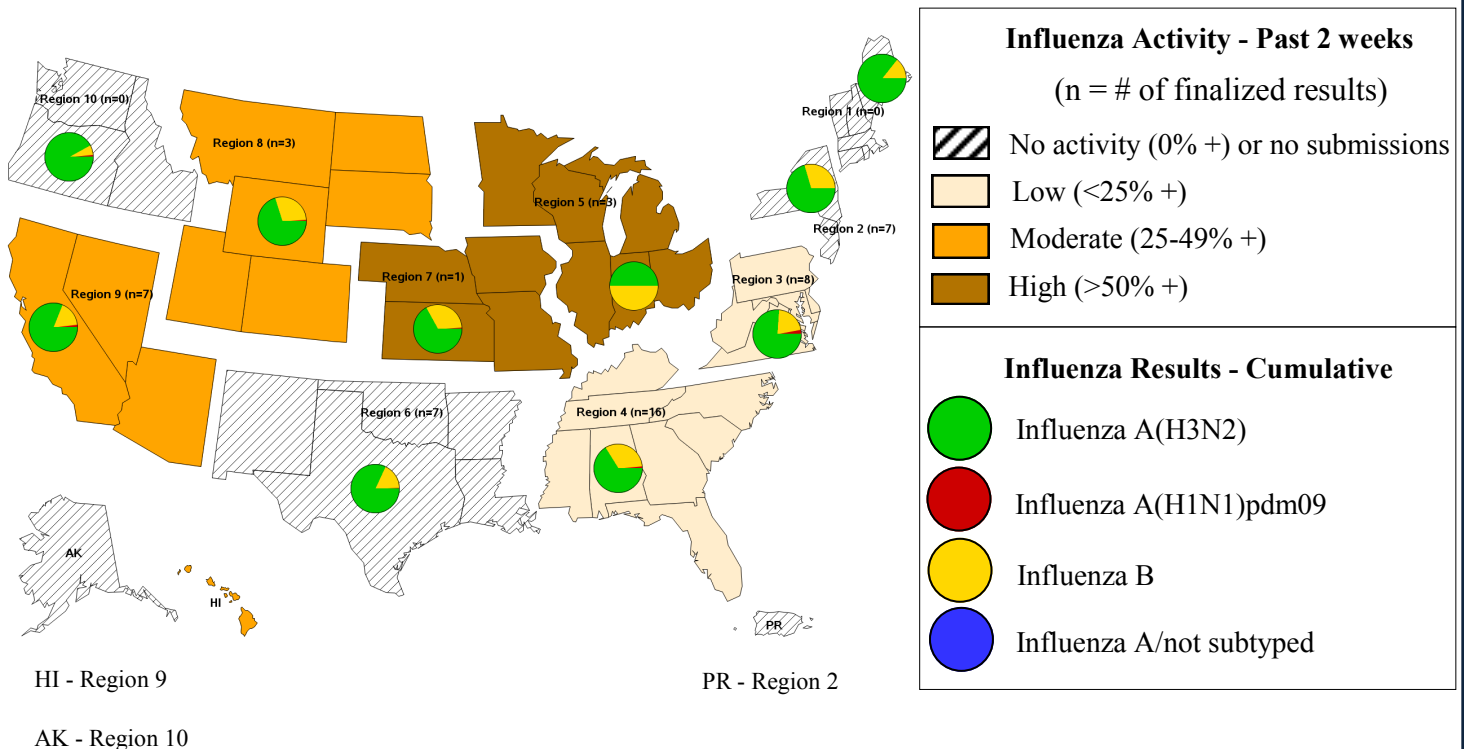


Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 18*



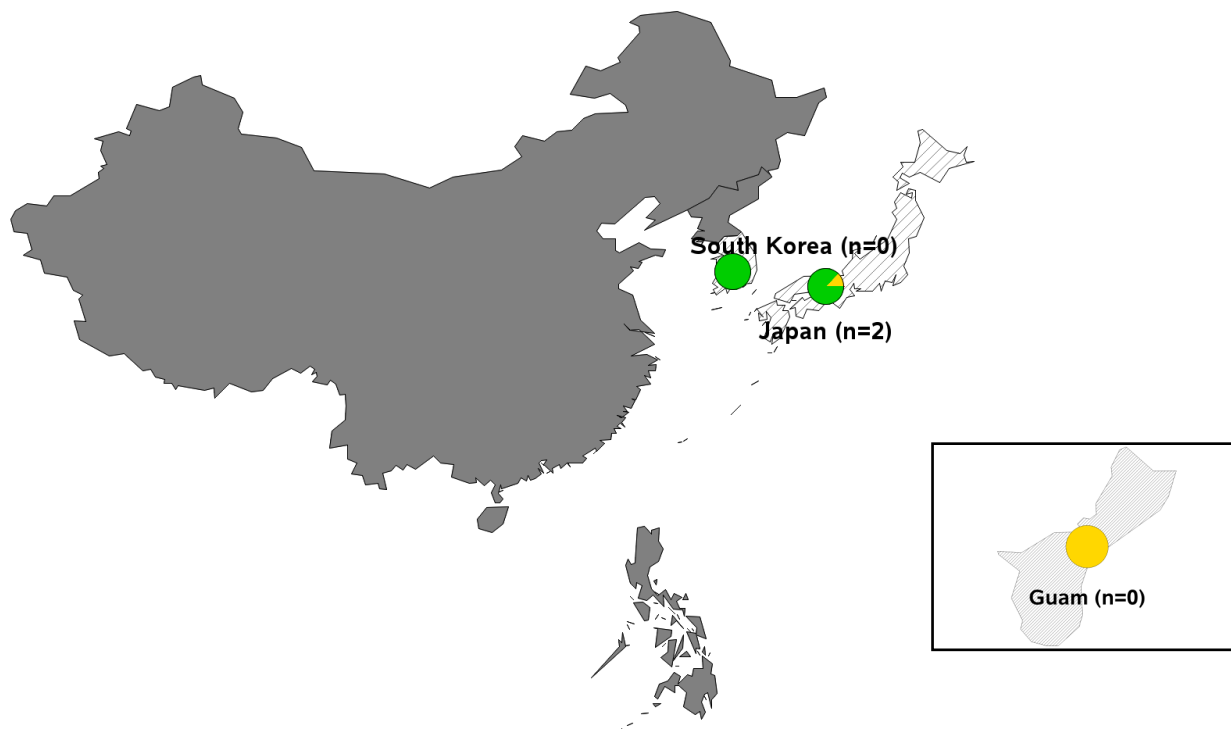
*Vaccination status by beneficiary type for Week 19 was not available at time of publication.

Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 19



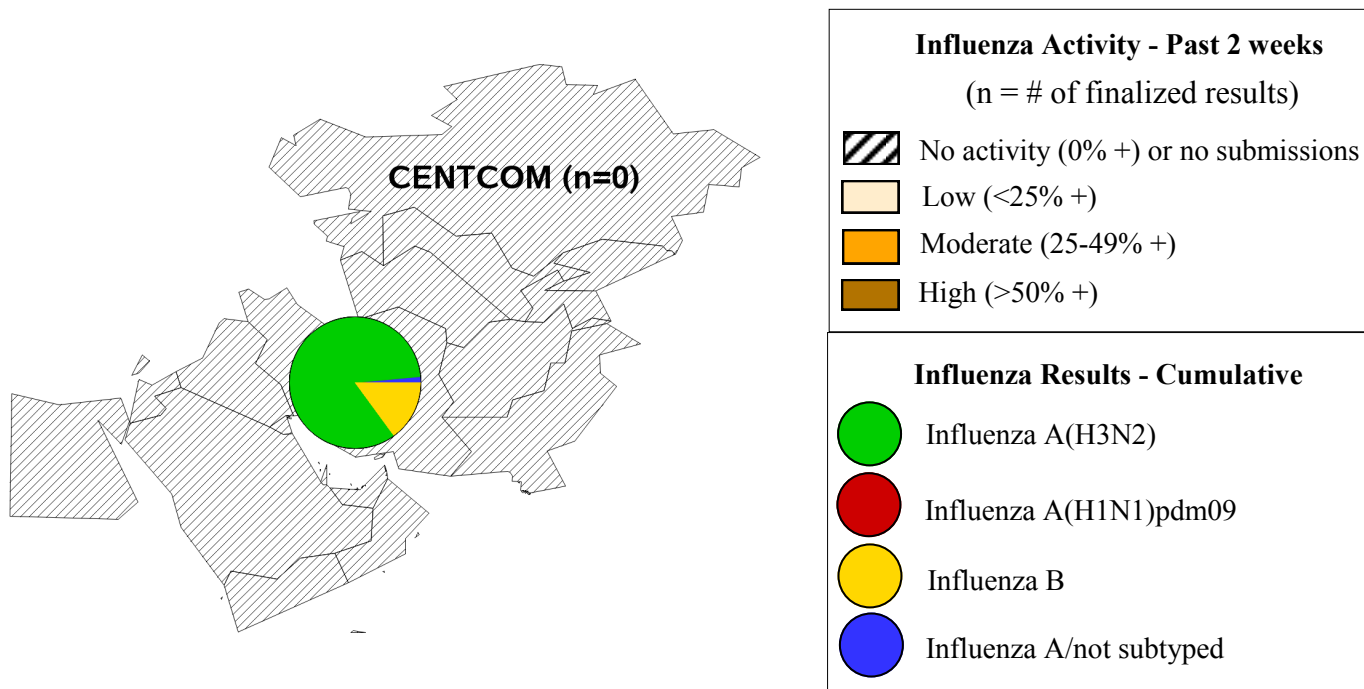
DoD Global, Laboratory-Based, Influenza Surveillance Program

Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 19 (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 19



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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 19

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

Region*		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 & hMPV & Rhino/Entero	Adenovirus	C. pneumoniae	Coronavirus	hMPV	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	-	-	-	-	-	-	1	-	-	-	-	-	5	7
	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	1	2	3	2	9	5	-	-	66	133
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	-	90	255	
	JB McGuire-Dix-Lakehurst, NJ	-	54	-	-	-	-	-	2	-	3	-	6	9	2	9	6	12	5	-	83	191	
	USMA - West Point, NY	-	86	-	-	-	-	-	15	-	12	-	5	7	2	10	13	10	7	-	152	319	
Region 3	Dover AFB, DE	-	18	-	-	-	-	-	10	-	2	-	2	1	1	-	1	4	-	-	-	48	87
	JB Anacostia-Bolling, DC	-	14	-	-	-	-	-	4	-	-	-	-	-	-	-	1	-	-	-	-	19	
	JB Andrews, MD	2	23	-	-	-	-	-	12	-	-	-	2	1	-	3	2	1	2	-	41	89	
	JB Langley-Eustis, VA	6	149	-	1	1	-	-	31	-	1	-	4	10	2	11	20	37	11	-	260	544	
	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	-	-	18	27
	Eglin AFB, FL	1	15	-	-	-	-	-	4	-	7	-	2	1	2	1	5	11	6	-	39	94	
	Ft Bragg, NC	1	8	-	-	-	-	-	6	-	-	-	1	1	1	3	2	7	4	3	38	75	
	Ft Campbell, KY	1	15	-	-	-	-	-	9	1	2	-	-	1	-	-	3	-	4	-	17	53	
	Hurlburt Field, FL	-	18	-	-	-	-	-	6	-	2	-	1	-	1	1	2	3	1	-	27	62	
	JB Charleston (AF), SC	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	17	
	Keesler AFB, MS	-	2	-	-	-	1	-	-	-	-	-	-	1	-	2	2	4	2	-	15	29	
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	6	7	
	Maxwell AFB, AL	-	10	-	-	-	-	-	2	-	-	-	-	1	-	2	-	1	-	-	14	30	
	Moody AFB, GA	-	36	-	-	-	-	-	44	-	1	-	2	7	1	13	8	16	14	1	87	230	
	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	1	3	2	-	25	65	
	Seymour Johnson AFB, NC	3	16	-	-	-	-	-	1	-	2	-	-	-	-	1	1	2	1	-	19	46	
	Shaw AFB, SC	-	70	-	-	-	-	-	34	-	1	1	7	5	1	5	1	11	2	-	64	202	
	Tyndall AFB, FL	-	11	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	16	16

(Cont'd on page 7)

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—Through Current Surveillance Week 19

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(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & hMPV & Rhino/Entero	Adenovirus	C. pneumoniae	Coronavirus	hMPV	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	1	1	1	1	1	-	1	8	21
	Wright-Patterson AFB, OH	-	10	-	-	-	-	-	-	10	-	-	-	1	1	1	1	-	2	2	-	39	67
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	3	-	4	1	-	39	67
	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	-	-	85	186
	Tinker AFB, OK	1	97	-	-	-	-	1	-	25	-	2	-	10	4	1	9	6	12	6	-	138	312
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	12
Region 7	McConnell AFB, KS	-	25	-	-	-	-	-	-	18	-	1	-	4	-	1	4	5	9	3	-	36	106
	Offutt AFB, NE	1	32	-	-	-	-	-	-	9	-	1	-	6	2	-	1	1	7	1	-	57	118
Region 8	Ellsworth AFB, SD	-	14	-	-	-	-	-	-	14	-	-	-	3	-	-	3	1	3	-	-	37	75
	FE Warren AFB, WY	-	36	-	-	-	-	-	-	7	-	3	-	4	1	2	4	6	4	-	-	52	119
	Hill AFB, UT	-	30	-	-	-	-	-	-	3	-	-	-	3	1	-	6	4	4	2	-	41	94
	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	11	3	4	-	26	82
	USAF Academy, CO	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	1	-	-	2	6
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	1	15	-	-	-	-	-	-	4	-	-	-	-	2	-	5	1	6	5	-	35	74
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	-	-	4	-	1	-	2	-	-	1	3	1	1	-	17	30
	Nellis AFB, NV	1	3	-	-	-	-	-	-	4	-	3	-	1	-	-	4	4	5	7	-	32	64
	Travis AFB, CA	-	58	-	-	-	-	-	-	5	-	1	1	6	7	-	6	13	15	5	-	42	159
	Vandenberg AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Fairchild AFB, WA	2	17	-	-	-	-	-	-	2	-	3	-	3	-	-	5	2	4	-	-	46	84
	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		24	1339	1	1	3	1	1	1	435	1	69	5	121	91	37	179	174	276	129	8	2202	5098

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

Molecular Sequence Analysis Report #9

This is the ninth USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 73 influenza specimens collected between 1 January 2017 and 22 February 2017. Five of these specimens were influenza A(H1N1)pdm09, 56 were influenza A(H3N2), three were influenza B/Victoria lineage, and nine 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.

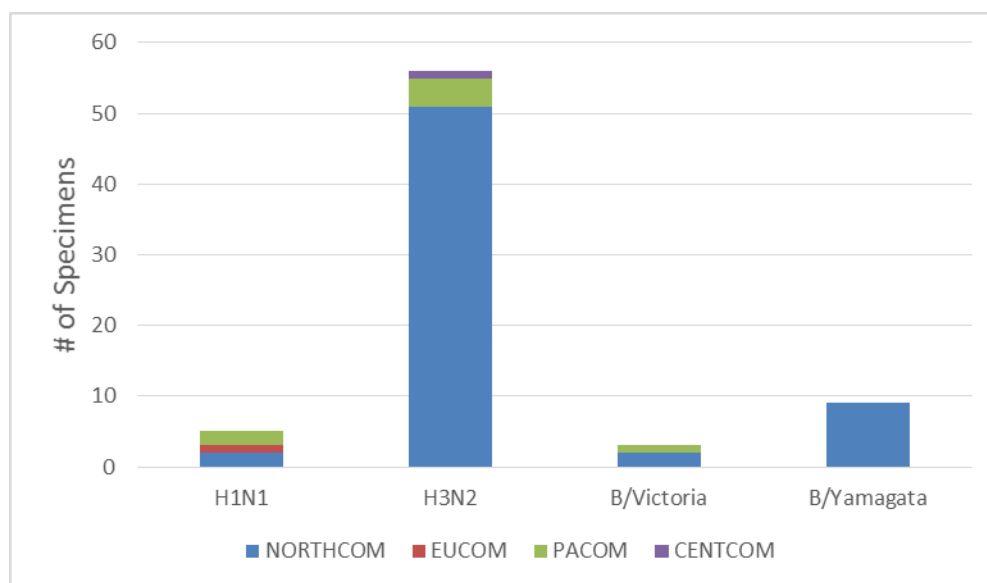


Figure 1: The total HA sequences of influenza A(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata from each of the United States Combatant Commands listed in this report.

DoD Global, Laboratory-Based, Influenza Surveillance Program

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

B/

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
CONUS					
Arizona					
Davis-Monthan AFB		1			1
Connecticut					
USCG Academy		2		1	3
Florida					
Eglin AFB		1			1
Hulburt Field AFB		2			2
Georgia					
Moody AFB		3			3
Robins AFB				1	1
Kansas					
McConnell AFB		4			4
Maryland					
JB Anacostia-Bolling		2			2
JB Andrews		1			1
Massachusetts					
Hanscom AFB		1			1
Nebraska					
Offutt AFB		3			3
Nevada					
Nellis AFB		1			1
New Jersey					
JB McGuire-Dix-Lakehurst		2			2
New Mexico					
Cannon AFB		2			2
New York					
Ft Drum		3		2	5
USMA - West Point		2			2
North Carolina					
Ft Bragg	1			1	2
North Dakota					
Minot AFB		1		1	2
Ohio					
Wright-Patterson AFB				1	1
Oklahoma					
Tinker AFB		6		1	7
South Carolina					
JB Charleston		1			1
Shaw AFB		1	2		3

DoD Global, Laboratory-Based, Influenza Surveillance Program

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

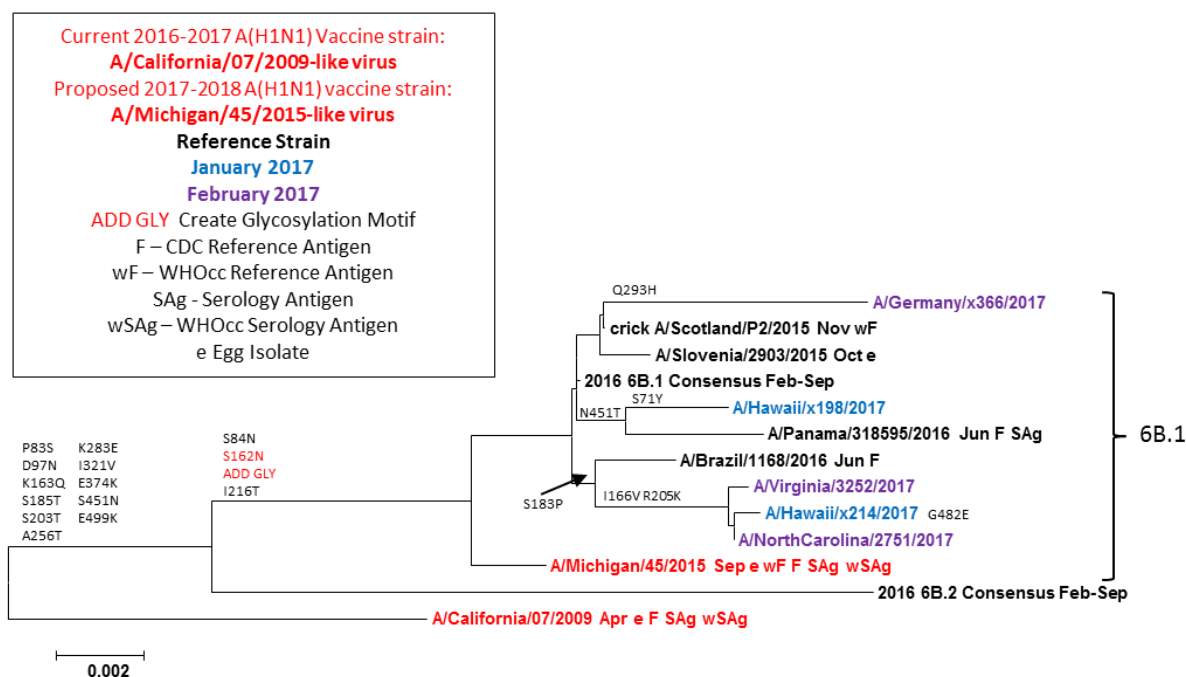
	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Total
South Dakota					
Ellsworth AFB		2			2
Texas					
Sheppard AFB		5			5
Utah					
Hill AFB		2			2
Virginia					
JB Langley-Eustis	1	1		1	3
Wyoming					
FE Warren AFB		2			2
OCONUS					
Country 2					
Location A		1			1
Germany					
USAG Wiesbaden	1				1
Hawaii					
Tripler AMC	2		1		3
Japan					
Kadena AB		1			1
Yokota AB		3			3
Total	5	56	3	9	73

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(H1N1)pdm09

- Among the 61 influenza A isolates, five (8.2%) 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 96.4 – 96.9% (average 96.6%) compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus. In addition, overall protein homology of 99.1 – 99.6% (average 99.36%) 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 22 mutations present in the A(H1N1)pdm09 isolates, eight occurred at predicted antigenic sites (none at site A, one at site B, none at site C, four at site D, and three at site E) and four occurred at the receptor binding site.^{2,5}

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



Influenza A(H3N2)

- Among the 61 influenza A isolates, 56 (91.8%) 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 – 98.9% (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 nine (16.1%) in subclade 3C.3a and 47 (83.9%) in subclade 3C.2a. Twenty-eight of the 56 3C.2a (59.6%) 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 26 (92.9%) of the 3C.2a1 isolates and 33 (58.9%) of the total A(H3N2) isolates. The mutation T135K was present in nine isolates (32.1% of 3C.2a1 and 16.1% of total).
- Among the influenza A(H3N2) isolates characterized in this report, seven mutations; N122D (asparagine to aspartic acid), S124N (serine to asparagine), 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 55 mutations present in the A(H3N2) specimens, 20 occurred at predicted antigenic sites (seven at site A, three 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}

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

ADD GLY Create Glycosylation Motif

LOSS GLY Loss of Glycosylation Motif

F – CDC Reference Antigen

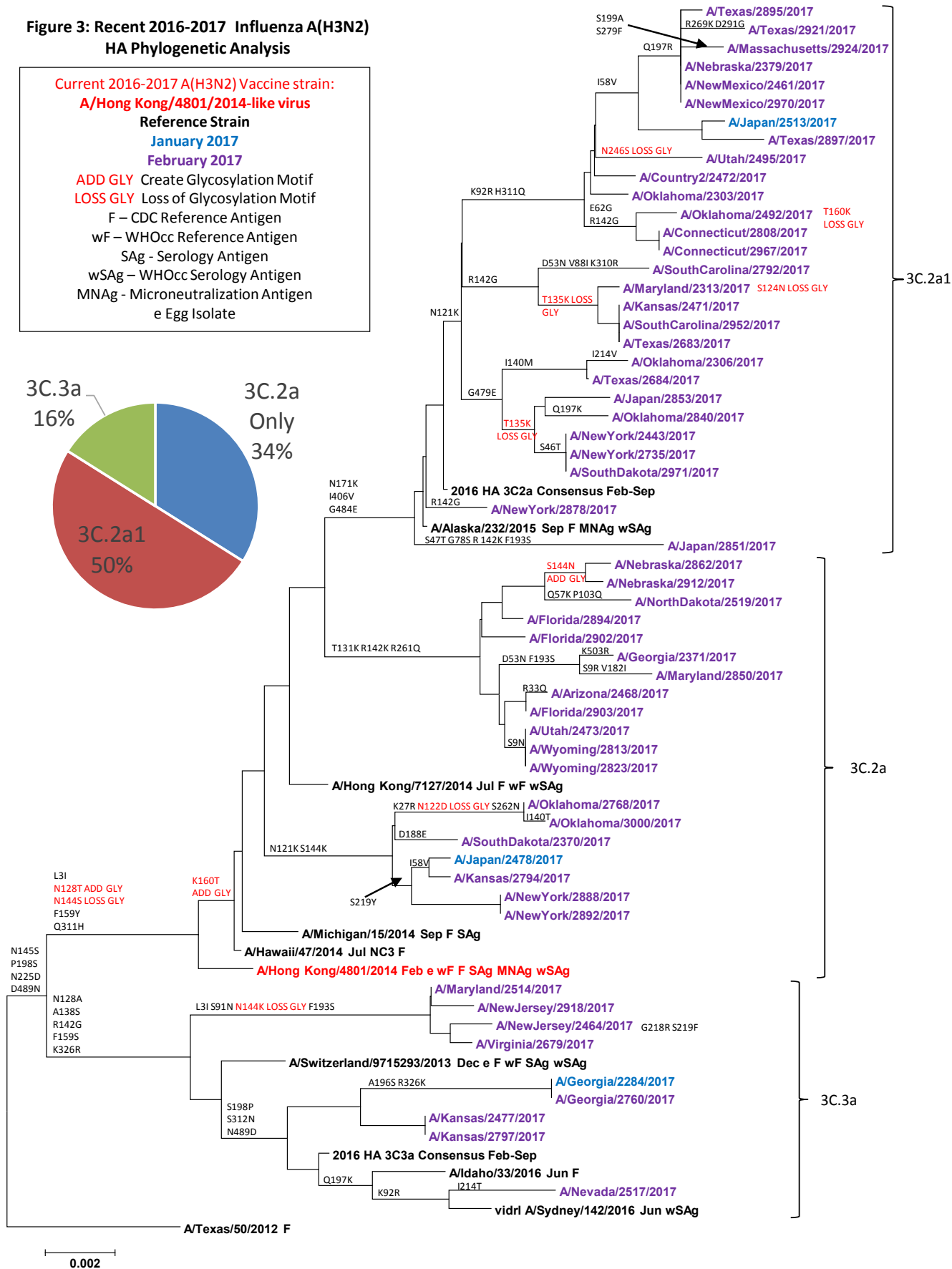
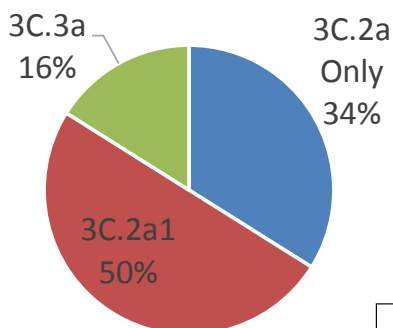
vF – WHOcc Reference Antigen

SAg - Serology Antigen

SAg – WHOcc Serology Antigen

MNAg - Microneutralization Antigen

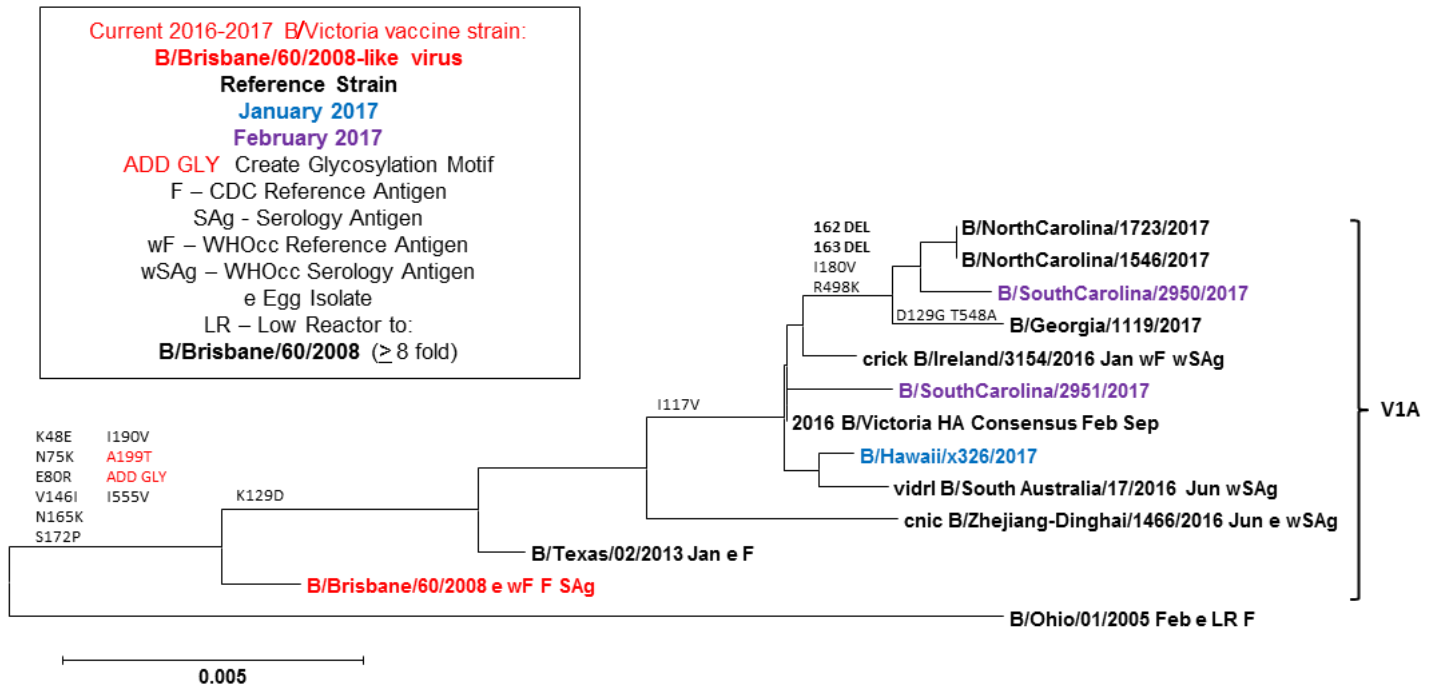
e Egg Isolate



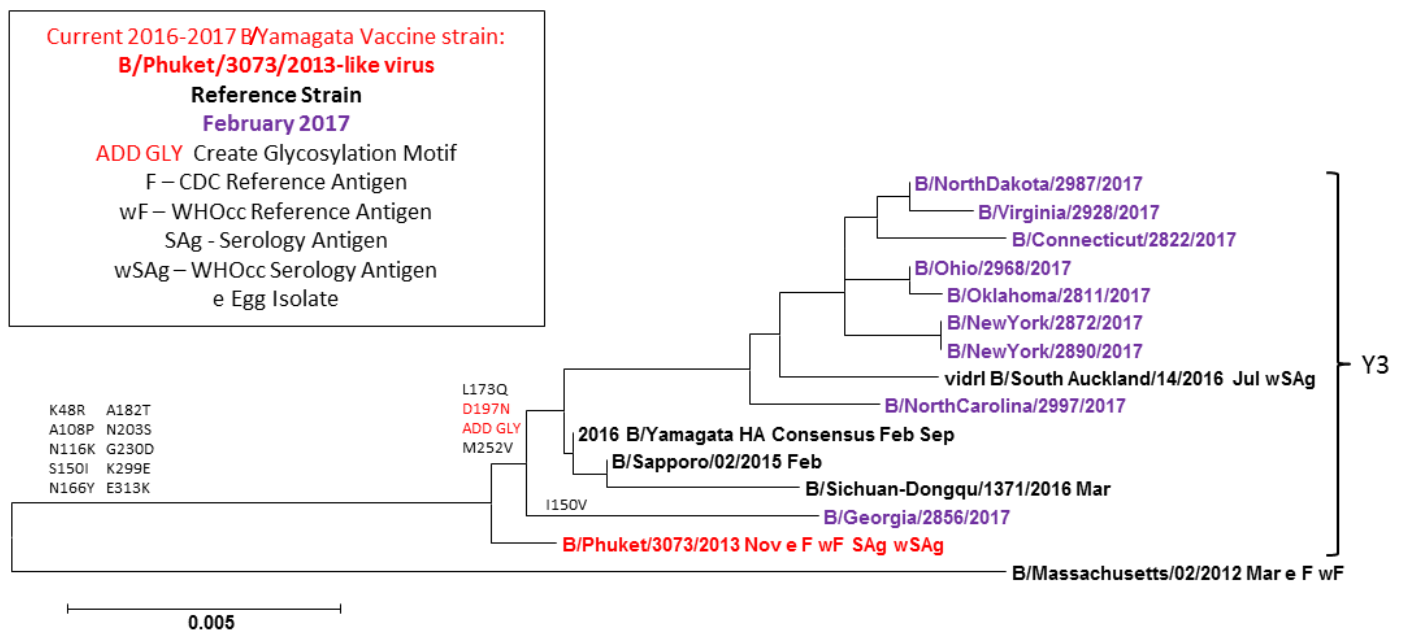
Influenza B

- 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 Three (25.0%) of the influenza B isolates characterized in this report fell into the B/Victoria lineage and nine (75.0%) fell into the B/Yamagata lineage.
- Of interest, one 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. Three B/Victoria sequences from the 2016-2017 season containing this deletion were previously reported by USAFSAM.
- Both of 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 99.1 – 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.

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



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



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. Kongchanagul, A., Suptawiwat, O., Kanrai, P., Uprasertkul, 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.
3. 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.
4. 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.
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).

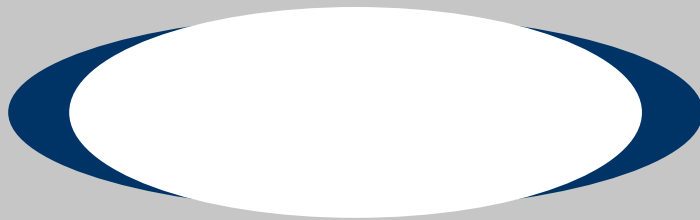
Sentinel Site Surveillance

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 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.

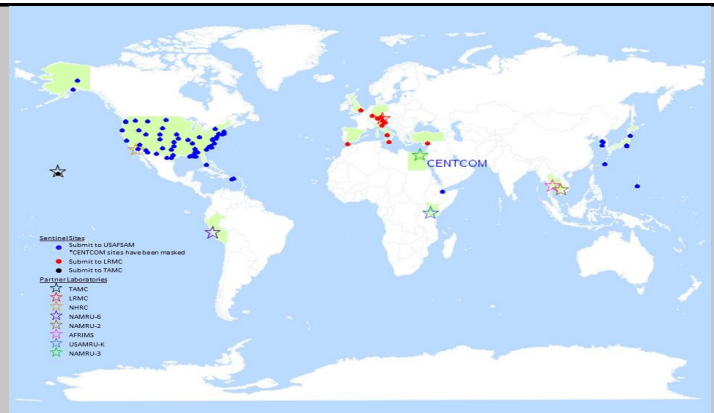
Errata:



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.

