DoD Global, Laboratory-Based, Influenza Surveillance Program

USAF School of Aerospace Medicine

2014 - 2015

Cumulative Results

Locations	87
Collected	5,411
Tested	5,289

Influenza A	**1,777**
A(H1N1)pdm09	2
A(H3N2)	1,769
A & B	1
A & Coronavirus	1
A & Parainfluenza	1
A(H3N2) & B & Adenovirus & Rhino/Enterovirus	1
A(H3N2) & Coronavirus	1
A(H3N2) & Rhino/Enterovirus	1

Influenza B	**220**
B/Unknown or pending lineage	193
B & Rhino/Enterovirus	1
B/Victoria	6
B/Yamagata	20

Other Respiratory Pathogens	**841**
Adenovirus	94
Bordetella pertussis	0
Chlamydophila pneumoniae	1
Coronavirus	71
Human Metapneumovirus	27
Mycoplasma pneumoniae	29
Parainfluenza	125
RSV	192
Rhino/Enterovirus	215
Non-influenza Co-infections	87

Lab data are current as of 30 March 2015. Results are preliminary and may change as more results are received.

Respiratory Highlights

15-28 March 2015 (Surveillance Weeks 11 & 12)

- During 15-28 March 2015, a total of 166 specimens were collected and received from 40 locations. Results were finalized for 104 specimens from 31 locations. During Week 11, the laboratory identified 12 influenza A(H3N2) and 15 influenza B. During Week 12, five influenza A(H3N2) and 10 influenza B were identified.
- Since the end of last season to present, influenza A(H3N2) has predominated. However, the proportion of influenza B has been increasing in recent weeks. In the past two weeks, approximately 25% of specimens tested positive for influenza (influenza B 15%, influenza A 10%). Overall, we are seeing a downward trend in influenza activity.
- In 2014, enterovirus-D68 (EV-D68) was implicated in a widespread outbreak across the US of severe respiratory illness with some patients experiencing acute flaccid myelitis. A recent study that included children at two Colorado and California hospitals strengthens the evidence that the polio-like illnesses were related to EV-D68 infection. The virus was identified in 48% of individuals with the condition and the proportion likely would have been higher if respiratory samples were collected earlier. For more information, please refer to the 31 March 2015 CIDRAP or the online abstract from The Lancet.

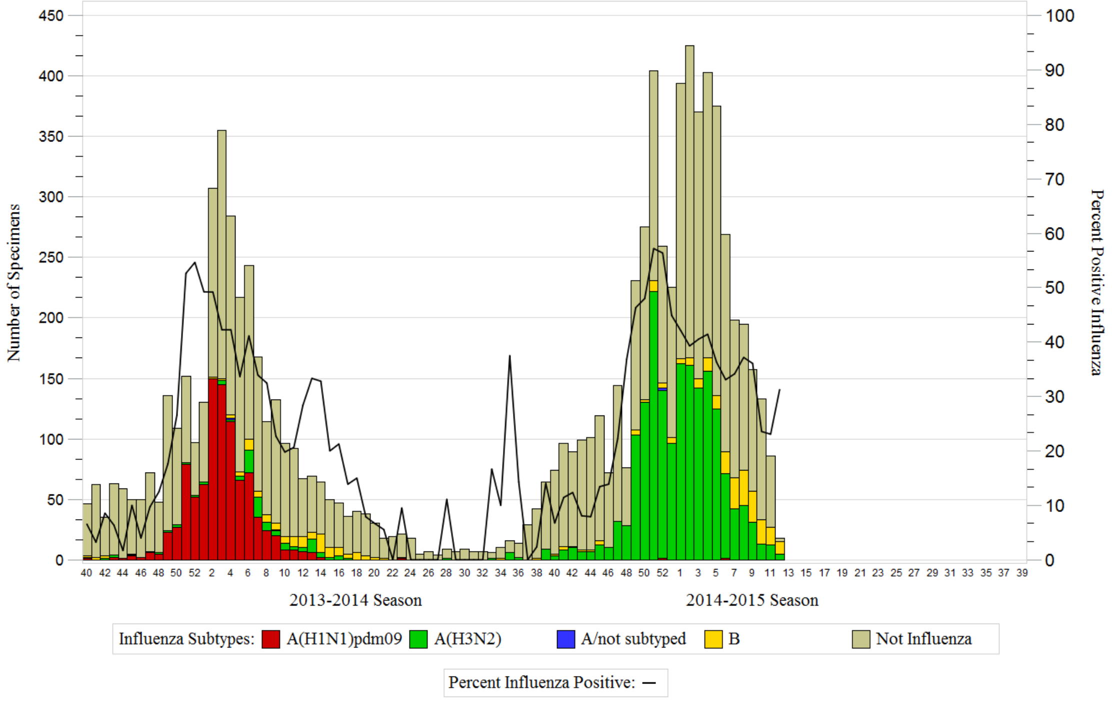
Table 1. Results by region and location for specimens collected and finalized during Weeks 11 & 12

Region*		A(H3N2)	B	Adenovirus	hMNV	Parainfluenza	RSV	No Pathogen	Total
PACOM	Misawa AB, Japan	-	-	-	-	-	-	1	1
	Yokota AB, Japan	1	-	-	-	-	-	-	1
Region 1	Hanscom AFB, MA	-	-	-	-	-	-	1	1
	NHCNE Newport, RI	-	1	-	-	-	-	-	1
	USCG Academy, CT	-	-	1	-	-	-	-	1
Region 2	Ft Drum, NY	7	5	-	-	-	-	3	15
	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	-	3	3
	USMA - West Point, NY	1	1	-	-	-	1	5	8
Region 3	Dover AFB, DE	-	1	-	-	-	-	-	1
Region 4	CGS Mobile, AL	-	1	-	-	-	-	1	2
	Eglin AFB, FL	-	-	-	-	1	-	1	2
	Maxwell AFB, AL	-	-	-	-	-	-	4	4
	Moody AFB, GA	-	1	3	-	1	-	5	10
	NH Beaufort, SC	-	1	-	-	-	-	1	2
	Tyndall AFB, FL	-	-	1	-	-	-	-	1
Region 5	Scott AFB, IL	-	3	1	-	-	-	1	5
	Wright-Patterson AFB, OH	-	-	-	1	-	-	-	1
Region 6	Altus AFB, OK	-	1	-	-	-	-	-	1
	Cannon AFB, NM	-	1	-	-	-	-	-	1
	Sheppard AFB, TX	-	2	-	-	-	-	2	4
	Tinker AFB, OK	1	2	-	-	-	2	3	8
Region 7	Offutt AFB, NE	-	2	-	-	-	-	1	3
Region 8	Ellsworth AFB, SD	2	2	-	-	-	1	2	7
	Minot AFB, ND	-	-	-	-	-	-	2	2
	Peterson AFB, CO	-	1	-	-	-	-	1	2
	USAF Academy, CO	-	-	-	-	-	-	1	1
Region 9	Beale AFB, CA	1	-	-	-	-	-	-	1
	Davis-Monthan AFB, AZ	2	-	-	-	-	-	1	3
	Edwards AFB, CA	1	-	-	-	-	-	-	1
	Travis AFB, CA	1	-	-	-	-	2	7	10
Region 10	Mt Home AFB, ID	-	-	-	-	1	-	-	1
Total		17	25	6	1	3	6	46	104

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

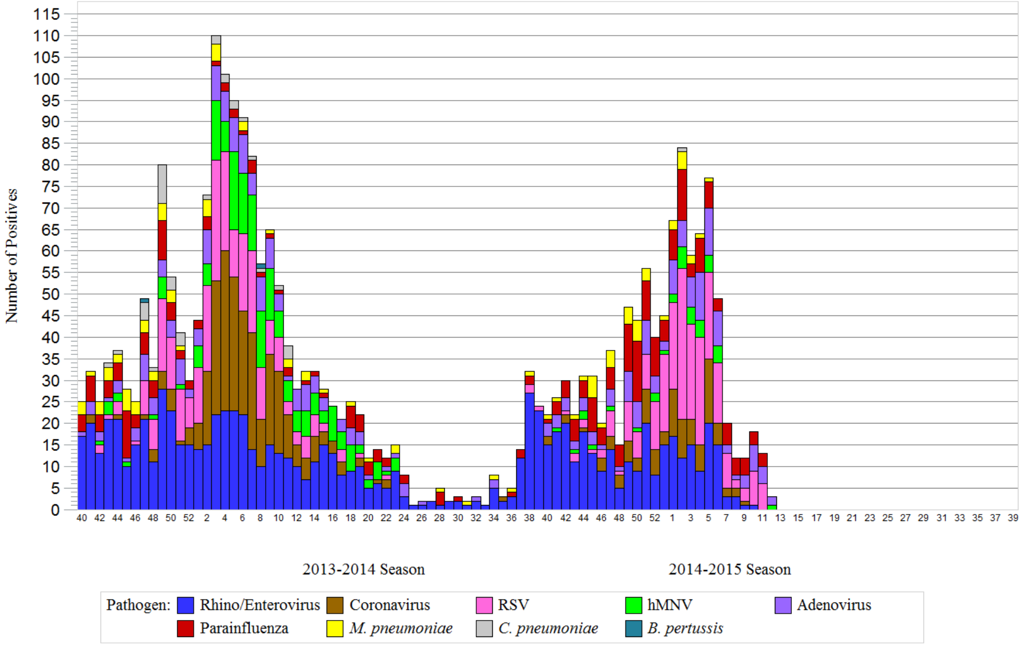
Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2013-2014 surveillance year and through Week 12 of the 2014-2015 surveillance year



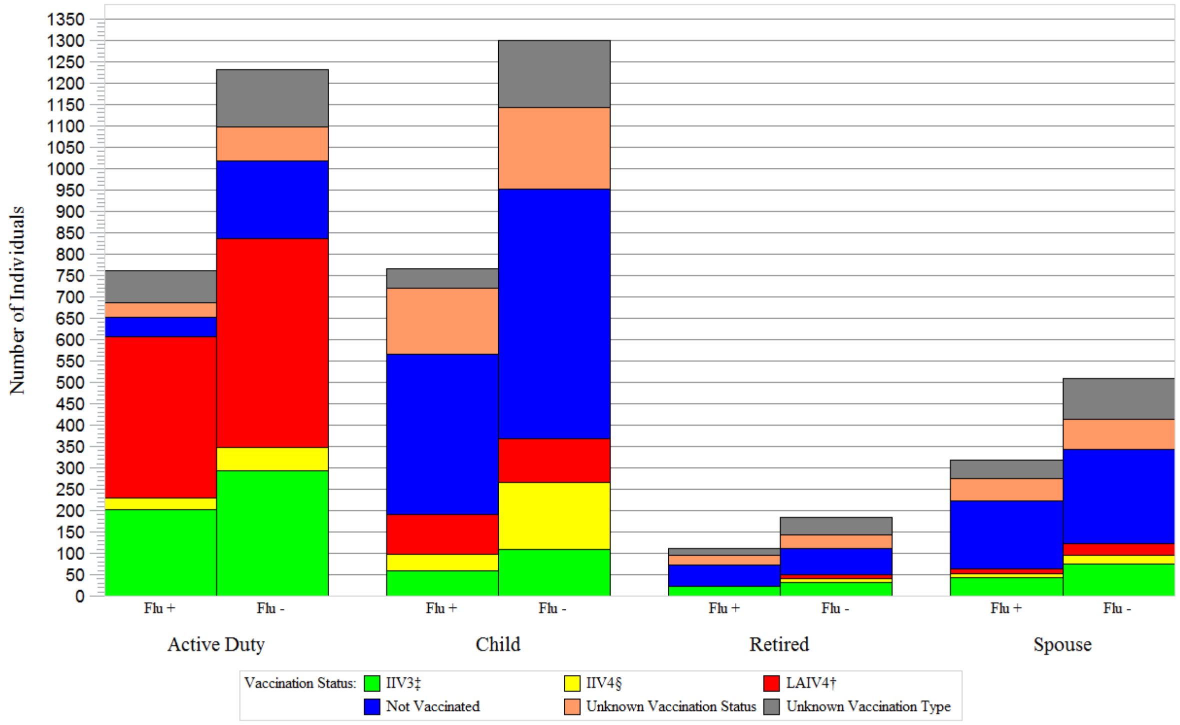
Note: One specimen positive for influenza A(H3N2)v during the 2013-2014 season has been excluded from the graph . Additionally, dual influenza co-infections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

Graph 2. Other respiratory pathogen results by week: 2013-2014 surveillance year and through Week 12 of the 2014-2015 surveillance year



Note: Due to change in protocol between the surveillance years 2013-2014 and 2014-2015, a direct comparison between the years cannot be made.

Graph 3. Vaccination status by beneficiary type for the 2014-2015 surveillance year through Week 12



‡ Influenza, inactivated vaccine (trivalent)

§ Influenza, inactivated vaccine (quadrivalent)

† Live, attenuated influenza vaccine (quadrivalent)

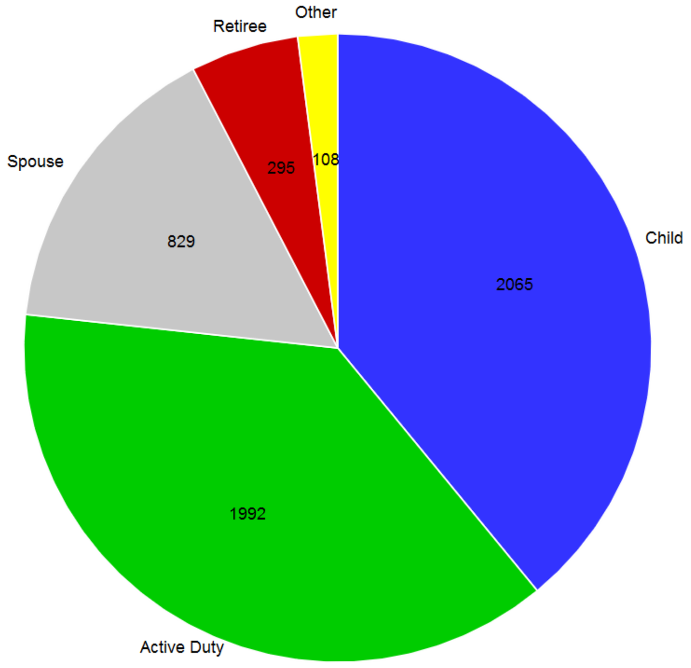
Table 2. ILI by age group for the 2014-2015 surveillance year through Week 12

Age Group	Frequency	Percent
0-5	1135	21.46
6-9	408	7.71
10-17	523	9.89
18-24	752	14.22
25-44	1776	33.58
45-64	535	10.12
65+	149	2.82
Unknown	11	0.21

Demographic Summary

Of 5,289 ILI cases, 1,992 are service members (37.7%), 2,065 are children (39.0%), 829 (15.7%) are spouses, and 403 (7.6%) are retirees & other beneficiaries. The median age of ILI cases with known age (n=5,278) is 23 (range 0, 94) and 2,066 (39.1%) of these specimens are from ILI cases less than 18 years of age.

Graph 4. ILI by beneficiary status for the 2014-2015 surveillance year through Week 12



Laboratory Results—Through Current Surveillance Week 12

Table 3. Cumulative results by region and location for specimens collected during the 2014-2015 surveillance year

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Corona	A/not subtyped & Para	A(H3N2) & B & Adeno & Rhino/Entero	A(H3N2) & Corona	A(H3N2) & Rhino/Entero	Influenza A & B	B	B/Victoria	B/Yamagata	B & Rhino/Entero	Adenovirus	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Co-Infection	No Pathogen	Total
Deployed	Country 1, Location B	-	26	-	-	-	-	-	-	1	-	-	-	-	-	4	2	-	-	-	12	3	46	94
	Country 2, Location A	1	48	-	-	-	-	1	-	5	-	3	-	-	-	-	-	-	-	-	5	-	22	85
PACOM	CFA Okinawa, Japan	-	4	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	2	-	20	28
	Camp Zama, Japan	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6
	Eielson AFB, AK	-	6	-	-	-	-	-	-	1	-	-	-	2	-	-	-	-	-	-	1	-	8	18
	JB Elmendorf-Richardson, AK	-	7	-	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-	-	5	14
	JR Marianas - Andersen AFB, Guam	-	11	-	-	-	-	-	-	1	-	4	-	4	-	-	3	-	1	3	5	1	25	58
	JR Marianas - NH Guam, Guam	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Kadena AB, Japan	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	6	12
	Kunsan AB, South Korea	-	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	12
	Misawa AB, Japan	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	7	19
	Osan AB, South Korea	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	22
	Tripler AMC, HI	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	16
	Yokota AB, Japan	-	80	-	-	-	-	-	-	1	-	1	-	2	-	2	-	-	1	-	3	1	26	117
Region 1	Hanscom AFB, MA	-	24	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	1	-	25	53
	NHCNE Newport, RI	-	15	-	-	-	-	-	-	1	-	-	-	1	-	-	-	-	-	2	1	2	17	39
	USCG Academy, CT	-	9	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	1	-	2	1	11	26
Region 2	Ft Drum, NY	-	61	-	-	-	-	-	-	14	-	2	-	4	-	3	-	1	3	10	12	6	55	171
	JB McGuire-Dix-Lakehurst, NJ	-	32	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	3	1	25	64
	USMA - West Point, NY	-	93	-	-	-	-	-	-	8	-	-	-	5	-	6	1	4	5	10	6	3	148	289
Region 3	CG Base Portsmouth, VA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Dover AFB, DE	-	21	1	-	-	-	-	-	1	-	-	-	-	-	-	1	1	1	-	-	-	14	40
	JB Anacostia-Bolling, DC	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5
	JB Andrews, MD	-	4	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	2	-	4	12
	JB Langley-Eustis, VA	-	7	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	11	21
	NCRM - Ft Belvoir CH, VA	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	4	1	4	11
	NCRM - Walter Reed NMMC, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	3
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2	3
Region 4	CGS Mobile, AL	-	11	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	2	-	4	18
	Columbus AFB, MS	-	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	19	26
	Eglin AFB, FL	-	14	-	-	-	-	-	-	3	-	1	-	2	-	-	-	1	2	6	1	2	43	75
	Ft Bragg, NC	-	30	-	-	-	-	-	-	-	-	-	-	2	-	3	2	-	2	7	3	2	36	87
	Ft Campbell, KY	-	30	-	-	-	-	-	-	1	1	-	-	5	-	1	1	-	4	2	6	3	37	91
	Hurlburt Field, FL	-	22	-	-	-	-	-	-	1	-	-	-	2	-	-	-	1	-	4	7	2	36	75
	JB Charleston (AF), SC	-	13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	14
	JB Charleston (Navy), SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	2	-	2	5
	Keesler AFB, MS	-	6	-	-	-	-	-	-	1	1	-	-	3	-	-	-	-	1	2	1	2	20	37
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	7
	Maxwell AFB, AL	-	31	-	-	-	-	-	-	14	-	1	-	2	-	1	-	-	1	1	5	-	78	134
	Moody AFB, GA	-	92	-	-	-	-	-	-	6	2	2	-	12	-	7	1	1	9	5	14	5	88	244
	NH Beaufort, SC	-	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	2	1	13	19
	NH Camp Lejeune, NC	-	61	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3	9	74
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	1	-	-	1	-	-	-	4	1	-	8
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1
	Robins AFB, GA	-	35	-	-	-	-	-	-	3	-	1	-	1	-	3	-	-	-	-	-	-	41	84
	Seymour Johnson AFB, NC	-	15	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	3	4	-	11	35
	Shaw AFB, SC	-	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	9	17
	Tyndall AFB, FL	-	14	-	-	-	-	-	-	-	-	3	-	3	-	-	1	-	-	2	-	1	15	39
	USCG Base Elizabeth City, NC	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4

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

Continued on Page 5

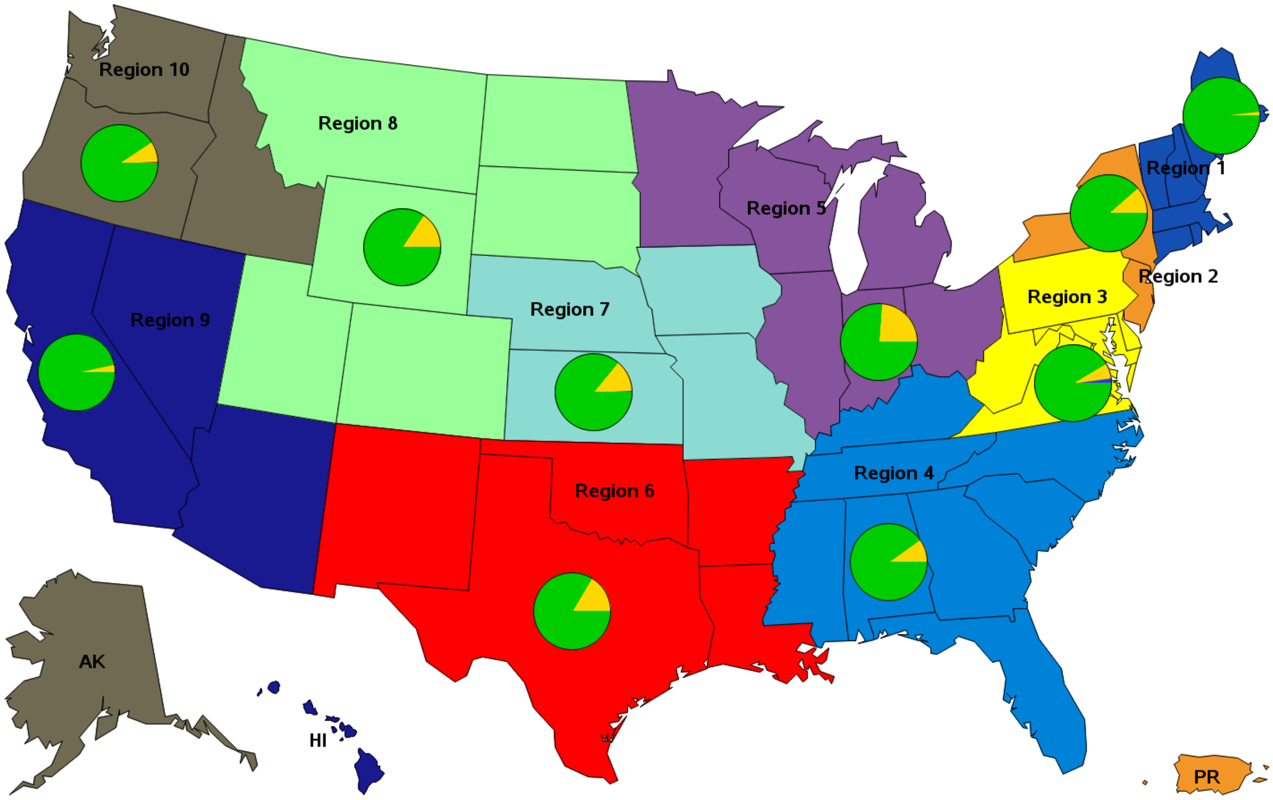
Laboratory Results—Through Current Surveillance Week 12

Table 3. Cumulative results by region and location for specimens collected during the 2014-2015 surveillance year (Continued from Page 4)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Corona	A/not subtyped & Para	A(H3N2) & B & Adeno & Rhino/Entero	A(H3N2) & Corona	A(H3N2) & Rhino/Entero	Influenza A & B	B	B/Victoria	B/Yamagata	B & Rhino/Entero	Adenovirus	*C. pneumoniae*	Coronavirus	hMNV	*M. pneumoniae*	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Co-Infection	No Pathogen	Total
Region 5	**Scott AFB, IL**	-	23	-	-	-	-	-	-	11	-	-	-	2	-	1	1	-	2	2	2	-	29	73
	Wright-Patterson AFB, OH	-	12	-	-	-	-	-	-	-	-	-	-	-	-	4	1	-	-	4	7	-	32	60
Region 6	**Altus AFB, OK**	-	16	-	-	-	-	-	-	6	-	-	1	2	-	1	-	-	2	6	3	2	104	143
	Barksdale AFB, LA	-	10	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	1	10	23
	Cannon AFB, NM	-	4	-	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-	1	-	-	7	14
	Ft Hood, TX	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Holloman AFB, NM	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Laughlin AFB, TX	-	9	-	-	-	-	-	-	-	-	-	-	1	-	1	-	2	-	2	2	2	14	33
	Little Rock AFB, AR	-	18	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	32	51
	SAMMC, TX	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	Sheppard AFB, TX	-	69	-	-	-	-	-	-	8	-	-	-	3	-	5	1	1	3	5	4	6	93	198
	Tinker AFB, OK	-	123	-	-	1	-	-	-	32	1	-	-	2	-	5	1	1	7	20	9	5	190	397
	USCG New Orleans, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	3
Region 7	**Ft Leavenworth, KS**	-	5	-	-	-	-	-	-	-	-	-	-	2	-	1	1	-	-	1	1	-	13	24
	McConnell AFB, KS	-	38	-	1	-	-	-	1	4	-	-	-	-	-	3	-	-	-	-	3	-	27	77
	Offutt AFB, NE	-	67	-	-	-	-	-	-	13	-	-	-	3	-	4	-	2	8	1	10	1	130	239
Region 8	**Buckley AFB, CO**	-	2	-	-	-	-	-	-	3	-	-	-	-	-	1	-	-	-	1	1	-	9	17
	Ellsworth AFB, SD	-	30	-	-	-	-	-	-	16	-	1	-	2	-	4	-	2	7	1	3	2	33	101
	FE Warren AFB, WY	-	35	-	-	-	-	-	-	9	-	-	-	2	-	-	-	-	11	1	3	1	36	98
	Hill AFB, UT	-	34	-	-	-	-	-	-	-	-	1	-	-	-	-	-	2	3	4	6	1	30	81
	Malmstrom AFB, MT	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	1	-	2	10
	Minot AFB, ND	-	19	-	-	-	-	-	-	1	-	-	-	2	-	2	-	3	4	10	3	3	31	78
	Peterson AFB, CO	-	50	-	-	-	-	-	-	3	-	-	-	-	-	-	-	1	2	2	3	1	36	98
	USAF Academy, CO	-	25	-	-	-	-	-	-	3	-	-	-	-	-	-	-	1	1	-	1	-	26	57
Region 9	**Beale AFB, CA**	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Davis-Monthan AFB, AZ	-	25	-	-	-	-	-	-	1	-	-	-	-	-	1	1	-	1	1	1	1	43	75
	Edwards AFB, CA	-	8	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	2	-	-	-	11	22
	Los Angeles AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	-	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	14	27
	Nellis AFB, NV	-	19	-	-	-	-	-	-	2	-	-	-	1	-	-	-	-	-	2	2	-	21	47
	Travis AFB, CA	-	55	-	-	-	-	-	-	1	-	-	-	1	-	2	-	2	11	17	12	3	182	286
	USCG Island Alameda, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	8
	Vandenberg AFB, CA	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	11	17
Region 10	**CGS North Bend, OR**	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
	Fairchild AFB, WA	-	22	-	-	-	-	-	-	1	-	-	-	1	-	1	-	-	1	7	1	1	13	48
	Mt Home AFB, ID	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	1	-	-	7	21
	NH Bremerton, WA	1	87	-	-	-	-	-	-	10	-	-	-	12	1	3	6	2	19	37	21	14	299	512
Total		2	1769	1	1	1	1	1	1	193	6	20	1	94	1	71	27	29	125	192	215	87	2451	5289

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

Map 1. Percentage of influenza positives by region for the 2014-2015 surveillance year through Week 12

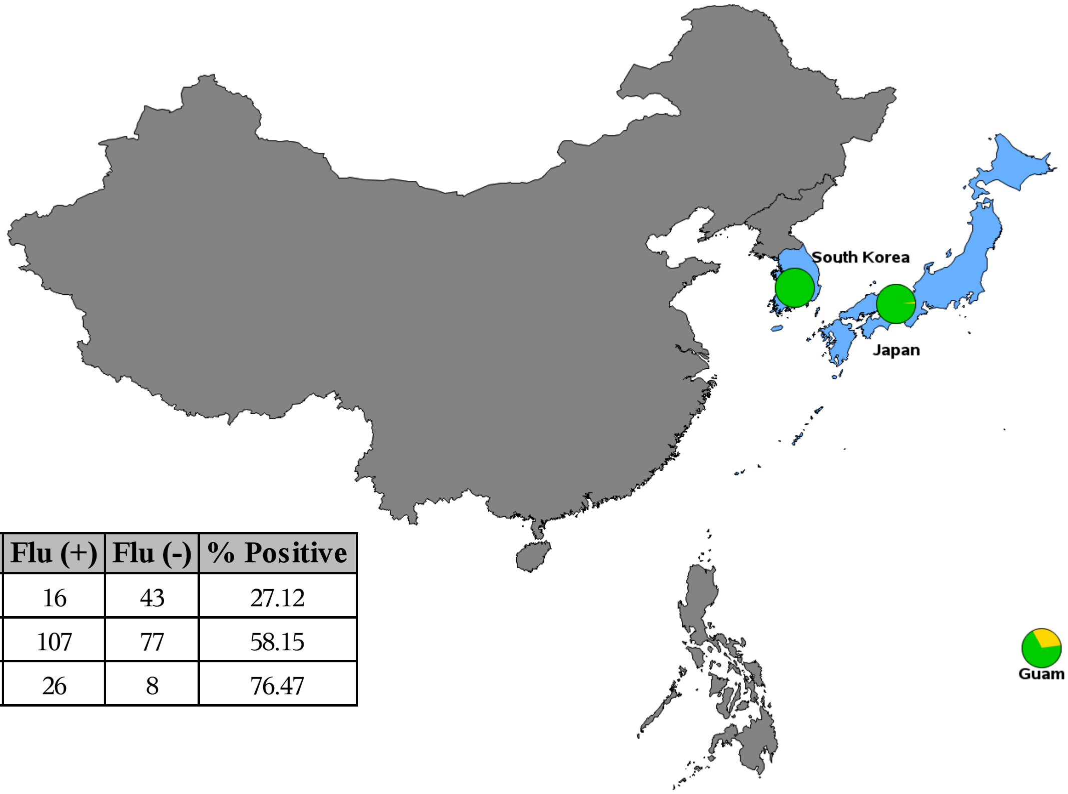


Region	Flu (+)	Flu (-)	% Positive
Region 1	49	72	40.5
Region 2	211	328	39.15
Region 3	46	54	46
Region 4	437	668	39.55
Region 5	46	90	33.82
Region 6	306	568	35.01
Region 7	128	211	37.76
Region 8	236	312	43.07
Region 9	154	356	30.2
Region 10	148	478	23.64

Legend

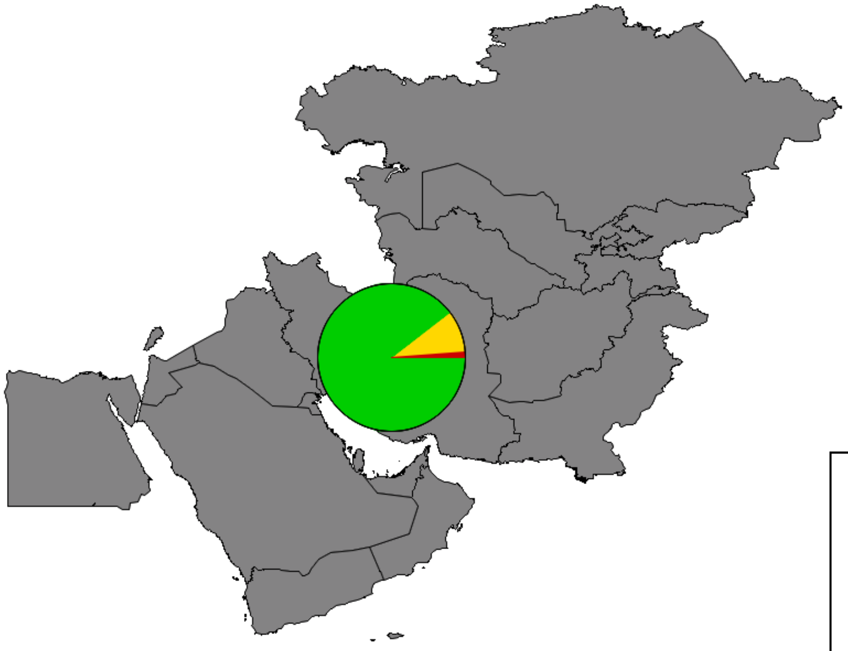
🟢	Influenza A(H3N2)
🔴	Influenza A(H1N1)pdm09
🟡	Influenza B
🔵	Influenza A/not subtyped

Map 2. Percentage of influenza positives by country for the 2014-2015 surveillance year through Week 12 (Pacific)



Country	Flu (+)	Flu (-)	% Positive
Guam	16	43	27.12
Japan	107	77	58.15
South Korea	26	8	76.47

Map 3. Percentage of influenza positives by country for the 2014-2015 surveillance year through Week 12 (CENTCOM)



Country	Flu (+)	Flu (-)	% Positive
Country 1	27	67	28.72
Country 2	58	34	63.04
Country 6	2	32	5.88

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

Legend

🟢 Influenza A(H3N2)

🔴 Influenza A(H1N1)pdm09

🟡 Influenza B

🔵 Influenza A/not subtyped

Countries marked in blue contain sentinel sites

Molecular Sequence Analysis Report

USAFSAM Epidemiology Laboratory Service

This is the sixth report for the 2014-2015 season. Out of 132 total specimens, collected between 16 December 2014 and 4 February 2015 and subsequently analyzed by USAFSAM, 119 were influenza A (H3N2) virus specimens (90.2%), six were influenza B/Yamagata virus specimens (4.5%), and seven were influenza B/Victoria virus specimens (5.3%).

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 potentially contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

		A(H3N2)	B/Yamagata	B/Victoria
CONUS	**Alabama** Maxwell AFB	1	2	
	Arkansas Little Rock AFB	2		
	Arizona Luke AFB	1		
	California Travis AFB	3		
	Colorado Peterson AFB	1		
	Colorado USAF Academy	1		
	Florida Eglin AFB	2		
	Florida Tyndall AFB	1		
	Georgia Moody AFB	1		
	Georgia Robins AFB	3		
	Kansas McConnell AFB	5		
	Massachusetts Hanscom AFB	1		
	Missouri Columbus AFB	2		
	Nebraska Offutt AFB	4	1	
	Nevada Nellis AFB	3	1	
	New Jersey JB McGuire-Dix-Lakehurst	2		
	New York Ft Drum	3		
	New York USMA – West Point	6		
	North Carolina Ft Bragg	2		
	North Carolina NH Camp Lejeune	2		
	North Carolina Seymour Johnson AFB	1		
	Oklahoma Tinker AFB	5	1	4
	Rhode Island NHCNE Newport	4		
	South Carolina JB Charleston (AF)	1		
	South Dakota Ellsworth AFB	1	1	1
	Texas Davis Monthan AFB	1		
	Texas Sheppard AFB	1		1
	Utah Hill AFB	1		
	Washington Fairchild AFB	3		
	Washington NH Bremerton	15		
	Wyoming FE Warren AFB	3		1
OCONUS	**Country 2** Location A	1		
	Germany Landstuhl RMC	24		
	Guam JR Marianas – Andersen AFB	1		
	Japan Kadena AB	2		
	Japan Misawa AB	4		
	Japan Yokota AB	5		
TOTAL		**119**	**6**	**7**

Influenza A(H3N2)

- Isolates are characterized in a neighbor-joining phylogenetic tree with reference strains and other recently sequenced isolates rooted from the previous vaccine, A/Victoria/361/2011-like virus [Figure 1].

- The A(H3N2) specimen characterized for this report by USAFSAM exhibited an overall protein identity of 97.3-98.9% as compared to the A(H3N2) component of the 2013-2014 vaccine formulation, A/Texas/50/2012-like virus.

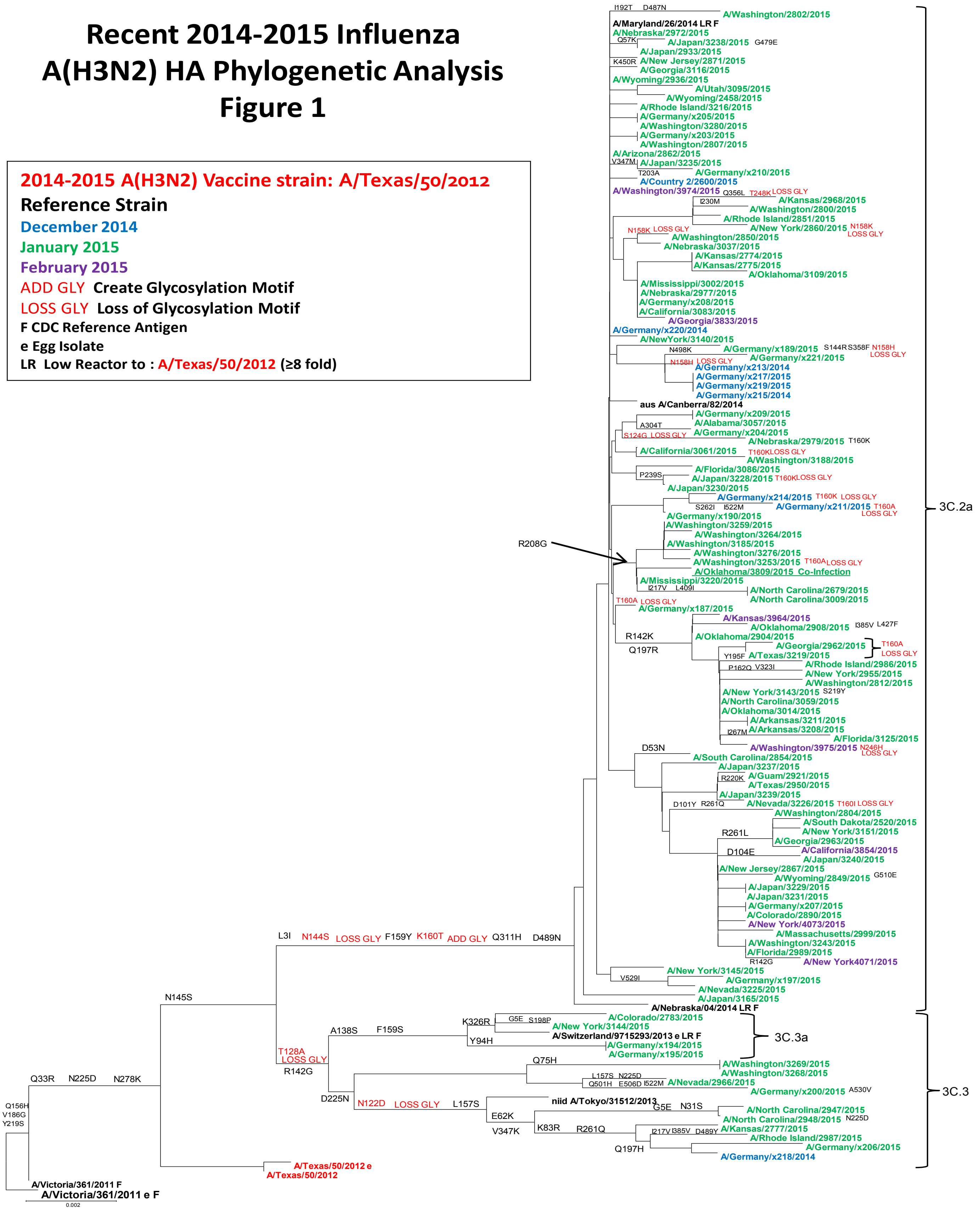
- Based on the mutations observed, all of the A(H3N2) viruses analyzed belong to clade 3C. Within this clade, 105 (88.2%) classify as group 3C.2a and 14 (11.8%) classify as group 3C.3. Four of the 3C.3 A(H3N2) viruses (3.4%) further classify as group 3C.3a.

- 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 119 influenza A(H3N2) specimens characterized in this report, 11 mutations: N122D (asparagine to aspartic acid), T128A (threonine to alanine), S124G (serine to glycine), N144S (asparagine to serine), N158K (asparagine to lysine), N158H (asparagine to histidine), T160A (threonine to alanine), T160K (threonine to lysine), T160I (threonine to isoleucine), N246H (asparagine to histidine), and T248K (threonine to lysine), were observed that could cause a loss of a glycosylation motif. One mutation, K160T (lysine to threonine), was observed that could cause a gain of a glycosylation motif. The amino acid residues 158 and 160 increasingly seem to be hotspots for variability of glycosylation within the 3C.2a clade.

- Out of the total 66 mutations, 23 occurred at predicted antigenic sites and 4 at the receptor binding site.[2,5]

Recent 2014-2015 Influenza A(H3N2) HA Phylogenetic Analysis
Figure 1

2014-2015 A(H3N2) Vaccine strain: A/Texas/50/2012
Reference Strain
December 2014
January 2015
February 2015
ADD GLY **Create Glycosylation Motif**
LOSS GLY **Loss of Glycosylation Motif**
F CDC Reference Antigen
e Egg Isolate
LR Low Reactor to : A/Texas/50/2012 (≥8 fold)



Distribution Statement A: Distribution is unlimited. 88ABW-2015-1795, 08 Apr 2015.

Email: USAFSAM.PHRFlu@us.af.mil, https://gumbo2.area52.afnoapps.usaf.mil/epi-consult/influenza

Influenza B

- The influenza B isolate is characterized in lineage specific; neighbor-joining phylogenetic trees with reference strains and other recently sequenced isolates. The phylogenetic trees are rooted from previous vaccines, B/Florida/04/2006-like virus for Yamagata specimens [Figure 2] and B/Ohio/01/2005-like virus for the Victoria specimen [Figure 3].

- The distinguishing characteristic between the two lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.[1] Six of the influenza B specimens characterized for this report reside within the Yamagata lineage (46.2%) while seven reside within the Victoria lineage (53.8%).

- The influenza B/Yamagata specimens characterized for this report exhibited an overall protein identity of 97.4-97.7% when compared to the 2013-2014 influenza B/Yamagata vaccine strain, B/Massachusetts/02/2012-like virus. When compared to the 2013-2014 influenza B/Victoria vaccine strain, B/Brisbane/60/2008-like virus, the B/Victoria specimens exhibited a protein homology of 99.3-99.5%.

- All six specimens of the influenza B/Yamagata lineage classify into group Y3, similar to the 2012-2013 B/Yamagata vaccine strain, B/Wisconsin/01/2010-like virus.

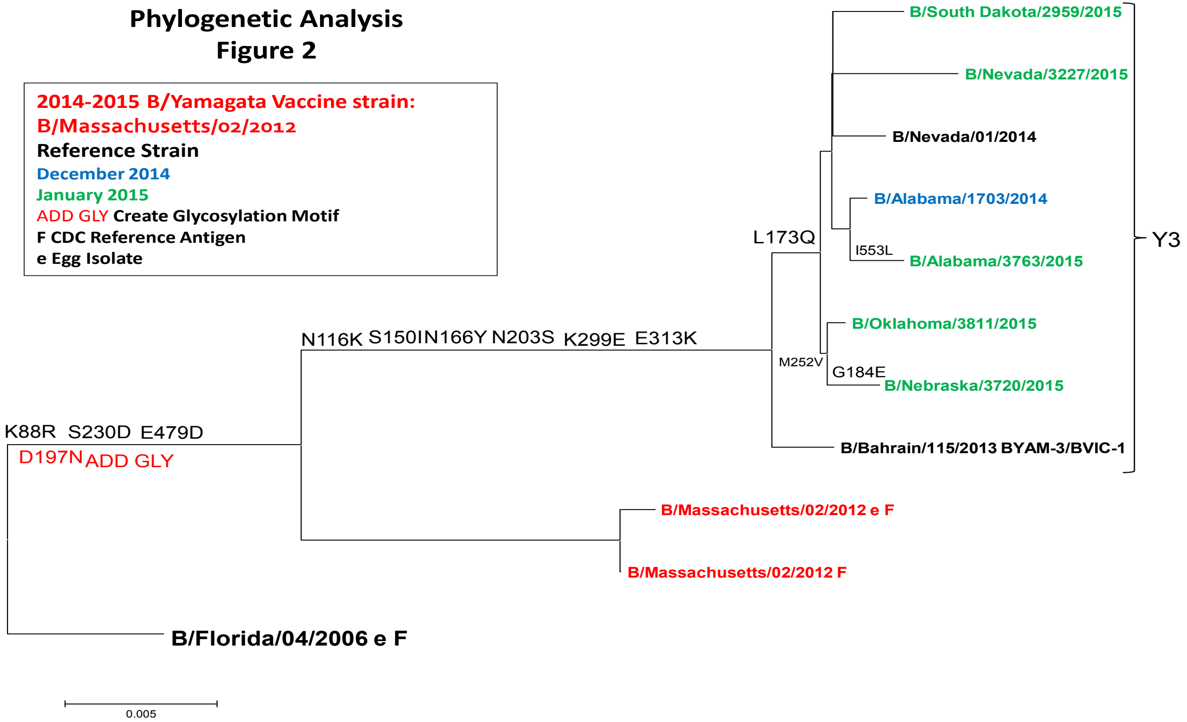
- All seven influenza B/Victoria specimens in this report were characterized as being in group 1A, identified by the mutations N75K (asparagine to lysine), N165K (asparagine to lysine), and S172P (serine to proline).

- 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. Within the influenza B specimens characterized in this report, two mutations: D197N (aspartic acid to asparagine) in the Yamagata lineage and A199T (alanine to threonine) in the Victoria lineage, were observed that could cause the gain of a glycosylation motif.

- The specimen from Tinker AFB in Oklahoma that had a co-infection of influenza A(H3N2) and influenza B (underlined) showed the influenza B portion to reside within the group 1A of the B Victoria lineage.

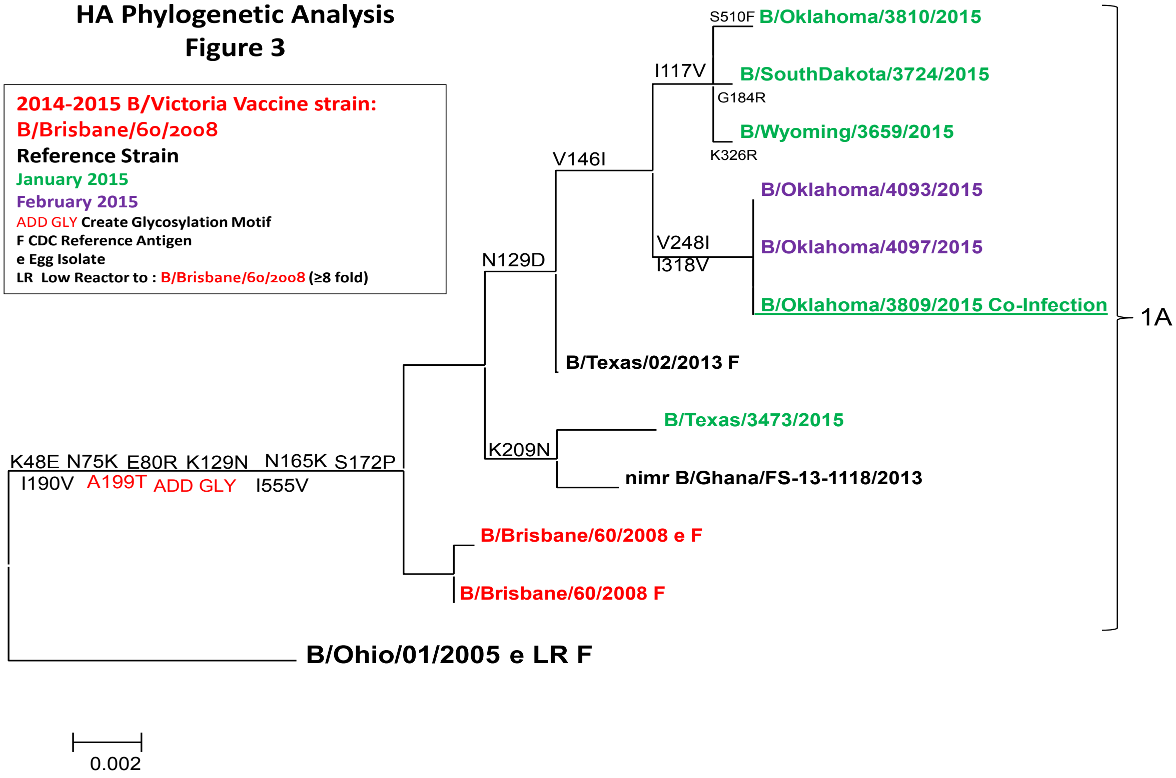
Recent 2014-2015 Influenza B/Yamagata HA Phylogenetic Analysis
Figure 2

2014-2015 B/Yamagata Vaccine strain:
B/Massachusetts/02/2012
Reference Strain
December 2014
January 2015
ADD GLY **Create Glycosylation Motif**
F CDC Reference Antigen
e Egg Isolate



Recent 2014-2015 Influenza B/Victoria HA Phylogenetic Analysis
Figure 3

2014-2015 B/Victoria Vaccine strain:
B/Brisbane/60/2008
Reference Strain
January 2015
February 2015
ADD GLY **Create Glycosylation Motif**
F CDC Reference Antigen
e Egg Isolate
LR Low Reactor to : B/Brisbane/60/2008 **(≥8 fold)**



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DoD Global Laboratory-Based Influenza Surveillance Program

USAF School of Aerospace Medicine 2014 - 2015

Respiratory Surveillance
2014-2015 Year
(beginning 28 September 2014)

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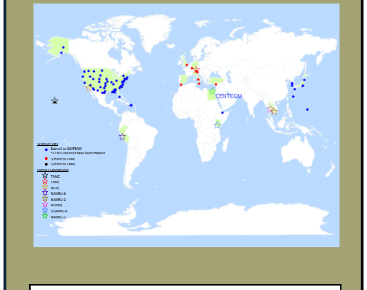

Contributions to the CDC for National Influenza Surveillance

All sequence data are sent to the CDC and selected original specimens or isolates are sent for further characterization and possible use as influenza vaccine seed viruses. Specimens may also undergo antiviral testing.

DoD Global, Influenza Surveillance Program

https://gumbo2.area52.afnoapps.usaf.mil/epi-consult/influenza

Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the 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-6 (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 the Division of Global Emerging Infections Surveillance and Response System (GEIS) Operations, a Division of the Armed Forces Health Surveillance Center (AFHSC).

Sentinel Site Surveillance at USAFSAM

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. USAFSAM manages the surveillance program that includes global surveillance among DoD beneficiaries at over 80 sentinel sites (including deployed locations) and many non-sentinel sites (please see map on the left). Unique sentinel sites include three DoD overseas medical research laboratories (AFRIMS, NAMRU-6, USAMRU-K) and the US Army Public Health Command Region South (PHCR-S). These sites collect specimens from local residents in surrounding countries that may not otherwise be covered in existing surveillance efforts.

Since the 2006-2007 season, Landstuhl Regional Medical Center (LRMC) has served EUCOM as a USAFSAM contributing laboratory. The initiative seeks to provide more timely results and efficient transport of specimens.

For an expanded view of this report, visit our website. Also available on the website is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and an overview of historical data. Please visit the AFHSC/GEIS website for an overview of influenza surveillance at all collaborating organizations.

Errata:

Collaborating Partners

In addition to all participating DoD military sentinel sites, several collaborating partners (described above) may be further understood by reviewing the partner's website.