



Cumulative Results

Locations	80
Collected	4,361
Tested	4,079

Influenza A 1,248

A(H1N1)pdm09	20
A(H1N1)pdm09 & Influenza B	1
A(H3N2)	1,222
A(H3N2) & Influenza B	2
A(H3N2) & RSV	1
A/not subtyped	1
A/not subtyped & Rhino/Enterovirus	1

Influenza B* 273

B	272
B & Human Metapneumovirus & Rhino/Enterovirus	1

Other Respiratory Pathogens 911

Adenovirus	58
<i>Bordetella pertussis</i>	0
<i>Chlamydomphila pneumoniae</i>	3
Coronavirus	107
Human Metapneumovirus	65
<i>Mycoplasma pneumoniae</i>	34
Parainfluenza	142
RSV	164
Rhino/Enterovirus	221
Non-influenza Viral Coinfections	109
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

12 - 25 March 2017 (Surveillance Weeks 11 & 12)

- During 12 - 25 March 2017, a total of 408 specimens were collected from 51 locations. Results were finalized for 275 specimens from 44 locations. During Week 11, two influenza A(H1N1)pdm09, one influenza A/not subtyped, 42 influenza A(H3N2), and 48 influenza B viruses were identified. During Week 12, three influenza A(H1N1)pdm09, 41 influenza A(H3N2), and 35 influenza B viruses were identified. Approximately 42% of specimens tested positive for influenza during Week 11. Approximately 44% of specimens tested positive for influenza during Week 12. The influenza percent positive for the season is approximately 37%.
- According to CDC FluView, during Week 12, influenza activity is still decreasing, but remained elevated in the United States. A cumulative rate for the season of 54.1 laboratory-confirmed influenza-associated hospitalizations per 100,000 population was reported. Six influenza pediatric deaths were reported in Week 12. (CDC, [Flu View Report Week 12](#), cited 31 March 2017).

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DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1. Finalized results by region and location for specimens collected during Weeks 11 & 12

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	B	Adenovirus	Coronavirus	hMPV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & Corona & Para	Adeno & RSV	Adeno & Rhino/Enterovirus	Corona & hMPV	Corona & Para	Para & Rhino/Enterovirus	RSV & Rhino/Enterovirus	No Pathogen	Total
Deployed	Country 1, Location B	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2
	Country 2, Location A	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
PACOM	Eielson AFB, AK	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1
	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2
	Yokota AB, Japan	-	1	-	4	-	-	-	1	-	1	-	-	-	-	-	-	-	-	2	9
Region 1	Hanscom AFB, MA	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 2	Ft Drum, NY	-	7	-	6	-	1	-	-	1	1	-	-	-	-	-	-	-	-	-	16
	JB McGuire-Dix-Lakehurst, NJ	-	2	-	1	1	-	1	-	-	1	-	-	-	-	-	-	-	-	1	7
	USMA - West Point, NY	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	2
Region 3	Dover AFB, DE	-	3	-	2	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	7
	JB Anacostia-Bolling, DC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	JB Andrews, MD	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	JB Langley-Eustis, VA	2	23	-	8	-	-	2	2	1	3	-	-	-	-	-	-	-	-	16	57
Region 4	Eglin AFB, FL	-	1	-	1	1	-	-	-	-	-	-	-	-	1	-	-	-	-	-	4
	Ft Bragg, NC	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	2
	Ft Campbell, KY	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	7
	Hurlburt Field, FL	-	3	-	2	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2	8
	Keesler AFB, MS	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2
	Maxwell AFB, AL	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2
	Moody AFB, GA	-	2	-	10	-	-	2	1	1	2	1	1	-	-	1	-	-	-	2	23
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Shaw AFB, SC	-	22	-	4	-	-	2	-	-	1	-	-	-	-	-	-	-	-	3	32
	Tyndall AFB, FL	-	4	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7
Region 5	Wright-Patterson AFB, OH	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4

(Cont'd on page 3)

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

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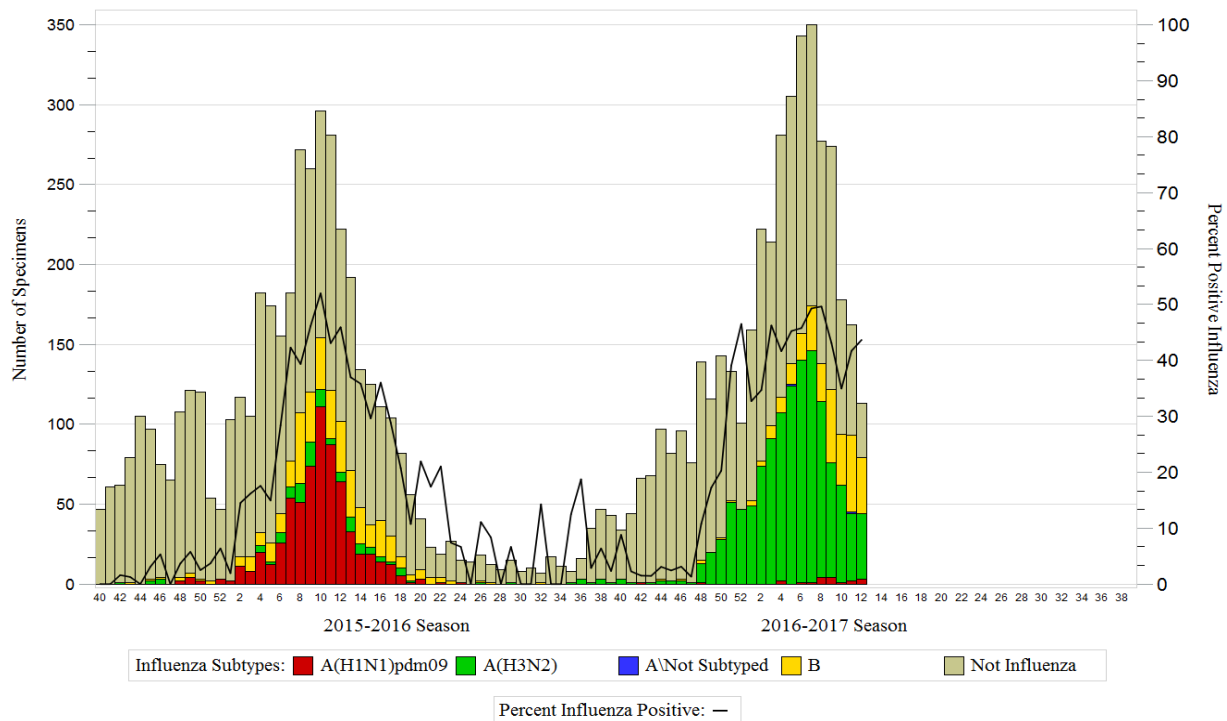
Table 1. Finalized results by region and location for specimens collected during Weeks 11 & 12
(Cont'd from page 2)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	B	Adenovirus	Coronavirus	hMPV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & Corona	Adeno & Corona & Para	Adeno & RSV	Adeno & Rhino/Entero	Corona & hMPV	Corona & Para	Para & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total
Region 6	Altus AFB, OK	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1
	Cannon AFB, NM	-	-	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	5
	Laughlin AFB, TX	1	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	4
	Little Rock AFB, AR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Sheppard AFB, TX	-	-	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	4
	Tinker AFB, OK	-	2	-	1	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	5
Region 7	McConnell AFB, KS	-	-	-	5	-	-	-	-	-	1	-	-	-	-	-	-	-	1	1	8
	Offutt AFB, NE	-	-	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	3
Region 8	Ellsworth AFB, SD	-	2	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	6
	EE Warren AFB, WY	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	3	5
	Hill AFB, UT	-	-	-	1	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	3
	Minot AFB, ND	1	1	-	4	-	-	-	1	1	1	-	-	-	-	-	-	-	-	3	12
	Peterson AFB, CO	1	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
Region 9	Davis-Monthan AFB, AZ	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Nellis AFB, NV	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Travis AFB, CA	-	1	-	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	5
Region 10	Fairchild AFB, WA	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	2
	NH Bremerton, WA	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Total		5	83	1	83	2	6	10	9	6	15	1	1	1	1	1	1	1	1	47	275

*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 12 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.

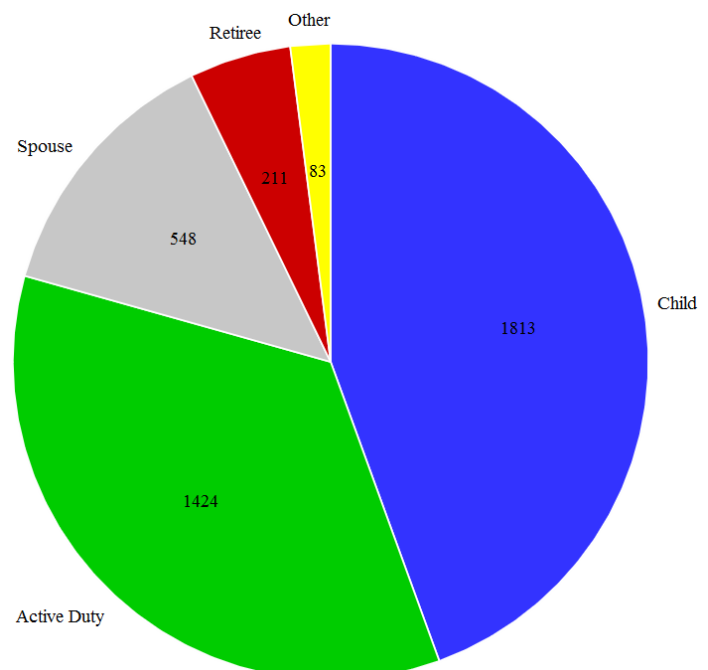
Table 2. ILI by age group for the 2016-2017 surveillance year through Week 12

Age Group	Frequency	Percent
0-5	954	23.39
6-9	372	9.12
10-17	492	12.06
18-24	562	13.78
25-44	1233	30.23
45-64	378	9.27
65+	88	2.16

Demographic Summary

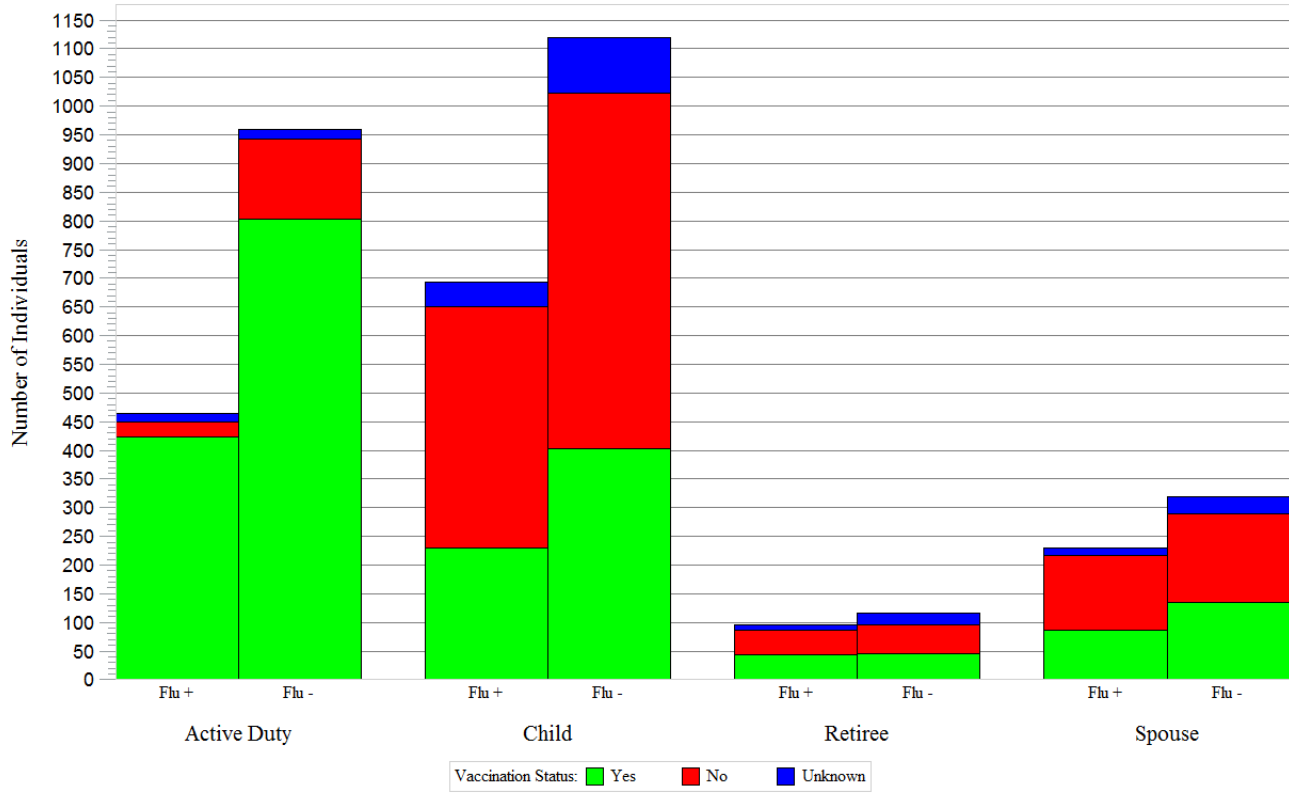
Of 4,079 ILI cases, 1,424 (34.9%) are service members, 1,813 (44.5%) are children, 548 (13.4%) are spouses, and 294 (7.2%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=4,079) is 21 (range 0, 96).

Graph 2. ILI by beneficiary status for the 2016-2017 surveillance year through Week 12

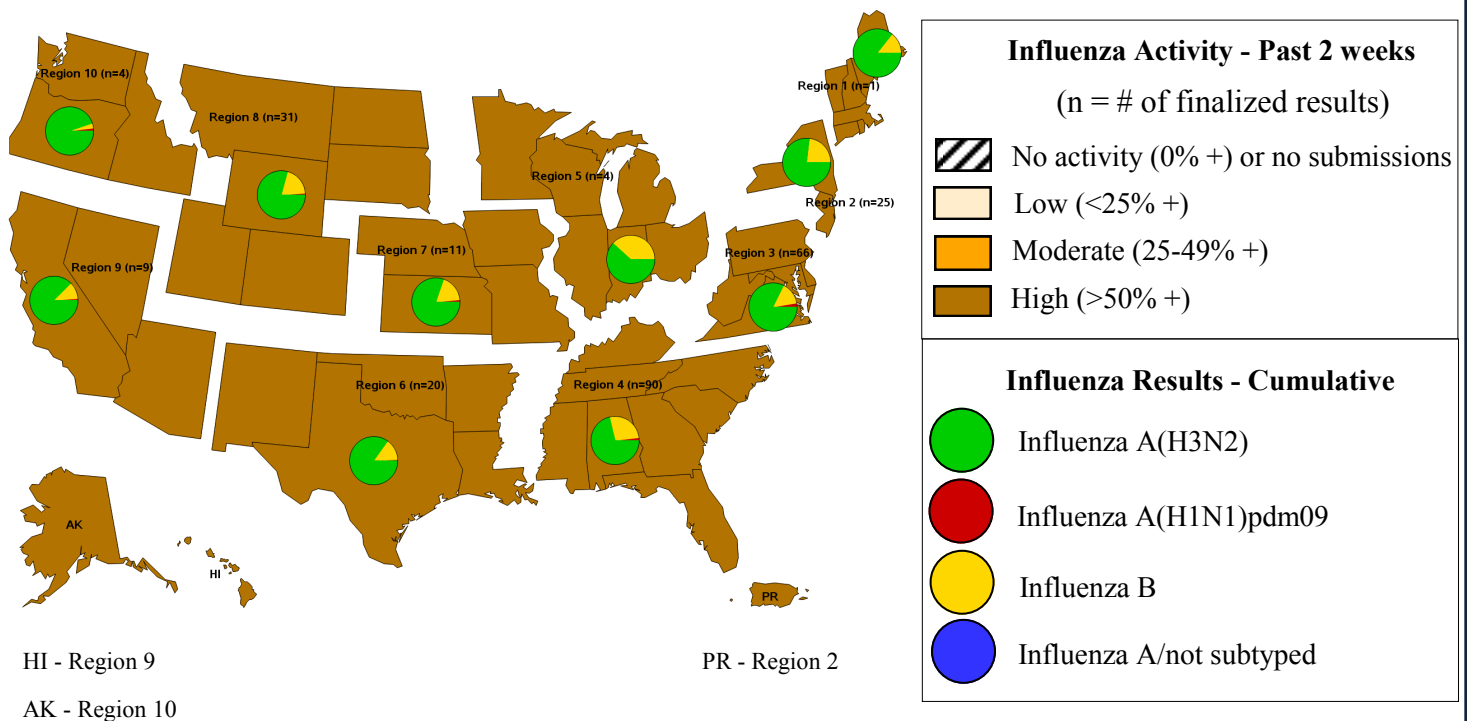


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Graph 3. Vaccination status by beneficiary type for the 2016-2017 surveillance year through Week 12

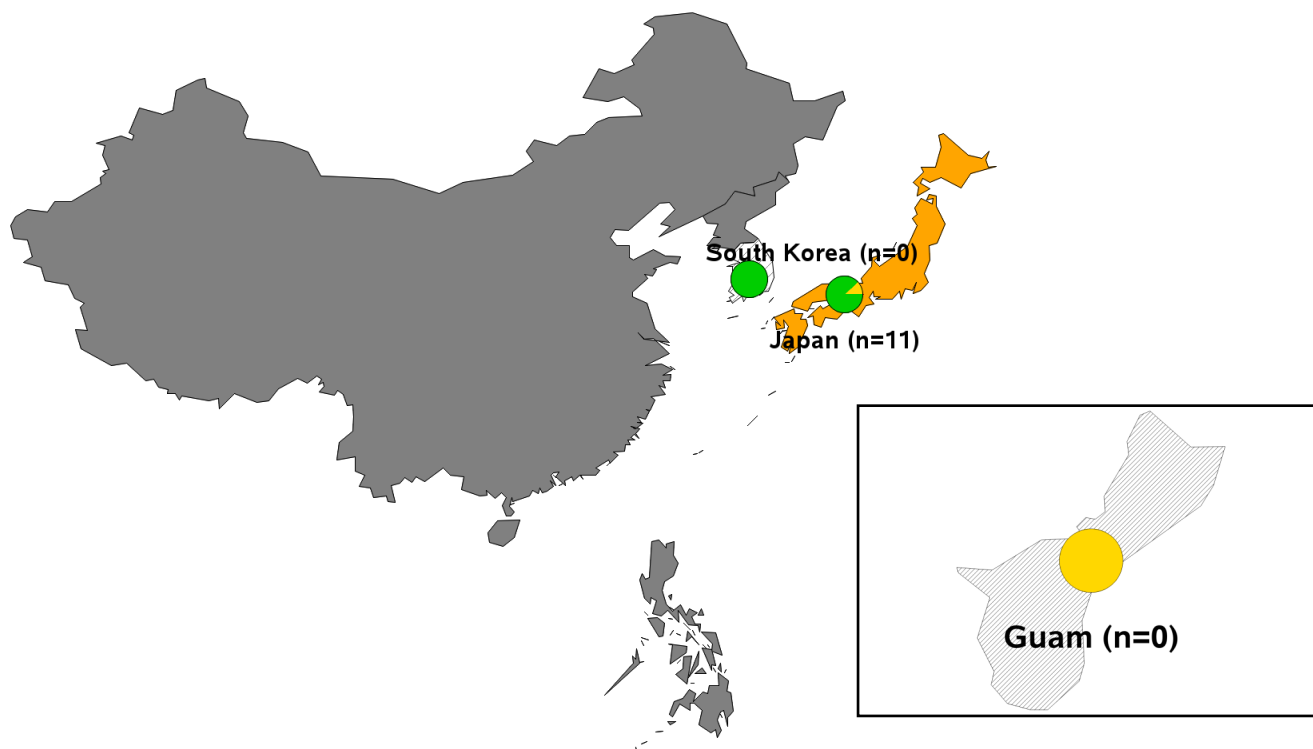


Map 1. Influenza subtypes and activity level by U.S. region for the 2016-2017 surveillance year through Week 12



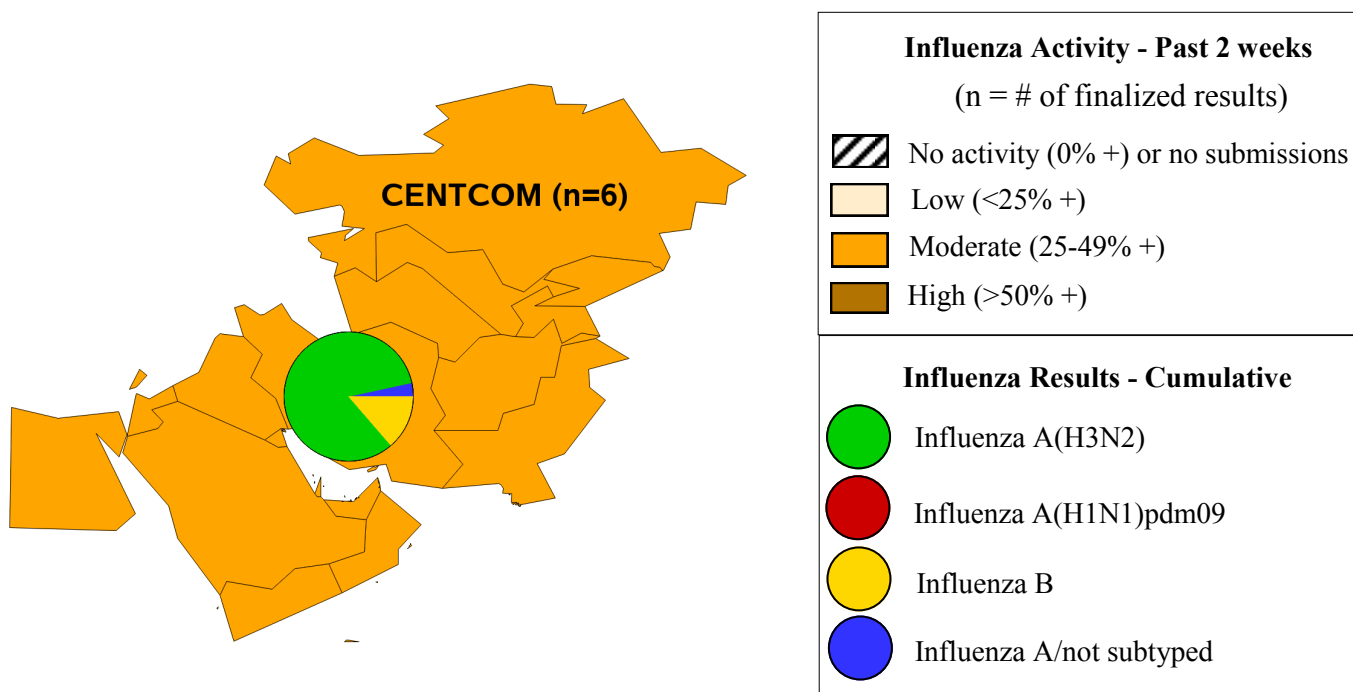
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Map 2. Influenza subtypes and activity level by country for the 2016-2017 surveillance year through Week 12 (Pacific)



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 12



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

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Laboratory Results—Through Current Surveillance Week 12

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/not subtyped & Rhino/Entero	A(H1N1)pdm09 & B	A(H3N2) & B	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	-	9	-	-	-	-	-	7	-	-	-	1	-	-	-	1	1	1	-	7	27
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	32	1	1	-	-	-	1	-	-	-	6	-	-	-	-	6	2	-	12	61
EUCOM	Incirlik AB, Turkey	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	2	4
PACOM	CFA Okinawa, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Eielson AFB, AK	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	5	7
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	5
	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-	1	3
	Kadena AB, Japan	-	4	-	-	-	-	-	-	-	-	-	1	-	3	-	-	2	1	1	22	34
	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	-	33	-	-	-	-	-	5	-	1	-	3	1	2	1	2	8	4	-	61	121
	Hanscom AFB, MA	-	3	-	-	-	-	-	1	-	1	-	-	-	1	2	-	-	1	-	2	11
	USCG Academy, CT	-	9	-	-	-	-	-	1	-	-	-	1	1	1	-	-	3	-	2	6	24
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	1	30	-	-	-	-	-	39	-	5	1	4	8	1	6	8	2	5	-	43	153
	JB McGuire-Dix-Lakehurst, NJ	-	47	-	-	-	-	-	1	-	3	-	6	8	2	7	5	11	5	-	70	165
	USMA - West Point, NY	-	86	-	-	-	-	-	8	-	10	-	5	6	2	7	12	7	4	-	117	264
Region 3	Dover AFB, DE	-	15	-	-	-	-	-	4	-	2	-	1	1	1	-	1	2	-	-	30	57
	JB Anacostia-Bolling, DC	-	13	-	-	-	-	-	3	-	-	-	-	-	-	-	1	-	-	-	-	17
	JB Andrews, MD	2	22	-	-	-	-	-	10	-	-	-	2	1	-	2	2	1	2	-	37	81
	JB Langley-Eustis, VA	4	136	-	-	1	1	-	18	-	-	-	3	7	2	9	20	29	9	-	192	431
	NCRM - Walter Reed NMMC, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	CGS Mobile, AL	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
Region 4	Columbus AFB, MS	-	5	-	-	-	-	-	1	-	-	-	2	-	-	-	-	1	-	-	14	23
	Eglin AFB, FL	1	13	-	-	-	-	-	4	-	4	-	1	-	1	-	5	9	4	-	28	70
	Ft Bragg, NC	1	8	-	-	-	-	-	4	-	-	-	1	1	1	3	2	6	4	3	28	62
	Ft Campbell, KY	1	15	-	-	-	-	-	6	1	2	-	-	1	-	-	3	-	4	-	14	47
	Hurlburt Field, FL	-	17	-	-	-	-	-	3	-	1	-	1	-	1	1	2	1	-	-	16	43
	JB Charleston (AF), SC	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	12
	Keesler AFB, MS	-	1	-	-	-	-	-	-	-	-	-	-	-	1	2	2	2	-	-	12	20
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	5	6
	Maxwell AFB, AL	-	10	-	-	-	-	-	1	-	-	-	-	1	-	1	-	1	-	-	13	27
	Moody AFB, GA	-	25	-	-	-	-	-	23	-	1	-	1	5	-	8	7	8	12	1	43	134
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	NH Camp Lejeune, NC	-	2	-	-	-	1	-	-	-	-	-	-	-	1	-	-	1	-	-	7	12
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	3
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	23	-	-	-	-	-	7	-	-	-	-	-	2	-	3	1	-	-	18	54
	Seymour Johnson AFB, NC	2	16	-	-	-	-	-	1	-	2	-	-	-	1	1	2	1	-	-	10	36
	Shaw AFB, SC	-	47	-	-	-	-	-	20	-	1	-	5	3	1	3	1	6	-	-	35	122
	Tyndall AFB, FL	-	7	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	12

(Cont'd on page 8)

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

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Laboratory Results—Through Current Surveillance Week 12

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/not subtyped	A/not subtyped & Rhino/Entero	A(H1N1)pdm09 & B	A(H3N2) & B	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	-	-	-	-	-	1	-	-	-	-	-	1	2	1	1	-	1	7	17
	Wright-Patterson AFB, OH	-	10	-	-	-	-	-	7	-	-	-	1	1	1	1	-	1	2	-	30	54
Region 6	Altus AFB, OK	-	7	-	-	-	-	-	-	-	1	-	1	1	-	-	5	6	3	-	34	58
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	1	-	-	-	-	2	-	1	-	-	8	12
	Cannon AFB, NM	-	12	-	-	-	-	-	3	-	-	-	2	-	1	1	-	4	1	-	26	50
	Ft Polk, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	3
	JBSA Lackland, TX	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1
	Laughlin AFB, TX	1	-	-	-	-	-	-	1	-	-	-	1	2	-	-	-	-	-	-	4	9
	Little Rock AFB, AR	-	11	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	6	18
	Sheppard AFB, TX	-	60	-	-	-	-	-	9	-	1	-	9	3	-	6	2	8	-	-	67	165
	Tinker AFB, OK	1	96	-	-	-	-	1	18	-	2	-	8	2	1	6	5	8	4	-	108	260
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	12
Region 7	McConnell AFB, KS	-	25	-	-	-	-	-	8	-	1	-	4	-	1	3	3	6	3	-	26	80
	Offutt AFB, NE	1	32	-	-	-	-	-	5	-	1	-	5	1	-	1	1	7	1	-	41	96
Region 8	Ellsworth AFB, SD	-	14	-	-	-	-	-	7	-	-	-	3	-	-	3	1	3	-	-	25	56
	FE Warren AFB, WY	-	35	-	-	-	-	-	2	-	3	-	4	-	2	4	6	4	-	-	44	104
	Hill AFB, UT	-	28	-	-	-	-	-	2	-	-	-	3	1	-	5	4	4	1	-	32	80
	Malmstrom AFB, MT	-	7	-	-	-	-	-	3	-	-	-	-	-	1	-	-	1	-	-	7	19
	Minot AFB, ND	1	22	-	-	-	-	-	8	-	-	-	2	1	1	1	4	4	2	-	27	73
	Peterson AFB, CO	1	19	-	-	-	-	-	9	-	-	-	3	-	-	1	9	3	4	-	24	73
	USAF Academy, CO	-	1	-	-	-	-	-	-	-	-	-	-	1	-	-	1	1	-	-	2	6
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	-	13	-	-	-	-	-	2	-	-	-	-	-	-	5	1	6	5	-	22	54
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Luke AFB, AZ	-	-	-	-	-	-	-	2	-	1	-	2	-	-	-	3	1	1	-	8	18
	Nellis AFB, NV	1	3	-	-	-	-	-	3	-	3	-	1	-	-	4	4	5	7	-	23	54
	Travis AFB, CA	-	55	-	-	-	-	-	3	-	-	1	4	4	-	6	13	12	4	-	35	137
	Vandenberg AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Fairchild AFB, WA	2	16	-	-	-	-	-	1	-	3	-	3	-	-	5	2	4	-	-	43	79
	JB Lewis-McChord, WA	-	2	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	3
	Mt Home AFB, ID	-	22	-	-	-	-	-	-	-	1	1	1	-	1	23	12	12	5	-	69	147
	NH Bremerton, WA	-	67	-	-	-	-	-	3	-	6	-	3	1	2	7	7	7	4	-	25	132
Total		20	1222	1	1	1	2	1	272	1	58	3	107	65	34	142	164	221	109	8	1647	4079

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

Molecular Sequence Analysis Report #6

This is the sixth USAFSAM influenza sequence surveillance report for the 2016-2017 influenza season and includes a total of 113 specimens collected between 13 July 2016 and 25 January 2017, with 78 influenza positive specimens sequenced at USAFSAM and 35 hemagglutinin sequences provided by the Naval Health Research Center (NHRC) in San Diego. Among the specimens analyzed, four (3.5%) were influenza A(H1N1)pdm09, 101 (89.4%) were influenza A(H3N2), two (1.8%) were influenza B/Victoria lineage, and six (5.3%) were influenza B/Yamagata lineage. Figure 1 shows the proportion of specimens sequenced at USAFSAM and NHRC for hemagglutinin (HA) and analyzed for this report by subtype or lineage. The number of sequences for each subtype and lineage included in this report are shown for each sentinel site and partner lab location in Table 1. Figures 2-5 display the phylogenetic relationships among HA sequences for influenza A(H1N1)pdm09, A(H3N2), and influenza B/Victoria and B/Yamagata lineages, respectively.

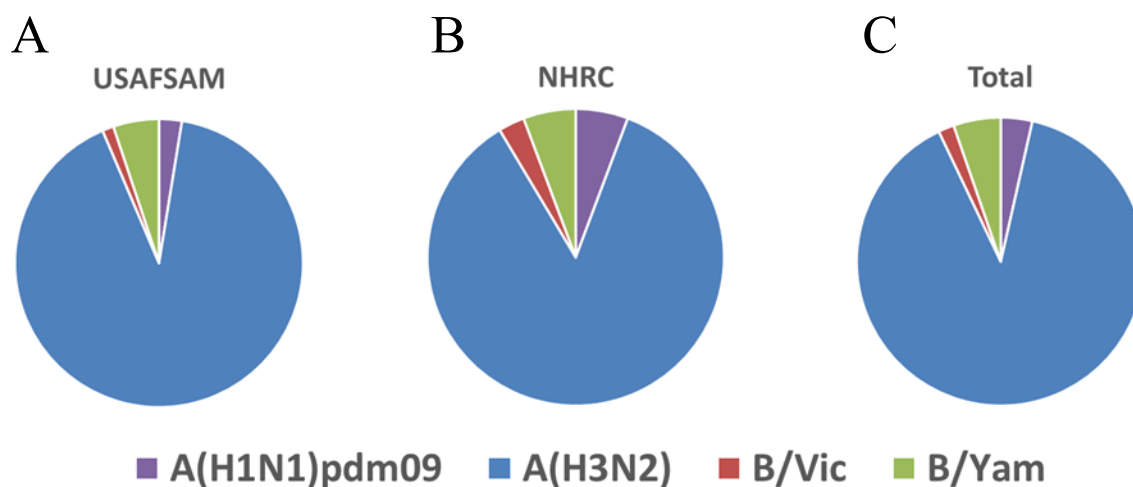


Figure 1: Proportion of hemagglutinin (HA) sequence subtypes and lineages analyzed for this report, sequenced at A) the United States Air Force School of Aerospace Medicine (USAFSAM), B) Naval Health Research Institute (NHRC), and C) total laboratories.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1: Influenza subtypes and lineages from corresponding sentinel sites and data from contributing labs included in the analyses for this report.

	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
CONUS					
Arizona					
Davis Monthan AFB		1			1
California					
Beale AFB		2			2
NHRC	2	16		1	19
Colorado					
Peterson AFB		2			2
Connecticut					
USCG Academy		1			1
Georgia					
Moody AFB		1			1
NHRC		2	1		3
Idaho					
Mt Home AFB		3			3
Illinois					
NHRC		1		1	2
Kansas					
McConnell AFB		1			1
Kentucky					
Ft Campbell		3			3
Maryland					
US Naval Academy		1			1
Massachusetts					
Hanscom AFB, MA		1			1
Missouri					
NHRC		3			3
Montana					
Malmstrom AFB				1	1
Nebraska					
Offutt AFB	1				1
New Jersey					
JB McGuire-Dix-Lakehurst		4			4

DoD Global, Laboratory-Based, Influenza Surveillance Program

Table 1 (Continued): Influenza subtypes and lineages from corresponding sentinel sites and data from contributing labs included in the analyses for this report.

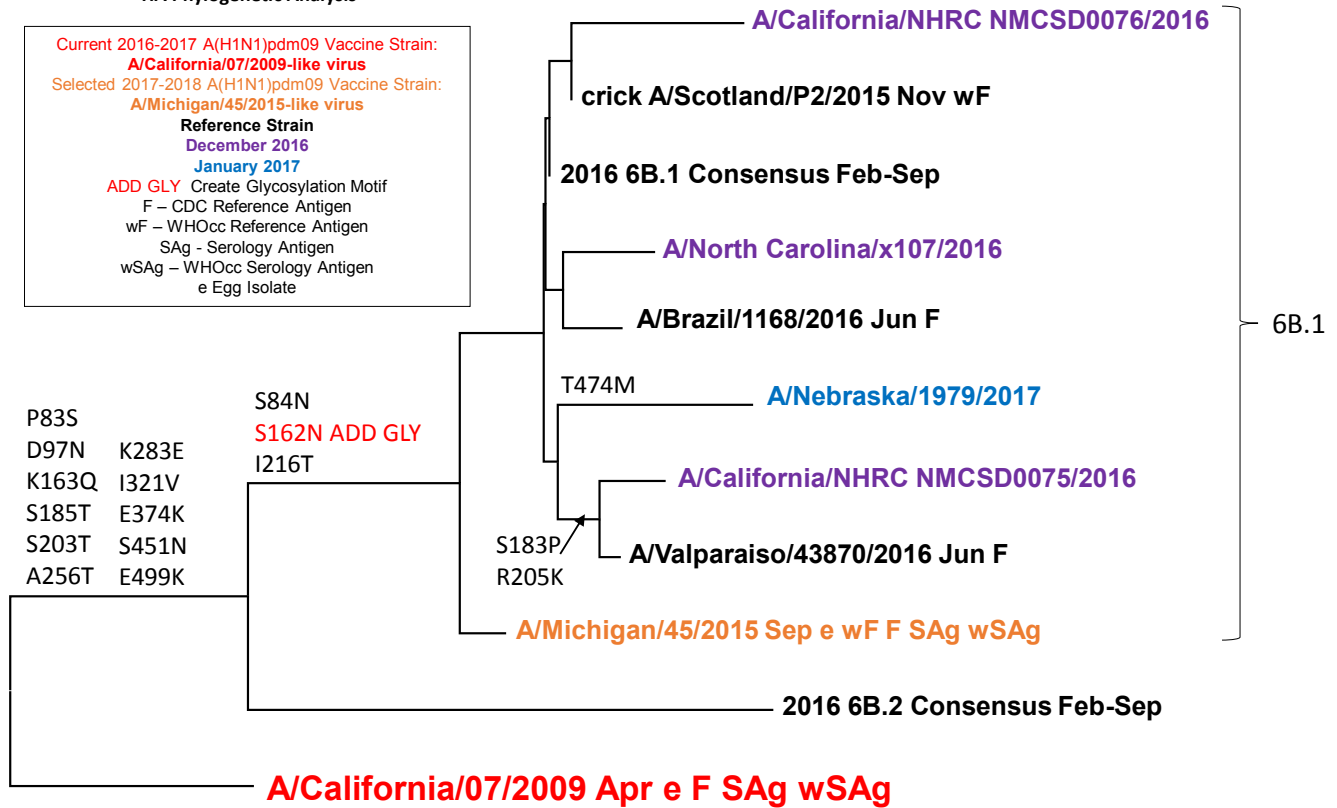
	A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata	Grand Total
New York					
USMA - West Point		3	1		4
Ft Drum				2	2
North Carolina					
NH Camp Lejeune	1	6			7
Ohio					
Wright-Patterson AFB		2			2
Oklahoma					
Altus AFB		2			2
South Carolina					
Shaw AFB		3			3
NHRC		8			8
Texas					
Sheppard AFB		7			7
SAMMC		5			5
Virginia					
JB Langley-Eustis		1			1
Washington					
Fairchild AFB		1			1
NH Bremerton AFB		8			8
Wyoming					
FE Warren AFB		5			5
OCONUS					
Country 1					
Location B		2			2
Country 2					
Location A		3			3
Germany					
Landstuhl RMC		1			1
Japan					
Yokota AB		1			1
South Korea					
Brian Allgood ACH		1			1
Turkey					
Incirlik AB				1	1
Grand Total	4	101	2	6	113

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 105 influenza A isolates, four (3.8%) 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 96.6%-97.0% (average 96.9%) compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus and 99.4%-99.8% (average 99.7%) compared to the A(H1N1)pdm09 vaccine component selection for the 2017-2018 season, A/Michigan/45/2015-like virus. Due to truncated sequences in the data set and low number available, the first 18 bases (six amino acids) and the last 48 bases (16 amino acids) were removed for calculation of the A(H1N1)pdm09 protein homology.
- 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 17 mutations present in the A(H1N1)pdm09 isolates, five occurred at predicted antigenic sites (none at site A, one at site B, none at site C, two at site D, and two at site E) and one occurred at the receptor binding site.^{2,5}

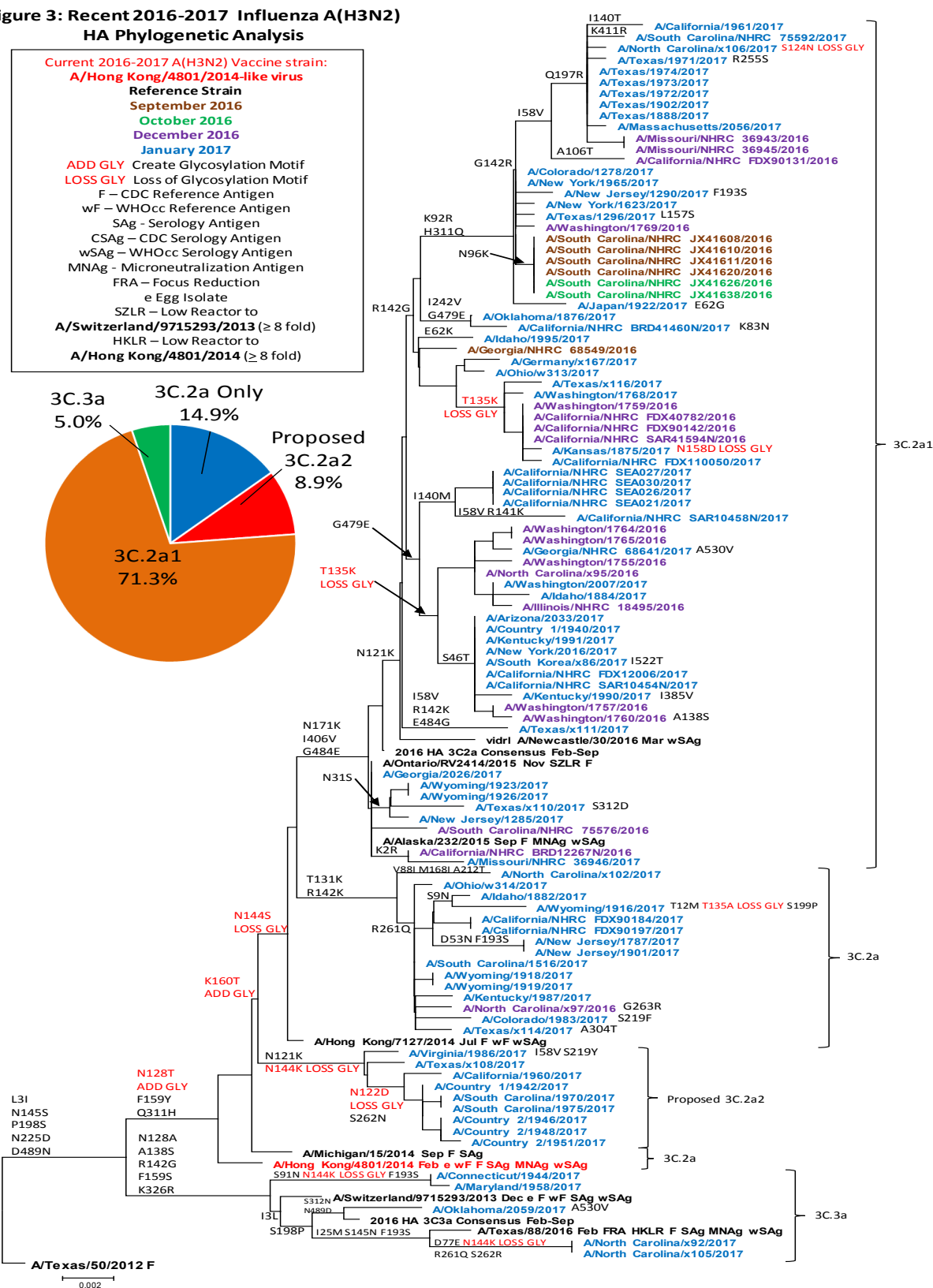
Figure 2: Recent 2016-2017 Influenza A(H1N1)pdm09 HA Phylogenetic Analysis



Influenza A(H3N2)

- Among the 105 influenza A isolates, 101 (96.2%) 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 96.9%-99.1% (average 98.3%) compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014-like virus. Due to truncated sequences in the data set, five sequences were removed for calculation of the A(H3N2) protein homology.
- All of the influenza A(H3N2) isolates sequenced for this report were in clade 3C. Ninety-six (95.0%) of the influenza A(H3N2) sequences classified as subclade 3C.2a with 72 (71.3%) further classified as the newly distinguished subclade within 3C.2a, 3C.2a1 (determined by the mutations N171K, I406V, and G484E) and nine (8.9%) further classified as the proposed subclade 3C.2a2. Five (5.0%) influenza A(H3N2) isolates classified as clade 3C.3a. The mutation N121K was present in 65 (90.3%) of the 3C.2a1 isolates and 74 (73.3%) of the total A(H3N2) isolates. The mutation T135K was present in 26 isolates (36.1% of 3C.2a1 and 25.7% of total) and the combination of mutations R142G and I242V were present in two isolates (2.8% of 3C.2a1 and 2.0% of total).
- Among the influenza A(H3N2) isolates characterized in this report, seven mutations; N122D (asparagine to aspartic acid), S124N (serine to asparagine), T135A (threonine to alanine), T135K (threonine to lysine), N144S (asparagine to serine), N144K (asparagine to lysine), and N158D (asparagine to aspartic acid) 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 59 mutations present in the A(H3N2) specimens, 20 occurred at predicted antigenic sites (seven at site A, four at site B, two at site C, two at site D, and five at site E) and two occurred at the receptor binding site.^{2,5}

Figure 3: Recent 2016-2017 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 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). Please note, one specimen on each B lineage phylogenetic tree was collected from the month of July prior to the 2016-2017 season.
- 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 Two (25.0%) of the influenza B isolates characterized in this report fell into the B/Victoria lineage and six (75.0%) fell into the B/Yamagata lineage.
- Both of the influenza B/Victoria isolates characterized for this report exhibited a protein homology of 99.1% when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-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. No changes in glycosylation motifs were observed for the B/Yamagata isolates.
- 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.

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

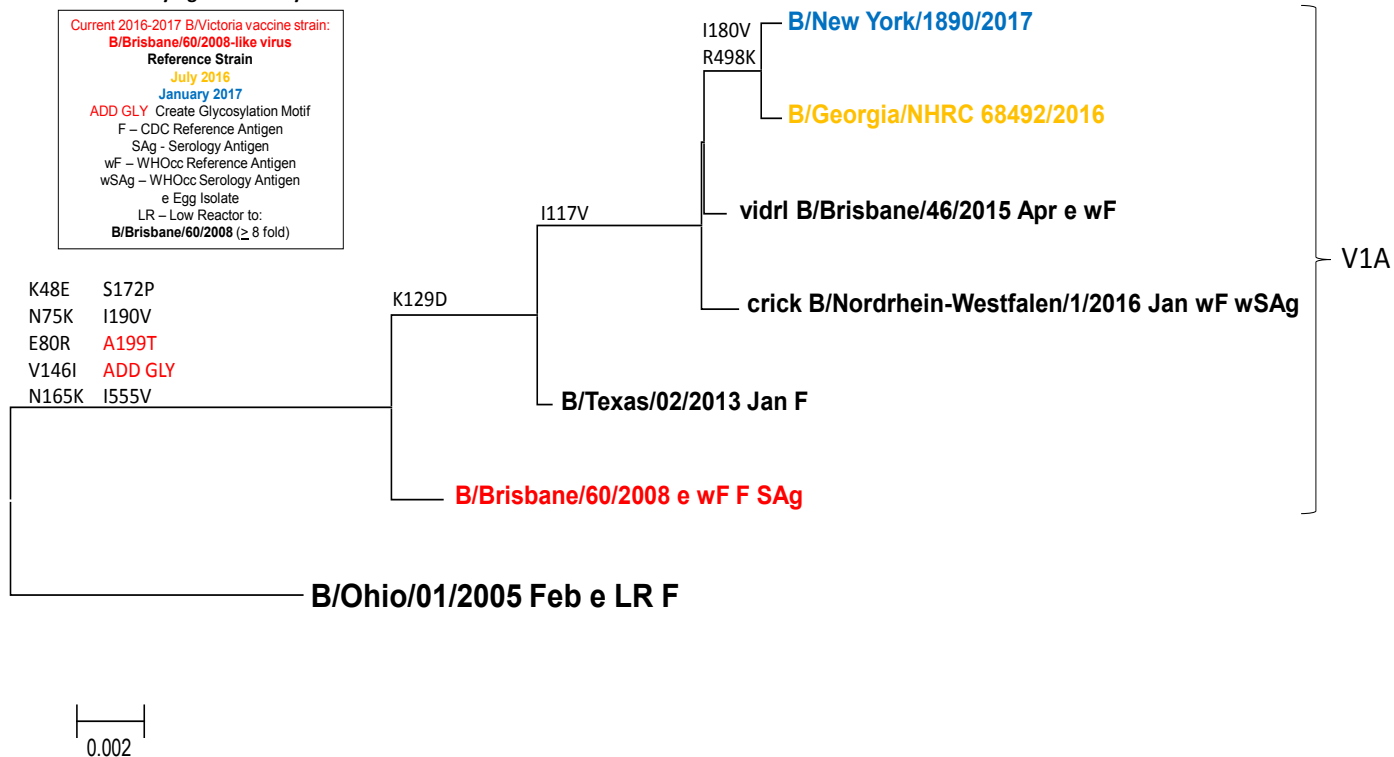
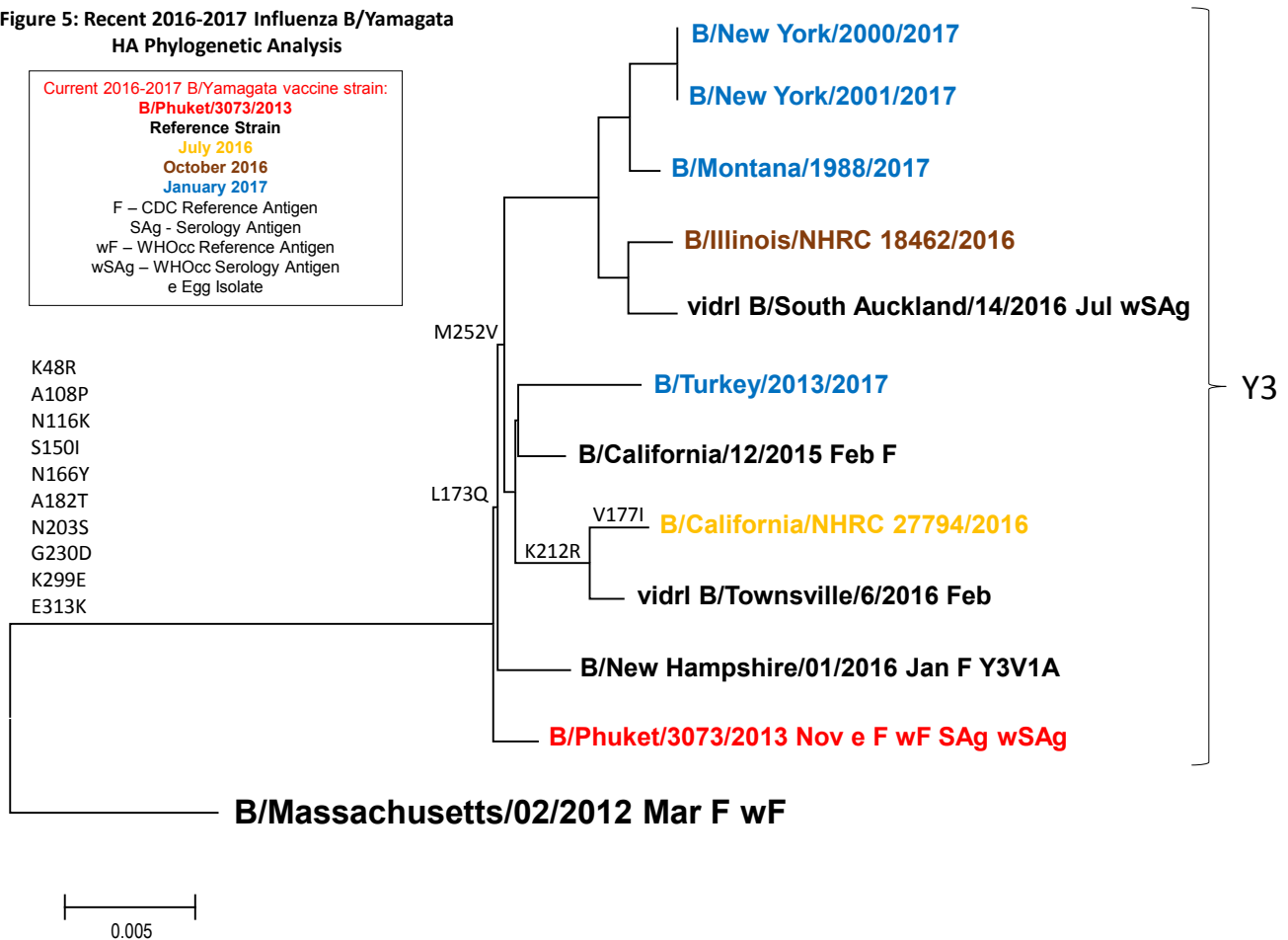


Figure 5: Recent 2016-2017 Influenza B/Yamagata HA Phylogenetic Analysis



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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).

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.

USAFSAM.PHRFlu@us.af.mil

