



Cumulative Results

Locations	74
Collected	1,499
Tested	1,397

Influenza A 238

A(H1N1)pdm09	2
A(H3N2)	235
A(H3N2) & RSV	1
A/not subtyped	0

Influenza B* 12

B	12
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Other Respiratory Pathogens 504

Adenovirus	31
<i>Bordetella pertussis</i>	0
<i>Chlamydomphila pneumoniae</i>	2
Coronavirus	43
Human Metapneumovirus	18
<i>Mycoplasma pneumoniae</i>	26
Parainfluenza	97
RSV	71
Rhino/Enterovirus	153
Non-influenza Viral Coinfections	55
Non-influenza Bacterial Coinfections	8
-M. pneumo coinfections (8)	

Lab data are current as of 17 January 2017.
Results are preliminary and may change as
more results are received.
*Influenza B lineages will be reported in the
periodic molecular sequencing reports.

Respiratory Highlights

1 - 14 January 2017 (Surveillance Weeks 1 & 2)

- During 1 - 14 January 2017, a total of 310 specimens were collected from 51 locations. Results were finalized for 233 specimens from 45 locations. During Week 1, 46 influenza A(H3N2) and three influenza B viruses were identified. During Week 2, 42 influenza A(H3N2) and three influenza B viruses were identified. Approximately 33% of specimens tested positive for influenza during Week 1. Approximately 30% of specimens tested positive for influenza during Week 2. The influenza percent positive for the season is approximately 18%.
- In May 2016, WHO released a new tool called Tool for Influenza Pandemic Risk Assessment (TIPRA). This tool was designed to standardize the approach to measuring the pandemic potential of influenza viruses. The tool focuses on the risk associated with a specific virus while also allowing access to other risk assessments to explore contextual and exposure issues. (WHO Influenza, *Tool for Influenza Pandemic Risk Assessment (TIPRA)*, cited 19 January 2017).

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DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1. Results by region and location for specimens collected during Weeks 1 & 2

Region*		A(H1N1)pdm09	A(H3N2)	A(H3N2) & RSV	B	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	-	1	-	1	-	-	1	-	-	-	1	-	-	-	1	5
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	16	-	-	-	-	2	-	-	-	-	1	2	-	3	24
PACOM	Eielson AFB, AK	-	-	-	-	-	-	-	-	1	-	-	-	-	-	4	5
	JB Elmendorf-Richardson, AK	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Kadena AB, Japan	-	3	-	-	-	-	-	-	-	2	-	2	-	1	16	24
	Kunsan AB, South Korea	-	2	-	-	-	-	1	-	-	-	-	1	-	-	-	4
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Osan AB, South Korea	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	6	-	-	-	-	2	-	2	-	2	7	3	-	37	59
Region 1	Hanscom AFB, MA	-	-	-	-	-	-	-	-	1	1	-	-	1	-	1	4
	USCG Academy, CT	-	-	-	-	-	-	-	-	1	-	-	3	-	2	2	8
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	-	-	-	1	4	-	1	6	1	5	3	1	2	-	10	34
	JB McGuire-Dix-Lakehurst, NJ	-	16	-	-	2	-	5	1	2	7	2	7	3	-	29	74
	USMA - West Point, NY	-	20	-	-	8	-	1	2	1	4	8	4	4	-	58	110
Region 3	Dover AFB, DE	-	3	-	-	1	-	1	-	1	-	1	1	-	-	8	16
	JB Anacostia-Bolling, DC	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
	JB Andrews, MD	-	3	-	-	-	-	-	-	-	-	2	1	1	-	7	14
	JB Langley-Eustis, VA	-	5	-	2	-	-	1	2	2	4	13	22	8	-	46	105
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
Region 4	Columbus AFB, MS	-	2	-	-	-	-	-	-	-	-	-	1	-	-	6	9
	Eglin AFB, FL	-	4	-	1	2	-	1	-	-	-	4	8	2	-	14	36
	Ft Bragg, NC	-	3	-	1	-	-	1	-	1	3	1	6	3	3	11	33
	Ft Campbell, KY	-	1	-	-	-	-	-	1	-	-	2	-	3	-	3	10
	Hurlburt Field, FL	-	4	-	-	-	-	-	-	-	1	-	-	-	-	3	8
	JB Charleston (AF), SC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	1	2	-	1	-	6	10
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	4
	Maxwell AFB, AL	-	1	-	-	-	-	-	-	-	1	-	1	-	-	6	9
	Moody AFB, GA	-	6	-	2	1	-	1	-	-	1	5	2	7	1	12	38
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	4
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	5	-	-	-	-	-	-	-	-	1	-	-	-	4	10
	Seymour Johnson AFB, NC	-	-	-	-	1	-	-	-	1	1	-	1	-	-	3	7
	Shaw AFB, SC	-	5	-	2	1	-	4	1	1	3	-	3	-	-	21	41

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

(Cont'd on page 3)

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1. Results by region and location for specimens collected during Weeks 1 & 2
(Cont'd from page 2)

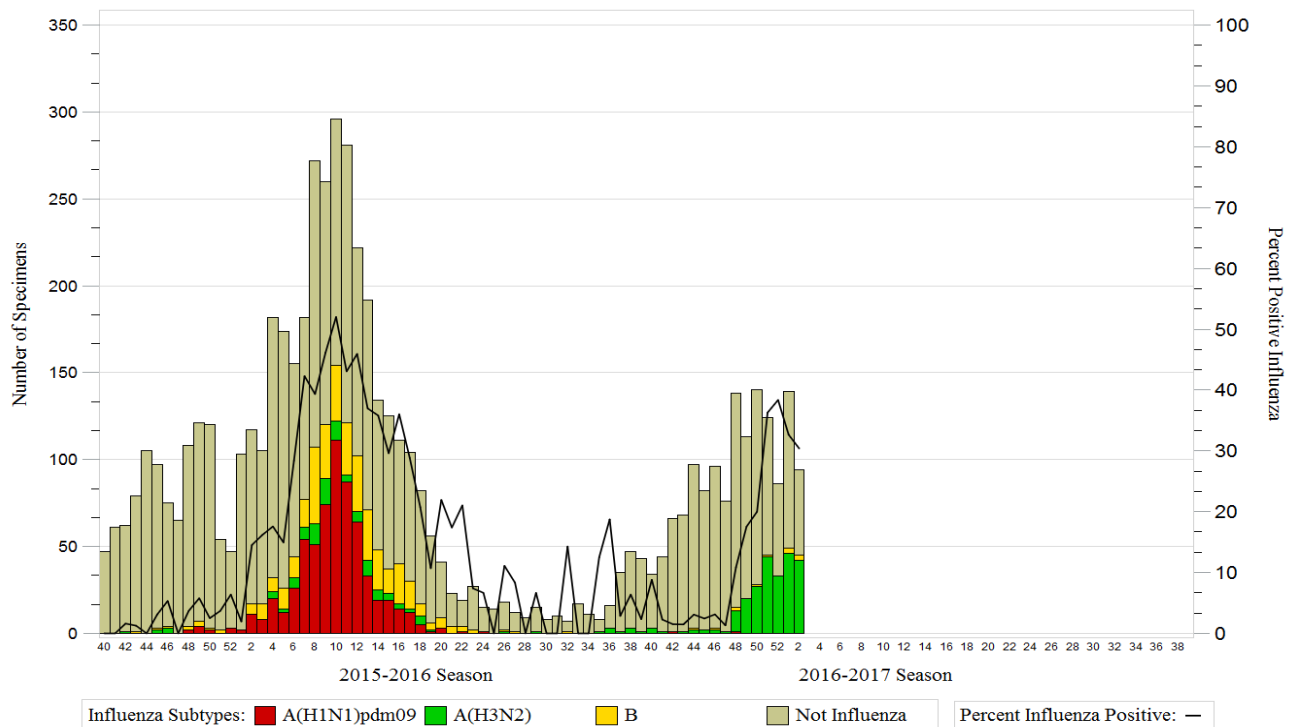
Region*		A(H1N1)pdm09	A(H3N2)	A(H3N2) & RSV	B	Adenovirus	C. pneumoniae	Coronavirus	hMPV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Viral Coinfection	Non-Influenza Bacterial Coinfection	No Pathogen	Total
Region 5	Scott AFB, IL	-	-	-	-	-	-	-	-	1	2	1	1	-	1	6	12
	Wright-Patterson AFB, OH	-	1	-	-	-	-	-	-	1	1	-	1	1	-	8	13
Region 6	Altus AFB, OK	-	-	-	-	1	-	-	-	-	-	-	4	-	-	14	19
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	1	-	1	-	-	3	5
	Cannon AFB, NM	-	2	-	-	-	-	-	-	1	1	-	3	-	-	8	15
	Ft Polk, LA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Laughlin AFB, TX	-	-	-	-	-	-	-	2	-	-	-	-	-	-	1	3
	Sheppard AFB, TX	-	10	-	-	-	-	3	1	-	4	-	4	-	-	13	35
	Tinker AFB, OK	-	11	1	-	-	-	1	-	1	4	3	6	-	-	25	52
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	7
Region 7	McConnell AFB, KS	-	5	-	-	-	-	1	-	1	2	-	4	-	-	13	26
	Offutt AFB, NE	-	2	-	-	1	-	2	-	-	-	-	4	-	-	10	19
Region 8	Ellsworth AFB, SD	-	-	-	-	-	-	2	-	-	3	-	3	-	-	6	14
	FE Warren AFB, WY	-	1	-	-	2	-	-	-	1	1	1	2	-	-	10	18
	Hill AFB, UT	-	14	-	-	-	-	2	-	-	4	2	4	-	-	19	45
	Malmstrom AFB, MT	-	3	-	-	-	-	-	-	1	-	-	1	-	-	3	8
	Minot AFB, ND	-	-	-	-	-	-	-	-	1	-	-	2	-	-	4	7
	Peterson AFB, CO	-	5	-	-	-	-	1	-	-	1	1	3	4	-	8	23
	USAF Academy, CO	-	1	-	-	-	-	-	1	-	-	1	1	-	-	1	5
Region 9	Beale AFB, CA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Davis-Monthan AFB, AZ	-	4	-	-	-	-	-	-	-	5	-	3	-	-	11	23
	Luke AFB, AZ	-	-	-	-	-	-	2	-	-	-	1	-	1	-	3	7
	Nellis AFB, NV	1	2	-	1	2	-	1	-	-	4	3	4	5	-	12	35
	Travis AFB, CA	-	32	-	-	-	1	1	1	-	5	1	8	-	-	26	75
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 10	CGS North Bend, OR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Fairchild AFB, WA	1	9	-	1	1	-	3	-	-	3	2	4	-	-	28	52
	JB Lewis-McChord, WA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	-	14	-	-	1	1	1	-	1	20	3	12	2	-	46	101
	NH Bremerton, WA	-	3	-	-	3	-	-	-	-	2	3	3	2	-	11	27
Total		2	235	1	12	31	2	43	18	26	97	71	153	55	8	643	1397

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

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2015-2016 surveillance year and through Week 2 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.

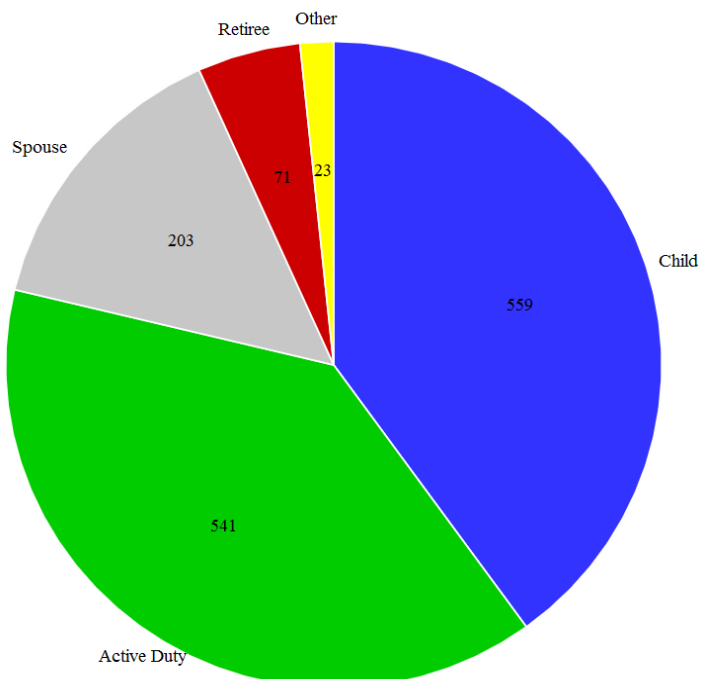
Table 2. ILI by age group for the 2016-2017 surveillance year through Week 2

Age Group	Frequency	Percent
0-5	325	23.26
6-9	93	6.66
10-17	141	10.09
18-24	217	15.53
25-44	466	33.36
45-64	112	8.02
65+	43	3.08

Demographic Summary

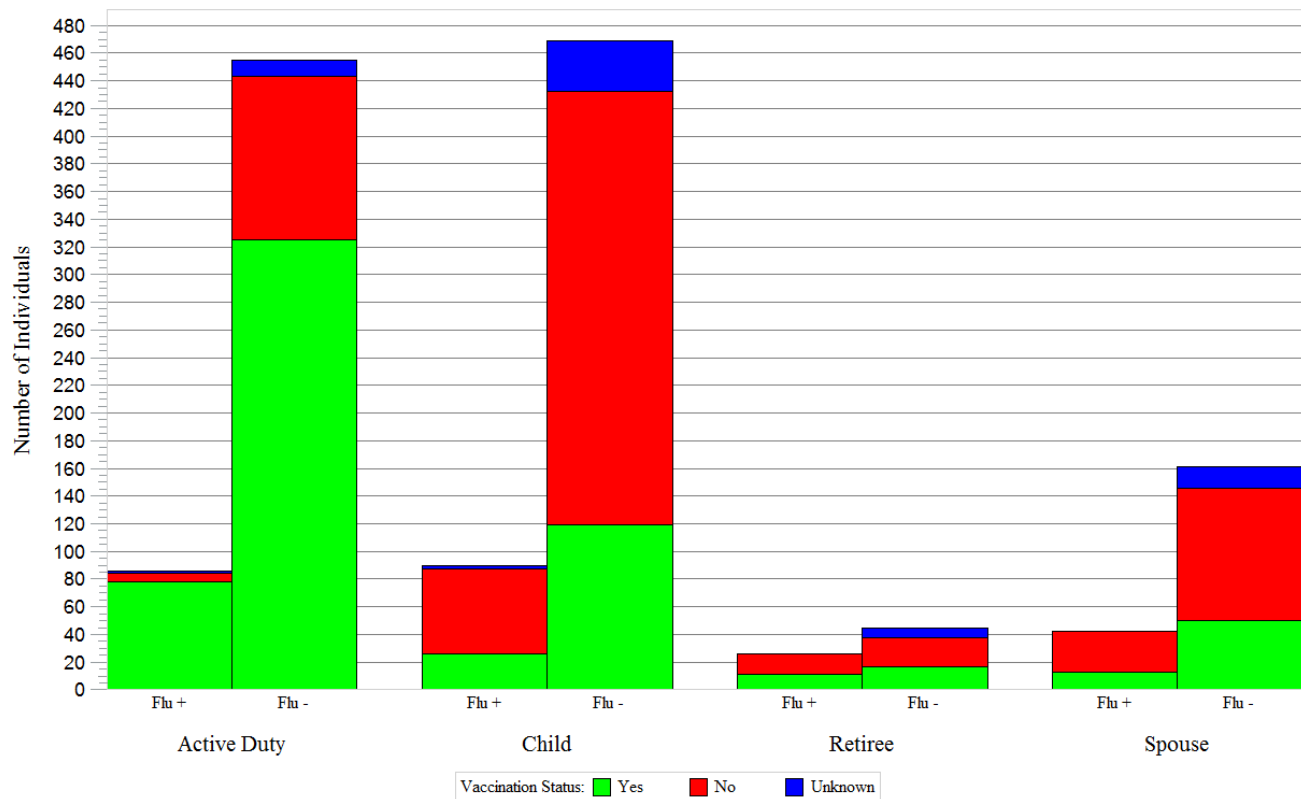
Of 1,397 ILI cases, 541 (38.7%) are service members, 559 (40.0%) are children, 203 (14.5%) are spouses, and 94 (6.8%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=1,397) is 22 (range 0, 91).

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

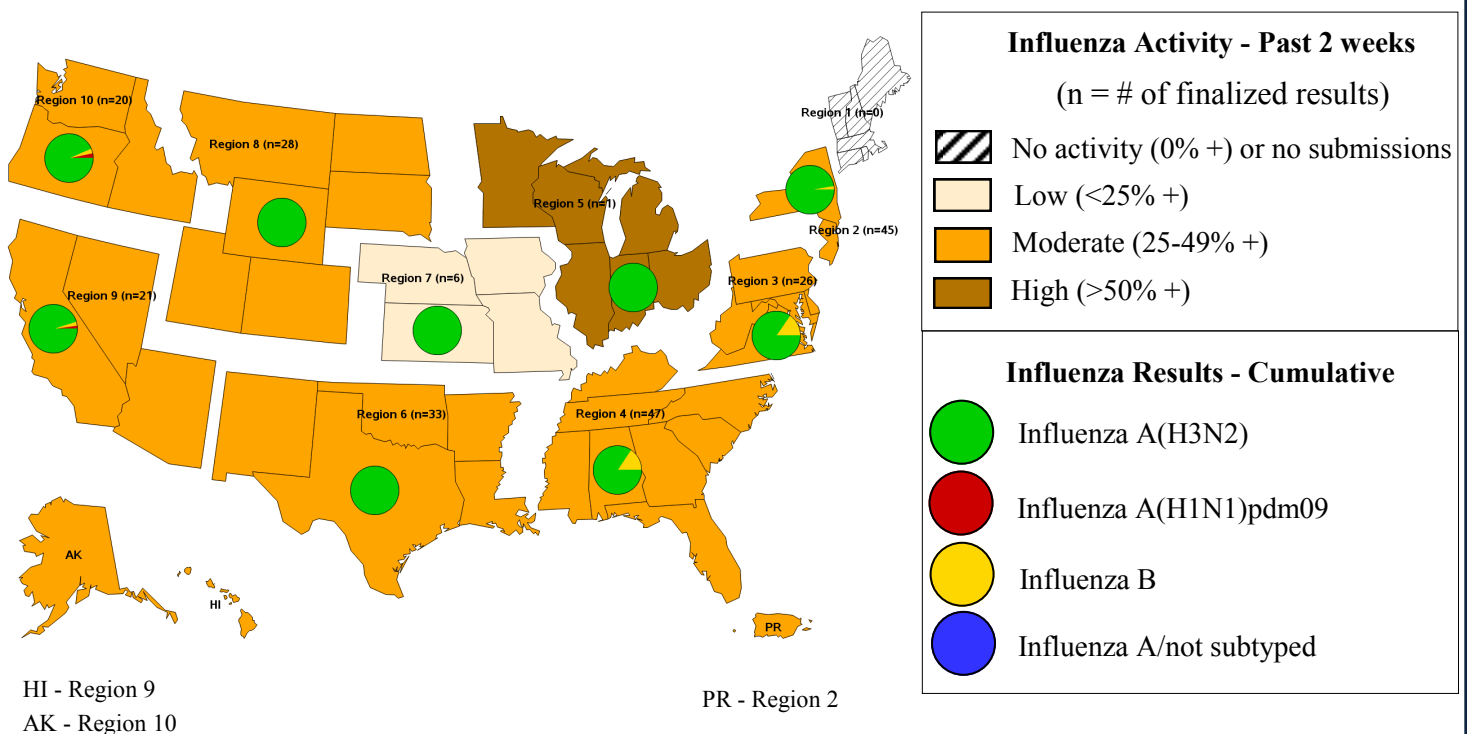


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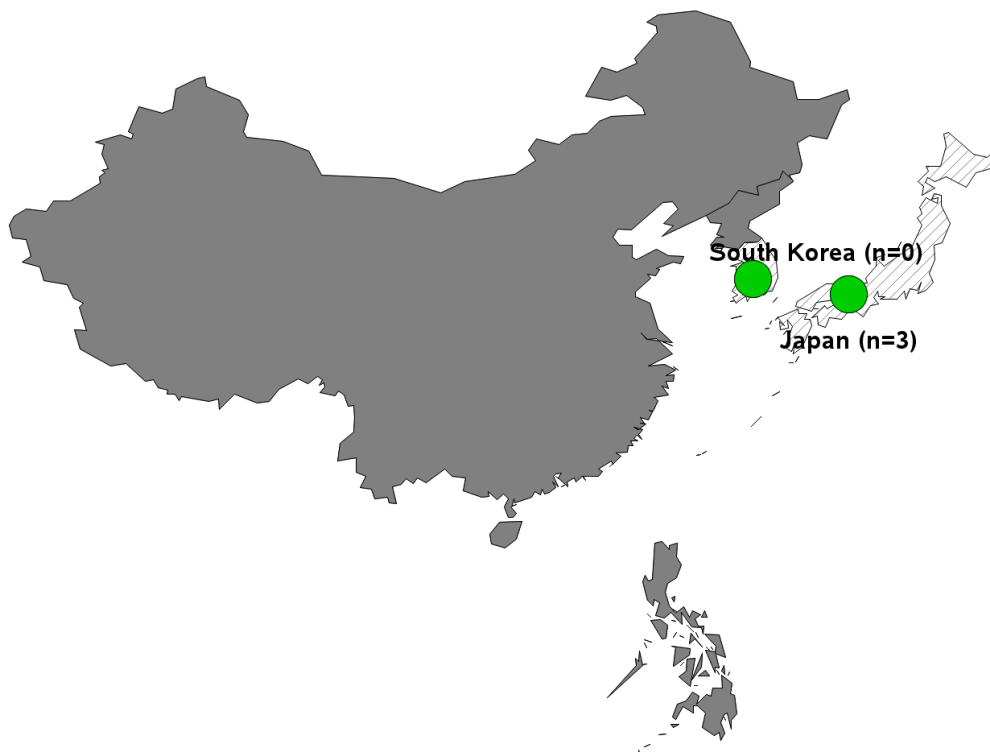
Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 2



Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 2

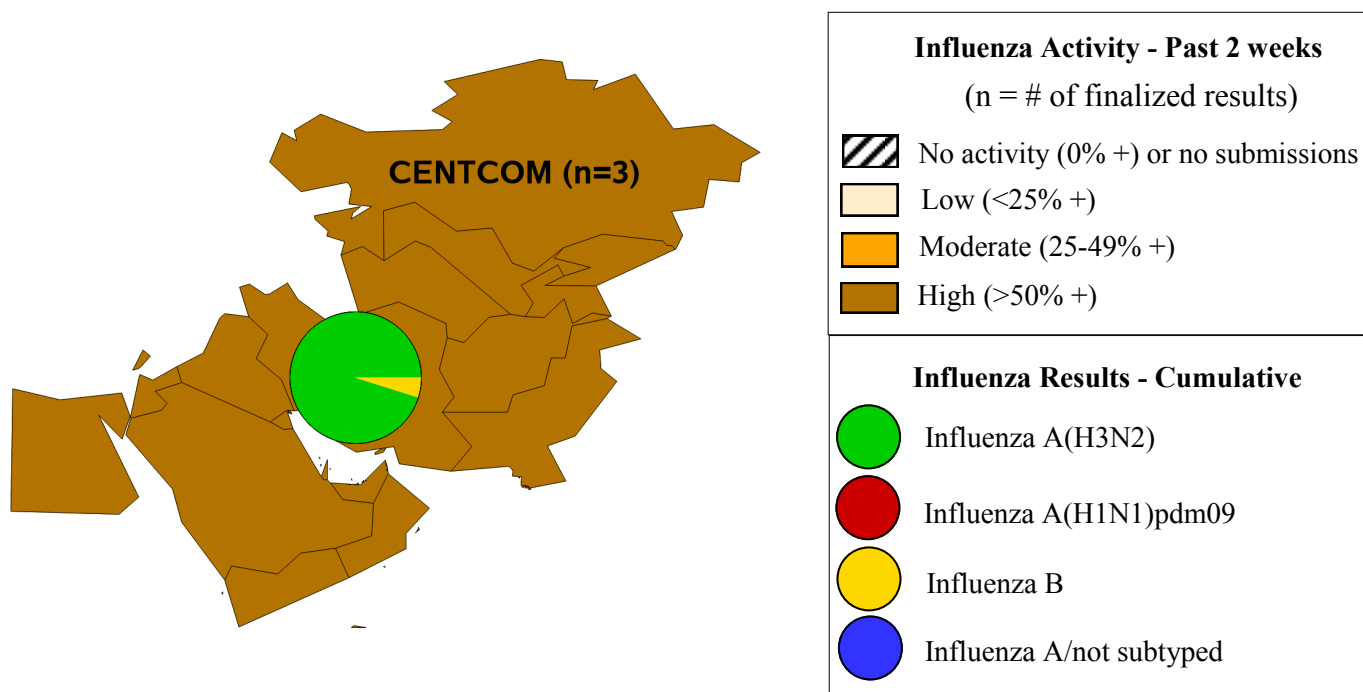


Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 2 (Pacific)



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 2



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 2

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

Region*		A(H1N1)pdm09	A(H3N2)	A(H3N2) & RSV	B	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	-	1	-	1	-	-	1	-	-	-	1	-	-	-	1	5
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	16	-	-	-	-	2	-	-	-	-	1	2	-	3	24
PACOM	Eielson AFB, AK	-	-	-	-	-	-	-	-	1	-	-	-	-	-	4	5
	JB Elmendorf-Richardson, AK	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Kadena AB, Japan	-	3	-	-	-	-	-	-	-	2	-	2	-	1	16	24
	Kunsan AB, South Korea	-	2	-	-	-	-	1	-	-	-	-	1	-	-	-	4
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Osan AB, South Korea	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Yokota AB, Japan	-	6	-	-	-	-	2	-	2	-	2	7	3	-	37	59
Region 1	Hanscom AFB, MA	-	-	-	-	-	-	-	-	1	1	-	-	1	-	1	4
	USCG Academy, CT	-	-	-	-	-	-	-	-	1	-	-	3	-	2	2	8
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	-	-	-	1	4	-	1	6	1	5	3	1	2	-	10	34
	JB McGuire-Dix-Lakehurst, NJ	-	16	-	-	2	-	5	1	2	7	2	7	3	-	29	74
	USMA - West Point, NY	-	20	-	-	8	-	1	2	1	4	8	4	4	-	58	110
Region 3	Dover AFB, DE	-	3	-	-	1	-	1	-	1	-	1	1	-	-	8	16
	JB Anacostia-Bolling, DC	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1
	JB Andrews, MD	-	3	-	-	-	-	-	-	-	-	2	1	1	-	7	14
	JB Langley-Eustis, VA	-	5	-	2	-	-	1	2	2	4	13	22	8	-	46	105
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
Region 4	Columbus AFB, MS	-	2	-	-	-	-	-	-	-	-	-	1	-	-	6	9
	Eglin AFB, FL	-	4	-	1	2	-	1	-	-	-	4	8	2	-	14	36
	Ft Bragg, NC	-	3	-	1	-	-	1	-	1	3	1	6	3	3	11	33
	Ft Campbell, KY	-	1	-	-	-	-	-	1	-	-	2	-	3	-	3	10
	Hurlburt Field, FL	-	4	-	-	-	-	-	-	-	1	-	-	-	-	3	8
	JB Charleston (AF), SC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Keesler AFB, MS	-	-	-	-	-	-	-	-	-	1	2	-	1	-	6	10
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	4
	Maxwell AFB, AL	-	1	-	-	-	-	-	-	-	1	-	1	-	-	6	9
	Moody AFB, GA	-	6	-	2	1	-	1	-	-	1	5	2	7	1	12	38
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	4
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	5	-	-	-	-	-	-	-	-	1	-	-	-	4	10
	Seymour Johnson AFB, NC	-	-	-	-	1	-	-	-	1	1	-	1	-	-	3	7
	Shaw AFB, SC	-	5	-	2	1	-	4	1	1	3	-	3	-	-	21	41

(Cont'd on page 8)

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

Laboratory Results—Through Current Surveillance Week 2

Table 3. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year
(Cont'd from page 7)

Region*		A(H1N1)pdm09	A(H3N2)	A(H3N2) & RSV	B	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	-	-	-	-	-	-	-	-	1	2	1	1	-	1	6	12
	Wright-Patterson AFB, OH	-	1	-	-	-	-	-	-	1	1	-	1	1	-	8	13
Region 6	Altus AFB, OK	-	-	-	-	1	-	-	-	-	-	-	4	-	-	14	19
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	1	-	1	-	-	3	5
	Cannon AFB, NM	-	2	-	-	-	-	-	-	1	1	-	3	-	-	8	15
	Ft Polk, LA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	2
	Laughlin AFB, TX	-	-	-	-	-	-	-	2	-	-	-	-	-	-	1	3
	Sheppard AFB, TX	-	10	-	-	-	-	3	1	-	4	-	4	-	-	13	35
	Tinker AFB, OK	-	11	1	-	-	-	1	-	1	4	3	6	-	-	25	52
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	7
		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Region 7	McConnell AFB, KS	-	5	-	-	-	-	1	-	1	2	-	4	-	-	13	26
	Offutt AFB, NE	-	2	-	-	1	-	2	-	-	-	-	4	-	-	10	19
Region 8	Ellsworth AFB, SD	-	-	-	-	-	-	2	-	-	3	-	3	-	-	6	14
	FE Warren AFB, WY	-	1	-	-	2	-	-	-	1	1	1	2	-	-	10	18
	Hill AFB, UT	-	14	-	-	-	-	2	-	-	4	2	4	-	-	19	45
	Malmstrom AFB, MT	-	3	-	-	-	-	-	-	1	-	-	1	-	-	3	8
	Minot AFB, ND	-	-	-	-	-	-	-	-	1	-	-	2	-	-	4	7
	Peterson AFB, CO	-	5	-	-	-	-	1	-	-	1	1	3	4	-	8	23
	USAF Academy, CO	-	1	-	-	-	-	-	1	-	-	1	1	-	-	1	5
		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Region 9	Beale AFB, CA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Davis-Monthan AFB, AZ	-	4	-	-	-	-	-	-	-	5	-	3	-	-	11	23
	Luke AFB, AZ	-	-	-	-	-	-	2	-	-	-	1	-	1	-	3	7
	Nellis AFB, NV	1	2	-	1	2	-	1	-	-	4	3	4	5	-	12	35
	Travis AFB, CA	-	32	-	-	-	1	1	1	-	5	1	8	-	-	26	75
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
Region 10	CGS North Bend, OR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Fairchild AFB, WA	1	9	-	1	1	-	3	-	-	3	2	4	-	-	28	52
	JB Lewis-McChord, WA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Mt Home AFB, ID	-	14	-	-	1	1	1	-	1	20	3	12	2	-	46	101
	NH Bremerton, WA	-	3	-	-	3	-	-	-	-	2	3	3	2	-	11	27
Total		2	235	1	12	31	2	43	18	26	97	71	153	55	8	643	1397

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

Molecular Sequence Analysis Report

USAFSAM Epidemiology Laboratory Service

This is the first USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 34 specimens collected between 13 August 2016 and 17 November 2016, with 25 specimens analyzed by USAFSAM and nine hemagglutinin sequences provided by the Naval Medical Research Unit 2 (NAMRU-2) in Cambodia. The influenza A virus subtypes submitted were as follows: three (8.8%) influenza A(H1N1)pdm09; 22 (64.7%) influenza A(H3N2); eight (23.5%) influenza B Victoria lineage; one (2.9%) influenza B Yamagata lineage. The proportions of each subtype/lineage submitted by each source and the proportion of data submitted from each source by influenza subtype/lineage are depicted in Figure 1. Sequences for each subtype/lineage included in this report are shown for each sentinel site and data submitting location in Table 1. Figures 2-5 display the phylogenetic relationships among NA sequences for each subtype and lineage.

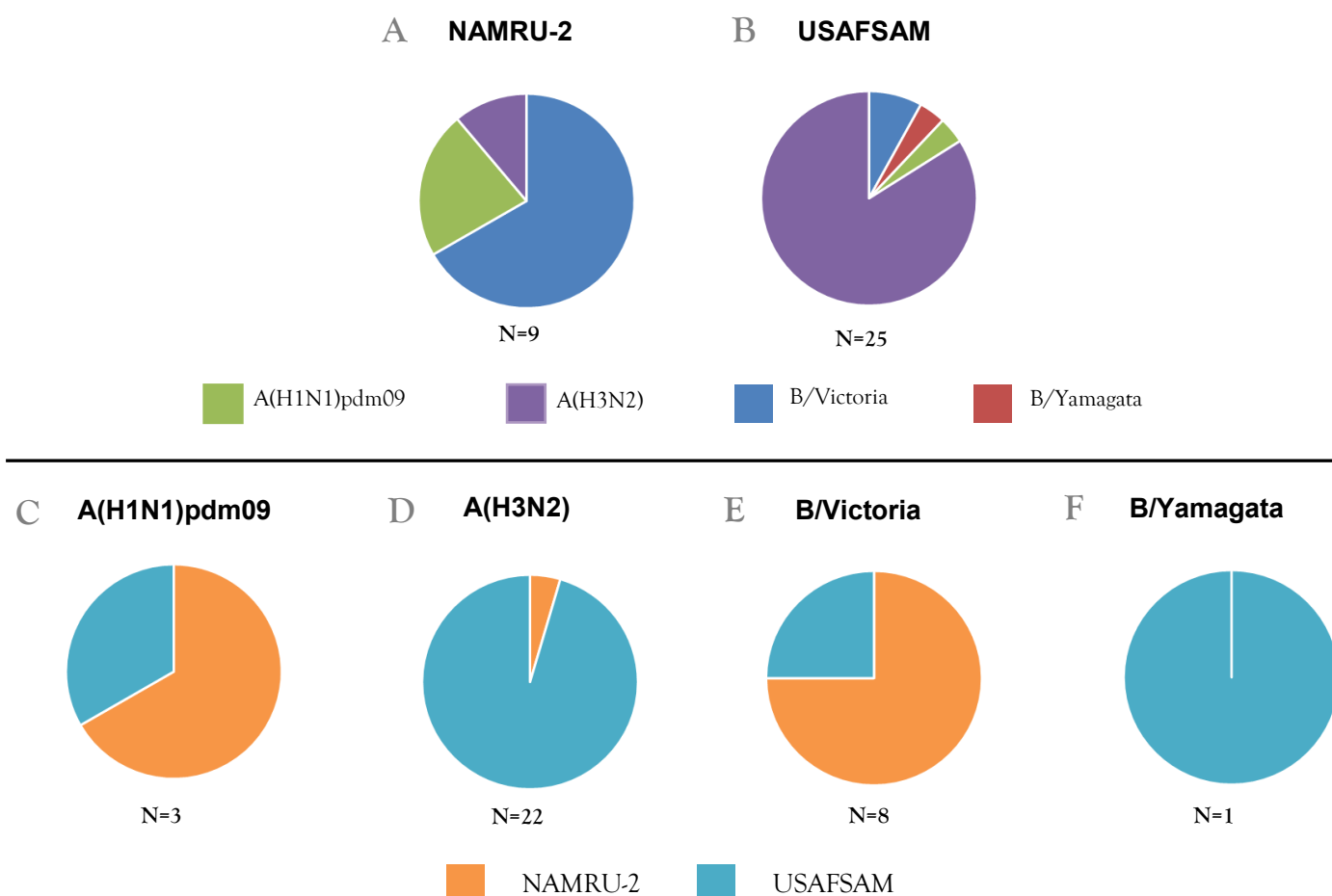


Figure 1: Proportion of influenza hemagglutinin segment sequence subtypes and lineages submitted by A) NAMRU-2 and B) USAFSAM; and the proportion of influenza hemagglutinin segment sequences submitted by NAMRU-2 and USAFSAM for C) A(H1N1)pdm09, D) A(H3N2), E) B/Victoria, and F) B/Yamagata.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1: Influenza subtypes and lineages from corresponding sentinel sites and contributing laboratory partners included in the 2016-2017 USAFSAM 1st sequencing report. Sites marked with an asterisk (*) contributed HA sequence data and the remaining sites contributed influenza positive specimens.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
CONUS					
California					
Beale AFB		1			1
Travis AFB		2			2
Vandenberg AFB		1			1
Connecticut					
USCG Academy		2			2
Maryland					
NCRM - Walter Reed NMMC		1			1
Mississippi					
Keesler AFB	1	1			2
Nevada					
Nellis AFB		1		1	2
New York					
USMA - West Point		2			2
Ohio					
Wright-Patterson AFB		1			1
Texas					
SAMMC		1	1		2
Washington					
Fairchild AFB			1		1
NH Bremerton		3			3
OCONUS					
Cambodia					
NAMRU-2 *	2	1	6		9
Germany					
Landstuhl RMC		1			1
Japan					
Kadena AB		2			2
Yokota AB		1			1
South Korea					
Osan AB		1			1
Grand Total	3	22	8	1	34

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

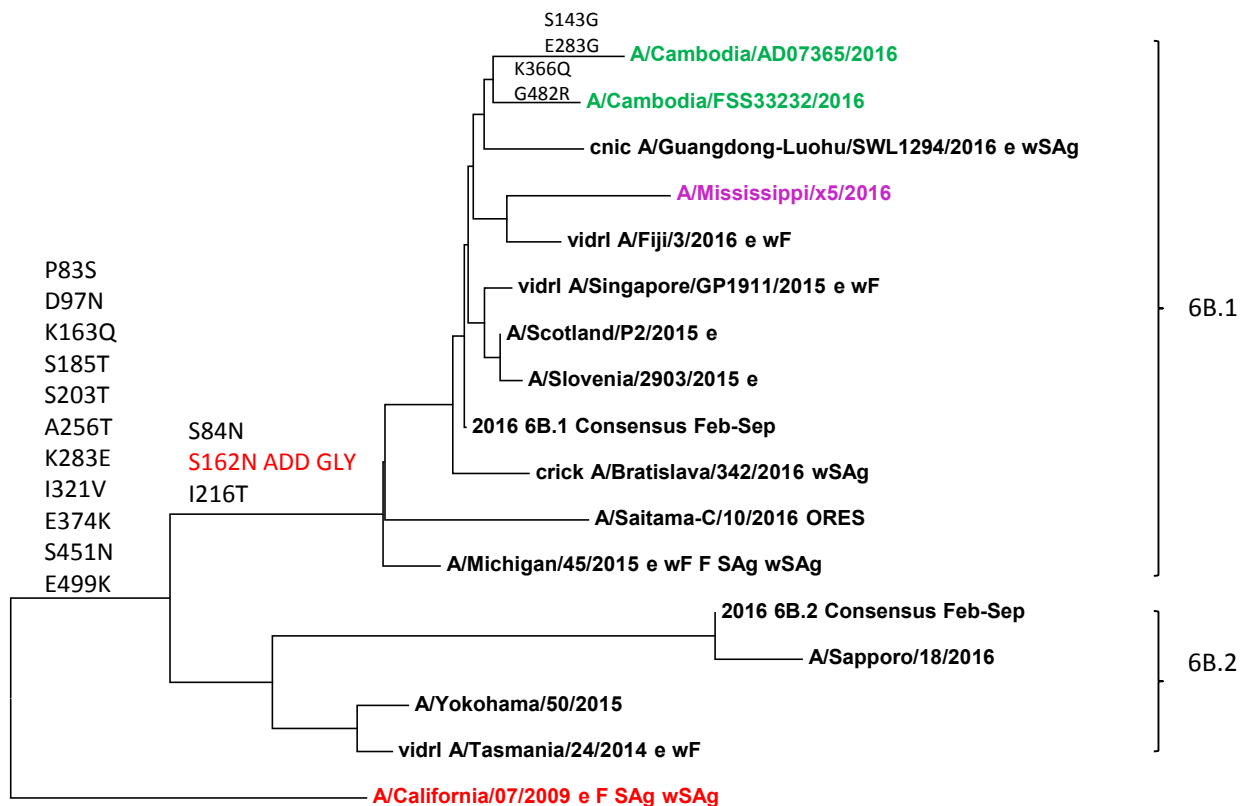
- Among the influenza A isolates, 12.0% were influenza A(H1N1)pdm09. The influenza A(H1N1)pdm09 sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009-like virus (Figure 2).
- The A(H1N1)pdm09 isolates characterized for this report exhibited an overall protein homology of 96.7-97.1% compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus.
- All three of the A(H1N1)pdm09 HA sequences for this report contain mutations consistent with one of the circulating subgroup, referred as group 6B, and all classified as clade 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 18 mutations present in the A(H1N1)pdm09 isolates, six occurred at predicted antigenic sites (zero at site A, one at site B, zero at site C, three at site D, and two at site E) and two occurred at the receptor binding site.^{2,5}

Figure 2. Influenza A(H1N1)pdm09 HA Phylogenetic Analysis

Current 2016-2017 A(H1N1)pdm09 Vaccine strain:
A/California/07/2009

Reference Strain
September 2016
November 2016

ADD GLY Create Glycosylation Motif
F – CDC Reference Antigen
wF – WHOcc Reference Antigen
SAg - Serology Antigen
wSAg – WHOcc Serology Antigen
e Egg Isolate
ORES - Oseltamivir Resistant

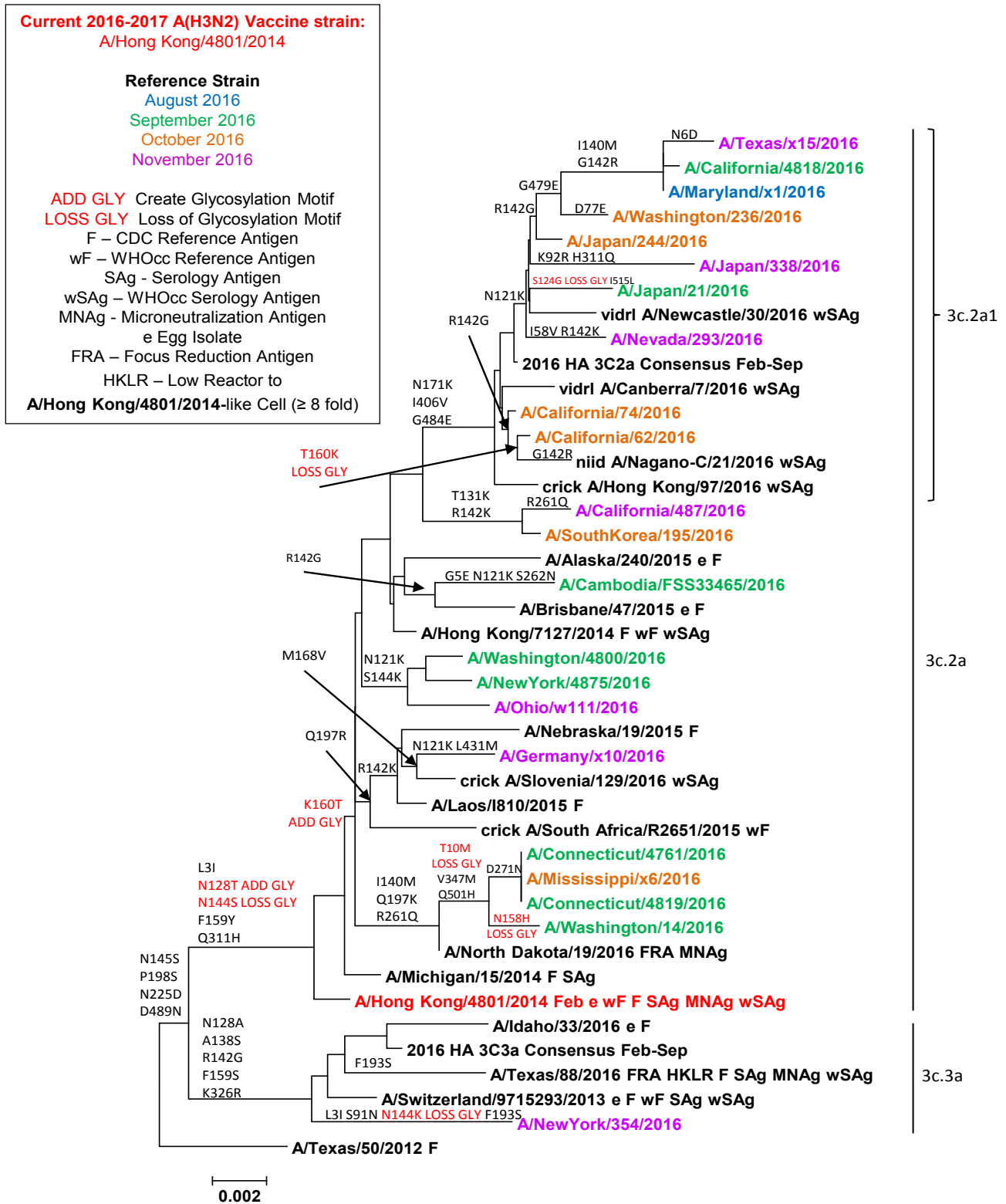


0.002

Influenza A(H3N2)

- Among the influenza A isolates, 88.0% 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 3).
- The A(H3N2) isolates characterized for this report exhibited an overall protein homology of 98.2-99.3% 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. Twenty-one (95.4%) of the influenza A(H3N2) sequences classified as subclade 3C.2a and one (4.5%) classified as subclade 3C.3a. Of note, 10 (47.6%) of the 3C.2a isolates fall into the newly defined subclade 3C.2a1 which is defined by the 171K, 406V, and 484E mutations.
- As Among the influenza A(H3N2) isolates characterized in this report, six mutations; T10M (threonine to methionine), S124G (serine to glycine), N144S (asparagine to serine), N144K (asparagine to lysine), N158H (asparagine to histidine), and T160K (threonine to lysine) 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 39 mutations present in the A(H3N2) specimens, 14 occurred at predicted antigenic sites (six at site A, four at site B, zero at site C, zero at site D, and four at site E) and two occurred at the receptor binding site.^{2,5}

Figure 3. Influenza A(H3N2) HA Phylogenetic Analysis



Influenza B

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains and are midpoint rooted for both the B/Victoria isolates (Figure 4) and B/Yamagata isolates (Figure 5).
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.¹ Eight (88.9%) of the nine influenza B isolates characterized in this report fall into the Victoria lineage, while the other one (11.1%) fall into the Yamagata lineage.
- The influenza B/Victoria isolates characterized for this report exhibited a protein homology of 98.7-98.9% when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-like virus, while the influenza B/Yamagata isolate exhibited a protein homology of 98.6% when compared to the 2016-2017 B/Yamagata vaccine strain, B/Phuket/3073/2013-like virus.
- All of the influenza B/Victoria isolates fall into clade V1A, while the influenza B/Yamagata isolate fall into clade Y3.
- In the Victoria lineage, one mutation, A199T (alanine to threonine) was observed that adds a glycosylation motif. In the Yamagata lineage, one mutation, D197N (aspartic acid to asparagine) was observed that adds a glycosylation motif.

Figure 4. Influenza B/Victoria HA Phylogenetic Analysis

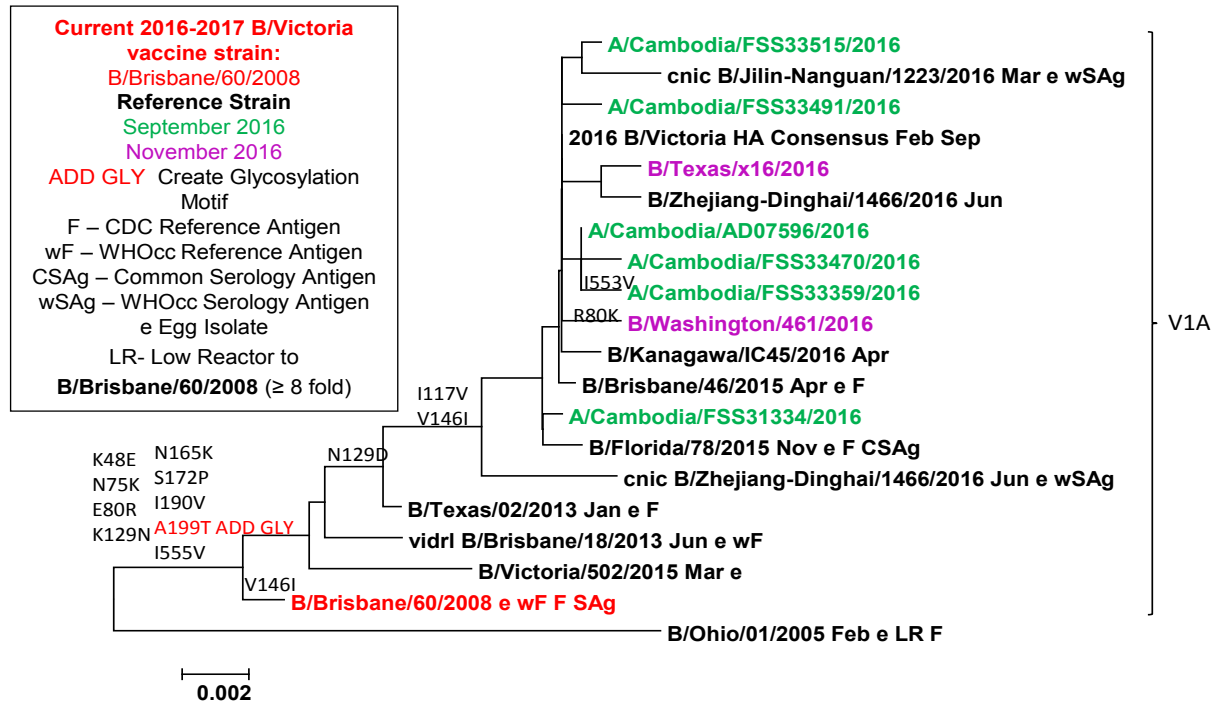
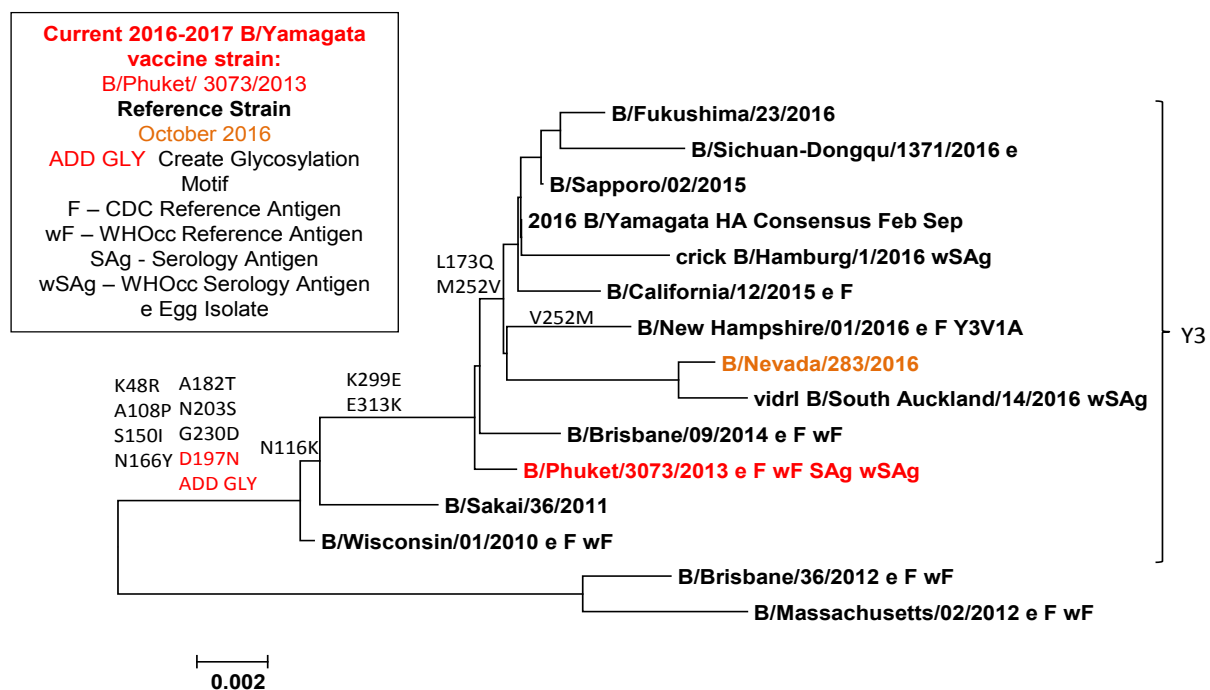


Figure 5. Influenza B/Yamagata HA Phylogenetic Analysis



References:

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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).

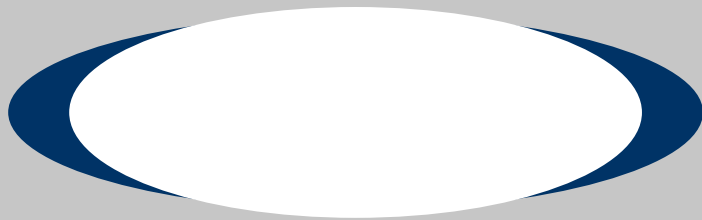
Sentinel Site Surveillance

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.

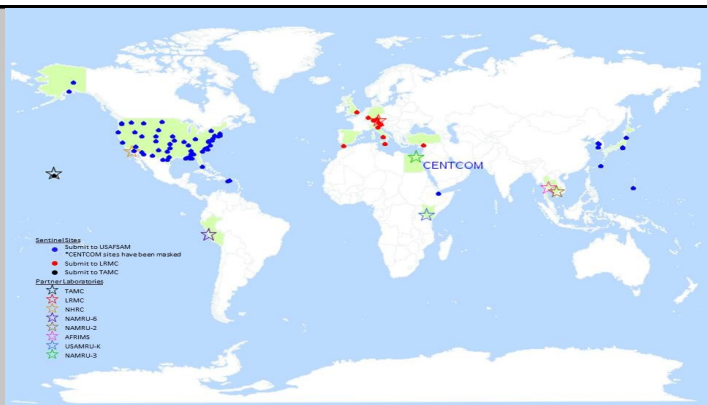
Errata:



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.

