

DoD Global, Laboratory-Based, Influenza Surveillance Program



USAF School of Aerospace Medicine

2014 - 2015

Cumulative Results

Locations	89
Collected	5,879
Tested	5,797

Influenza A 1,790

A(H1N1)pdm09	3
A(H3N2)	1,782
A & B	1
A & Parainfluenza	1
A(H3N2) & B/Victoria & Adenovirus & Rhino/Enterovirus	1
A(H3N2) & Coronavirus	1
A(H3N2) & Rhino/Enterovirus	1

Influenza B 253

B/Unknown or pending lineage*	142
B & Rhino/Enterovirus	1
B/Victoria	30
B/Yamagata	80

Other Respiratory Pathogens 1,061

Adenovirus	112
<i>Bordetella pertussis</i>	0
<i>Chlamydia pneumoniae</i>	2
Coronavirus	88
Human Metapneumovirus	65
<i>Mycoplasma pneumoniae</i>	33
Parainfluenza	167
RSV	206
Rhino/Enterovirus	272
Non-influenza Co-infections	116

Lab data are current as of 2 June 2015. Results are preliminary and may change as more results are received.
*USAFSAM does not sequence all influenza B specimens to determine lineage.



Respiratory Highlights

3-30 May 2015 (Surveillance Weeks 18-21)

- During 3-30 May 2015, a total of 117 specimens were collected and received from 38 locations. Results were finalized for 88 specimens from 32 locations. A total of six influenza viruses were identified. Four influenza B viruses were identified during Week 19, with one influenza B and one influenza A/H3 identified during Week 20. There were no influenza viruses identified during Week 18 and 21.
- This report contains the latest molecular sequence report. The sequences reported are from USAFSAM sentinel sites and influenza sequence data sent by AFRIMS. The report can be found on pages 10-15. Two additional sequence reports will be published and distributed immediately following the release of this report.
- On 2 June 2015, the CDC released a Health Alert Network (HAN) Advisory to notify public health workers and clinicians of the potential for human infection with highly-pathogenic avian influenza A/H5 viruses and describe recommendations for human health investigations and response. To access the HAN, please refer to <http://emergency.cdc.gov/han/han00378.asp>.

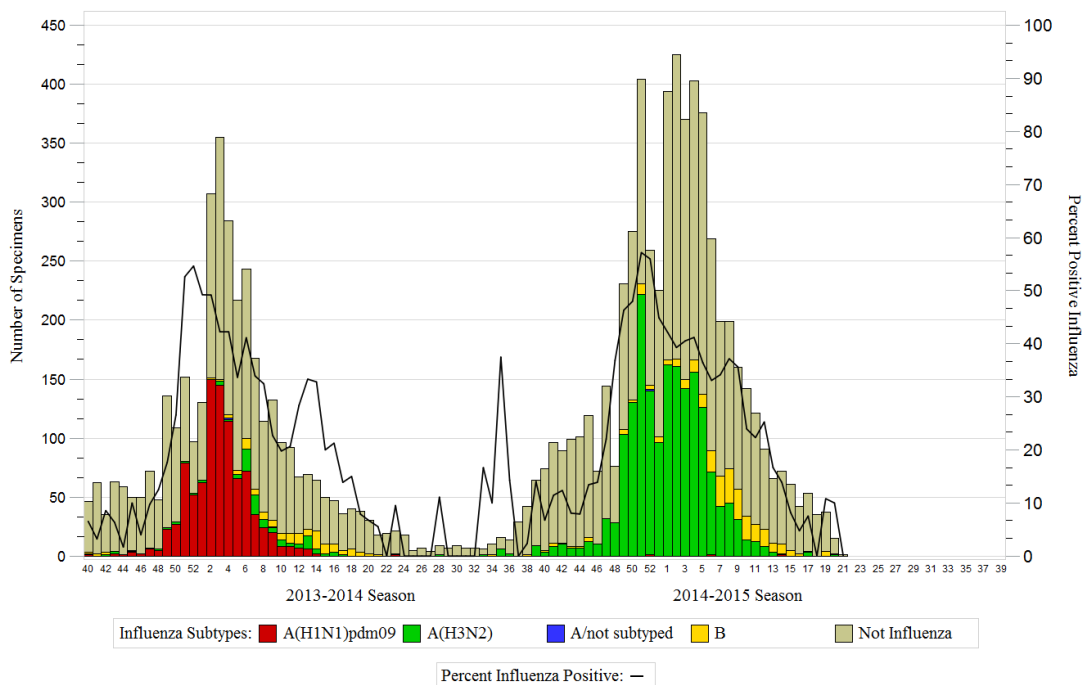
Table 1. Results by region and location for specimens collected and finalized during Weeks 18-21

Region*		A(H3N2)	B	Adenovirus	hMPV	M. pneumoniae	Parainfluenza	Rhino/Enterovirus	Adeno & Rhino/Enterovirus	M. pneumoniae & Rhino/Enterovirus	Para & Rhino/Enterovirus	No Pathogen	Total
PACOM	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	1
Region 1	NHCNE Newport, RI	-	2	-	-	-	1	-	-	-	-	-	4
Region 2	JB McGuire-Dix-Lakehurst, NJ	-	-	-	-	-	-	1	-	-	-	-	1
	USMA - West Point, NY	-	-	-	-	-	1	-	2	-	-	-	6
Region 3	NCRC - Walter Reed NMMC, MD	1	-	-	-	-	-	-	-	-	-	-	1
Region 4	Eglin AFB, FL	-	-	-	-	-	-	1	-	-	-	-	3
	Hurlburt Field, FL	-	-	-	-	-	-	-	-	-	-	-	1
	Keesler AFB, MS	-	-	1	-	-	-	-	-	-	-	-	3
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	2
	Maxwell AFB, AL	-	-	-	-	-	-	-	-	-	-	-	1
	Moody AFB, GA	-	1	-	-	-	1	-	-	-	-	-	6
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	1
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	1
Region 5	Wright-Patterson AFB, OH	-	-	-	-	-	-	-	-	-	-	2	2
Region 6	Altus AFB, OK	-	-	-	-	-	-	-	-	-	-	-	2
	Cannon AFB, NM	-	-	-	-	-	-	2	-	-	-	-	4
	Holloman AFB, NM	-	-	-	-	-	-	-	-	-	-	-	1
	Laughlin AFB, TX	-	-	1	-	-	-	2	-	-	-	-	4
	Sheppard AFB, TX	-	-	-	1	-	-	-	-	-	-	-	3
	Tinker AFB, OK	-	-	-	-	-	1	-	-	-	-	-	2
Region 7	McConnell AFB, KS	-	-	-	-	-	1	-	-	-	-	-	1
Region 8	Ellsworth AFB, SD	-	-	-	-	-	-	-	-	-	-	-	1
	FE Warren AFB, WY	-	1	-	-	-	-	-	-	-	-	-	1
	Hill AFB, UT	-	-	-	-	-	-	2	-	-	-	-	2
	Peterson AFB, CO	-	1	-	-	-	1	-	-	-	-	-	4
	USAF Academy, CO	-	-	-	-	-	-	-	-	-	-	-	1
Region 9	Davis-Monthan AFB, AZ	-	-	1	-	-	-	-	-	-	-	-	1
	Edwards AFB, CA	-	-	-	-	-	1	-	-	-	-	-	1
	Travis AFB, CA	-	-	-	-	-	-	-	-	-	-	-	3
	Vandenberg AFB, CA	-	-	-	-	-	-	-	-	-	-	-	3
Region 10	Fairchild AFB, WA	-	-	-	-	-	-	-	-	-	-	-	1
	NH Bremerton, WA	-	-	-	-	1	2	3	-	-	-	-	14
Total		1	5	3	1	1	8	12	2	1	1	53	88

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

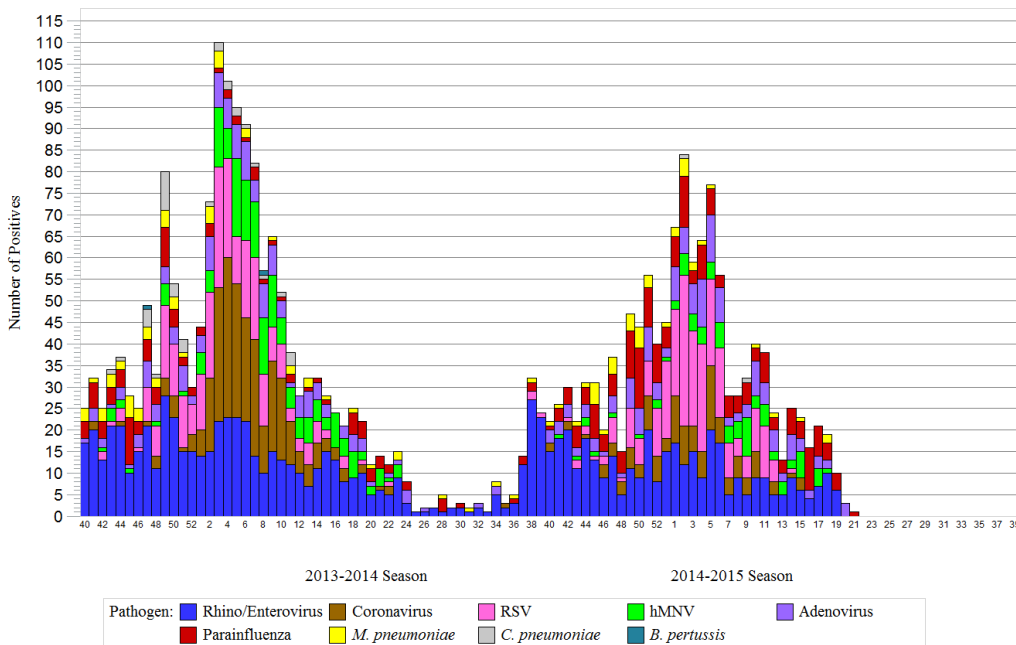
Laboratory Results - Cumulative for Season

Graph 1. Percent influenza positive by week: 2013-2014 surveillance year and through Week 21 of the 2014-2015 surveillance year



Note: One specimen positive for influenza A(H3N2)v has been excluded from the graph during the 2013-2014 season. 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 21 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.

Distribution Statement A: Distribution is unlimited. 88ABW-2015-2196 and PA email guidance dated 1May2015.

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

Graph 3. Vaccination status by beneficiary type for the 2014-2015 surveillance year through Week 21

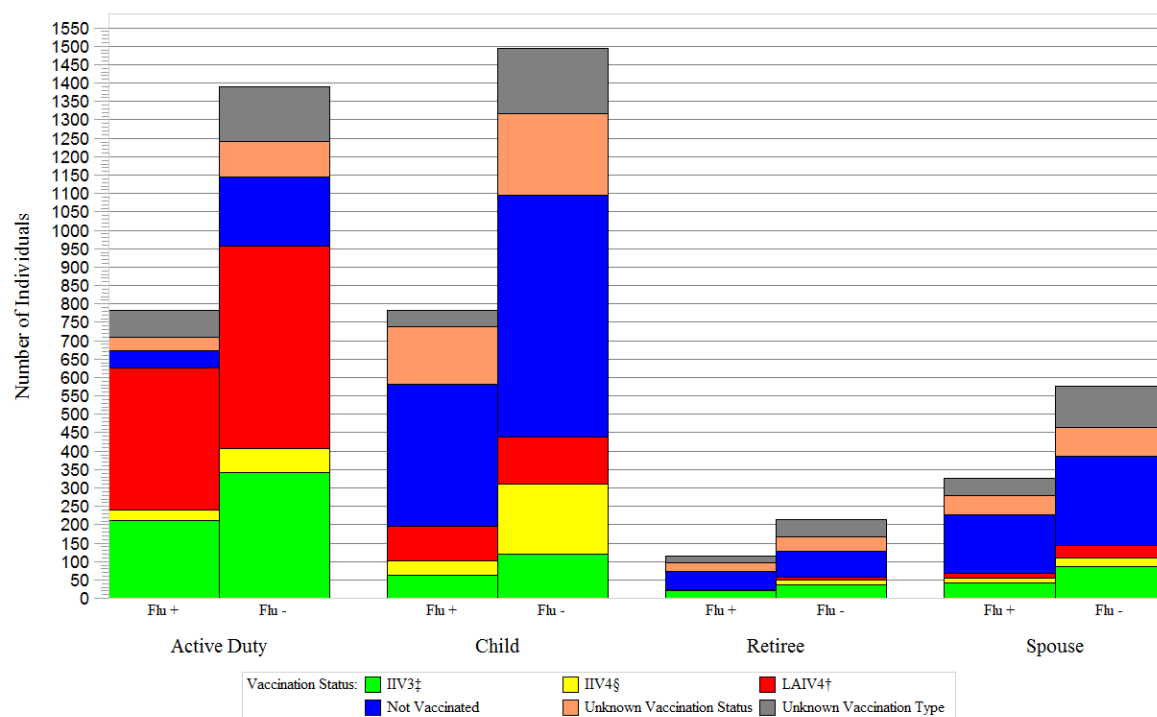


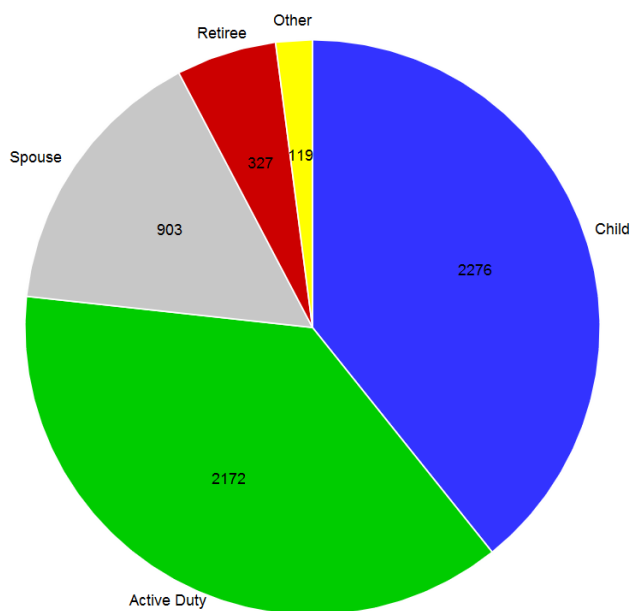
Table 2. ILI by age group for the 2014-2015 surveillance year through Week 21

Age Group	Frequency	Percent
0-5	1262	21.77
6-9	441	7.61
10-17	573	9.88
18-24	818	14.11
25-44	1928	33.26
45-64	593	10.23
65+	171	2.95
Unknown	11	0.19

Demographic Summary

Of 5,797 ILI cases, 2,172 are service members (37.5%), 2,276 are children (39.3%), 903 (15.6%) are spouses, and 446 (7.7%) are retirees & other beneficiaries. The median age of ILI cases with known age (n=5,786) is 23 (range 0, 95) and 2,276 (39.3%) 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 21



Laboratory Results—Through Current Surveillance Week 21

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

		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Para	A(H3N2) & B/Victoria & 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	hMPV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Co-Infection	No Pathogen	Total
Deployed	Country 1, Location B	-	26	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	18	3	52	107
	Country 2, Location A	1	48	-	-	-	-	-	1	-	7	-	-	-	-	-	-	-	-	6	1	27	92
	Country 3, Location A	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
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	-	5	-	-	3	-	1	3	5	1	26	60
	JR Marianas - NH Guam, Guam	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Kadena AB, Japan	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	7	14
	Kunsan AB, South Korea	-	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	12
	Misawa AB, Japan	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	-	11	24
	Osan AB, South Korea	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	23
	Tripler AMC, HI	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	16
	Yokota AB, Japan	-	80	-	-	-	-	-	-	-	2	-	2	-	2	4	-	1	-	4	1	26	122
	Region 1	Hanscom AFB, MA	-	24	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	3	1	-	27
NHCNE Newport, RI		-	16	-	-	-	-	-	3	-	3	-	2	-	-	-	-	1	2	1	2	23	53
USCG Academy, CT		-	10	-	-	-	-	-	1	-	-	-	1	-	-	-	1	1	-	2	1	11	28
Region 2	Ft Drum, NY	-	64	-	-	-	-	-	12	-	9	-	5	-	5	5	1	4	10	19	10	59	203
	JB McGuire-Dix-Lakehurst, NJ	-	32	-	-	1	-	-	-	-	2	-	-	-	-	-	-	-	2	5	1	28	71
	USMA - West Point, NY	1	95	-	-	-	-	-	8	-	2	-	5	-	9	2	4	8	12	7	7	154	314
Region 3	CG Base Portsmouth, VA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Dover AFB, DE	-	21	-	-	-	-	-	-	-	1	-	-	-	1	1	1	1	-	-	-	18	44
	JB Anacostia-Bolling, DC	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5
	JB Andrews, MD	-	4	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	2	-	4	12
	JB Langley-Eustis, VA	-	7	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	12	22
	NCRM - Ft Belvoir CH, VA	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	4	1	4	11
	NCRM - Walter Reed NMMC, MD	-	2	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	4
	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	-	2	-	2	-	-	-	1	4	6	2	4	55	93
	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	-	-	3	-	-	-	-	1	1	4	7	2	39	80
	JB Charleston (AF), SC	-	13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	14
	JB Charleston (Navy), SC	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	2	-	2	5
	Keesler AFB, MS	-	6	-	-	-	-	-	-	1	1	-	4	-	-	-	-	1	2	1	2	27	45
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10	10
	Maxwell AFB, AL	-	31	-	-	-	-	-	10	-	5	-	2	-	2	1	-	1	1	5	-	80	138
	Moody AFB, GA	-	92	-	-	-	-	-	6	3	2	-	15	-	8	9	1	12	5	17	9	100	279
	NH Beaufort, SC	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	2	1	15	21
	NH Camp Lejeune, NC	-	61	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3	10	75
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	1	-	-	1	-	-	-	4	1	-	8
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1
	Robins AFB, GA	-	35	-	-	-	-	-	3	-	2	-	1	-	3	1	-	-	-	-	-	41	86
	Seymour Johnson AFB, NC	-	15	-	-	-	-	-	-	-	-	-	2	-	-	1	-	1	3	5	-	13	40
	Shaw AFB, SC	-	7	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	2	-	10	21
Tyndall AFB, FL	-	14	-	-	-	-	-	-	-	3	-	4	-	1	1	-	-	2	1	1	15	42	
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 21

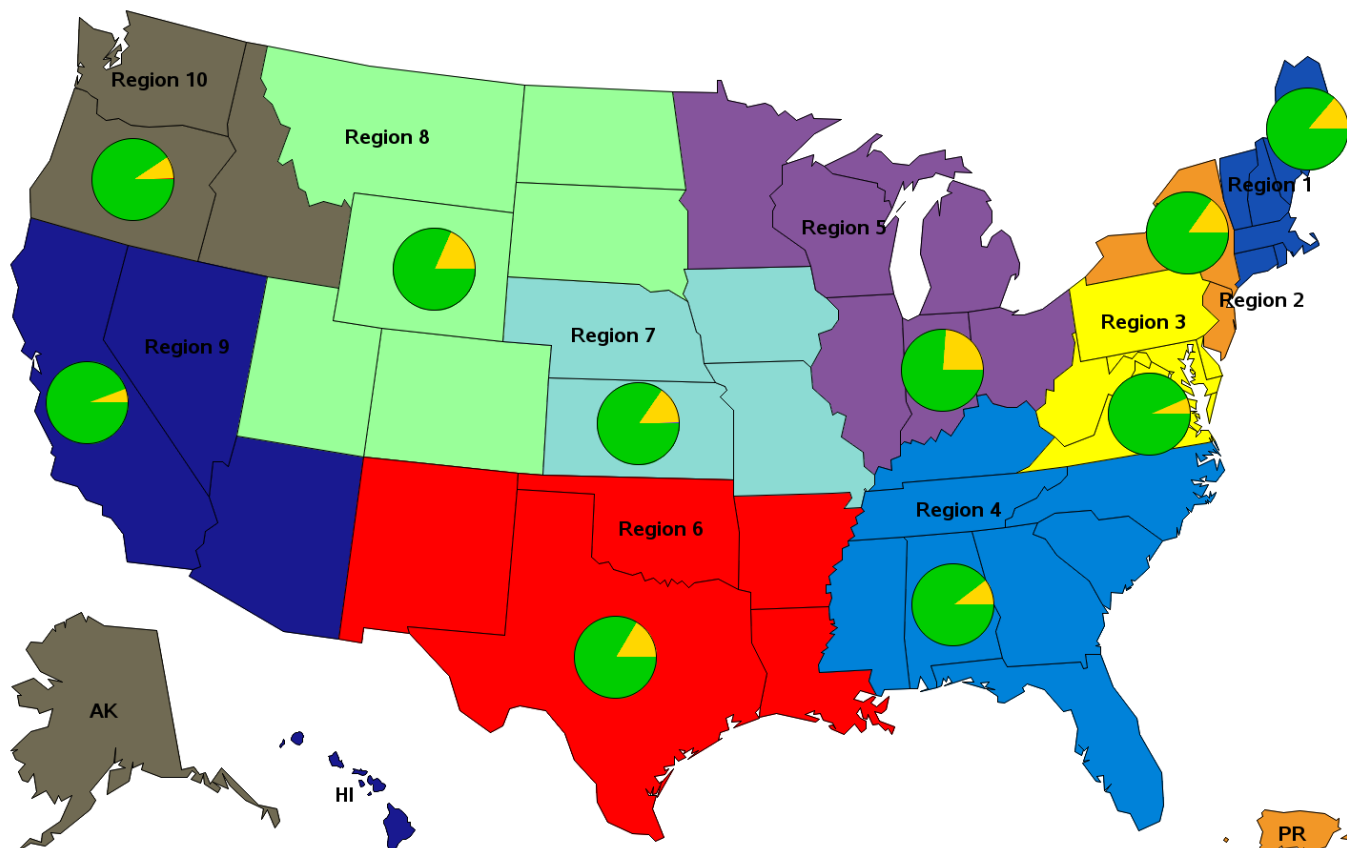
Table 3. Cumulative results by region and location for specimens collected during the 2014-2015 surveillance year
(Continued from Page 4)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Para	A(H3N2) & B/Victoria & 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	hMPV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Co-Infection	No Pathogen	Total
Region 5	Scott AFB, IL	-	23	-	-	-	-	-	6	1	4	-	2	-	1	1	-	2	2	2	-	34	78
	Wright-Patterson AFB, OH	-	12	-	-	-	-	-	-	-	-	-	-	-	4	1	-	-	4	8	-	38	67
Region 6	Altus AFB, OK	-	16	-	-	-	-	-	4	-	2	1	3	-	1	-	-	6	7	3	2	116	161
	Barksdale AFB, LA	-	10	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	1	11	24
	Cannon AFB, NM	-	4	-	-	-	-	-	1	-	-	-	-	-	1	-	-	1	1	2	-	12	22
	Ft Hood, TX	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Holloman AFB, NM	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Laughlin AFB, TX	-	9	-	-	-	-	-	-	-	-	-	2	-	1	-	2	2	3	6	3	16	44
	Little Rock AFB, AR	-	18	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	33	52
	SAMMC, TX	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	Sheppard AFB, TX	-	69	-	-	-	-	-	4	3	1	-	3	-	6	2	1	5	5	6	7	102	214
	Tinker AFB, OK	-	123	-	1	-	-	-	26	6	1	-	2	1	5	7	1	12	22	12	8	189	416
	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	2	-	2	-	-	-	3	-	-	1	-	4	-	28	80
	Offutt AFB, NE	-	67	-	-	-	-	-	9	-	6	-	3	-	5	-	2	8	1	11	1	135	248
Region 8	Buckley AFB, CO	-	2	-	-	-	-	-	1	2	-	-	-	-	1	-	-	-	1	1	-	9	17
	Ellsworth AFB, SD	-	30	-	-	-	-	-	12	2	4	-	2	-	5	1	4	7	1	3	2	40	113
	FE Warren AFB, WY	-	35	-	-	-	-	-	8	4	-	-	2	-	-	-	-	15	3	3	2	38	110
	Hill AFB, UT	-	34	-	-	-	-	-	-	-	2	-	-	-	-	-	2	3	4	8	2	33	88
	Malmstrom AFB, MT	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	1	-	2	10
	Minot AFB, ND	-	19	-	-	-	-	-	1	-	-	-	2	-	3	1	3	5	11	3	3	30	81
	Peterson AFB, CO	-	50	-	-	-	-	-	2	2	2	-	-	-	-	-	1	4	3	4	2	39	109
	USAF Academy, CO	-	26	-	-	-	-	-	2	1	-	-	-	-	-	-	1	1	-	1	-	31	63
	Beale AFB, CA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
Region 9	Davis-Monthan AFB, AZ	-	26	-	-	-	-	-	-	-	2	-	1	-	2	4	-	2	1	2	1	46	87
	Edwards AFB, CA	-	8	-	-	-	-	-	1	1	1	-	-	-	-	-	-	3	-	-	-	12	26
	Los Angeles AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	-	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	14	28
	Nellis AFB, NV	-	19	-	-	-	-	-	1	1	1	-	1	-	-	-	-	-	2	2	-	26	53
	Travis AFB, CA	-	56	-	-	-	-	-	1	-	-	-	1	-	2	1	2	12	18	13	3	201	310
	USCG Island Alameda, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	8
	Vandenberg AFB, CA	-	6	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	20	27
	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3
Region 10	Fairchild AFB, WA	-	22	-	-	-	-	-	1	-	1	-	1	-	2	2	-	1	7	1	1	11	50
	Mt Home AFB, ID	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	1	-	-	8	22
	NH Bremerton, WA	1	87	-	-	-	-	-	7	-	2	-	16	1	4	6	4	25	38	34	19	347	591
Total		3	1782	1	1	1	1	1	142	30	80	1	112	2	88	65	33	167	206	272	116	2693	5797

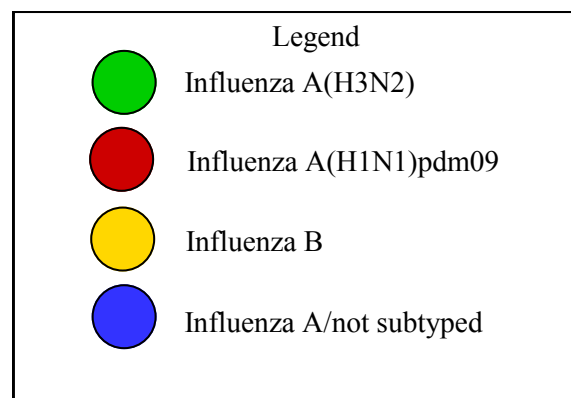
*US Regions are based on Health & Human Services regions. Other locations are defined by COCOM.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Map 1. Percentage of influenza positives by HHS region for the 2014-2015 surveillance year through Week 21

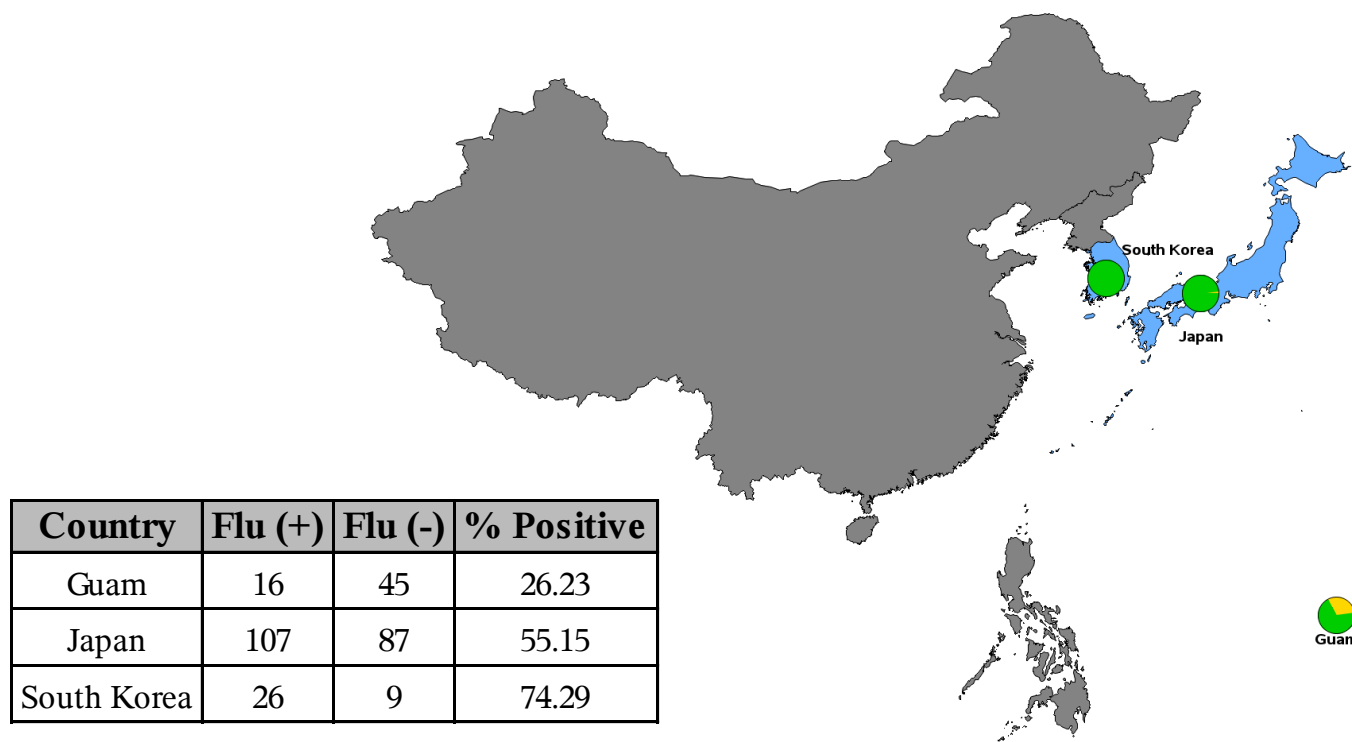


Region	Flu (+)	Flu (-)	% Positive
Region 1	58	79	42.34
Region 2	226	365	38.24
Region 3	46	60	43.4
Region 4	440	749	37.01
Region 5	46	100	31.51
Region 6	306	644	32.21
Region 7	130	223	36.83
Region 8	245	347	41.39
Region 9	160	400	28.57
Region 10	148	560	20.9

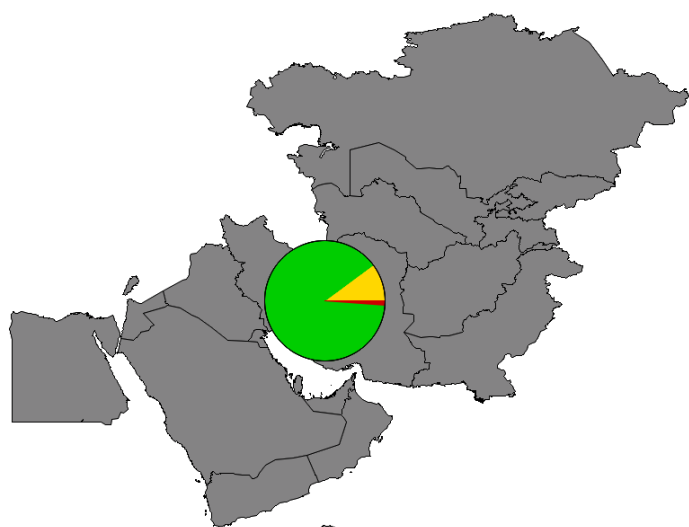


DoD Global, Laboratory-Based, Influenza Surveillance Program

Map 2. Percentage of influenza positives by country for the 2014-2015 surveillance year through Week 21 (Pacific)

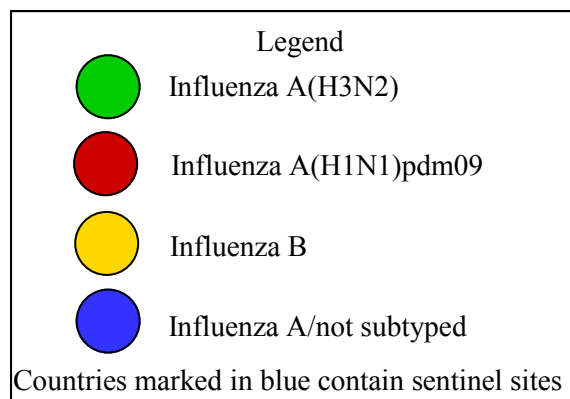


Map 3. Percentage of influenza positives by country for the 2014-2015 surveillance year through Week 21 (CENTCOM)



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

Country	Flu (+)	Flu (-)	% Positive
Country 1	27	80	25.23
Country 2	58	34	63.04
Country 3	2	0	100
Country 6	2	40	4.76



Monthly EUCOM Respiratory Surveillance Supplemental Report Through 30 May 2015

In cooperation and agreement with U.S. Army Public Health Command Region-Europe (PHCR-E), the DoD Global, Laboratory-based, Influenza Surveillance Program has analyzed data from surveillance sites that submit specimens to Landstuhl Regional Medical Center (LRMC), Germany. LRMC's laboratory is the forward laboratory for military sites in Europe.

Lab results are preliminary and may change as more results are received.

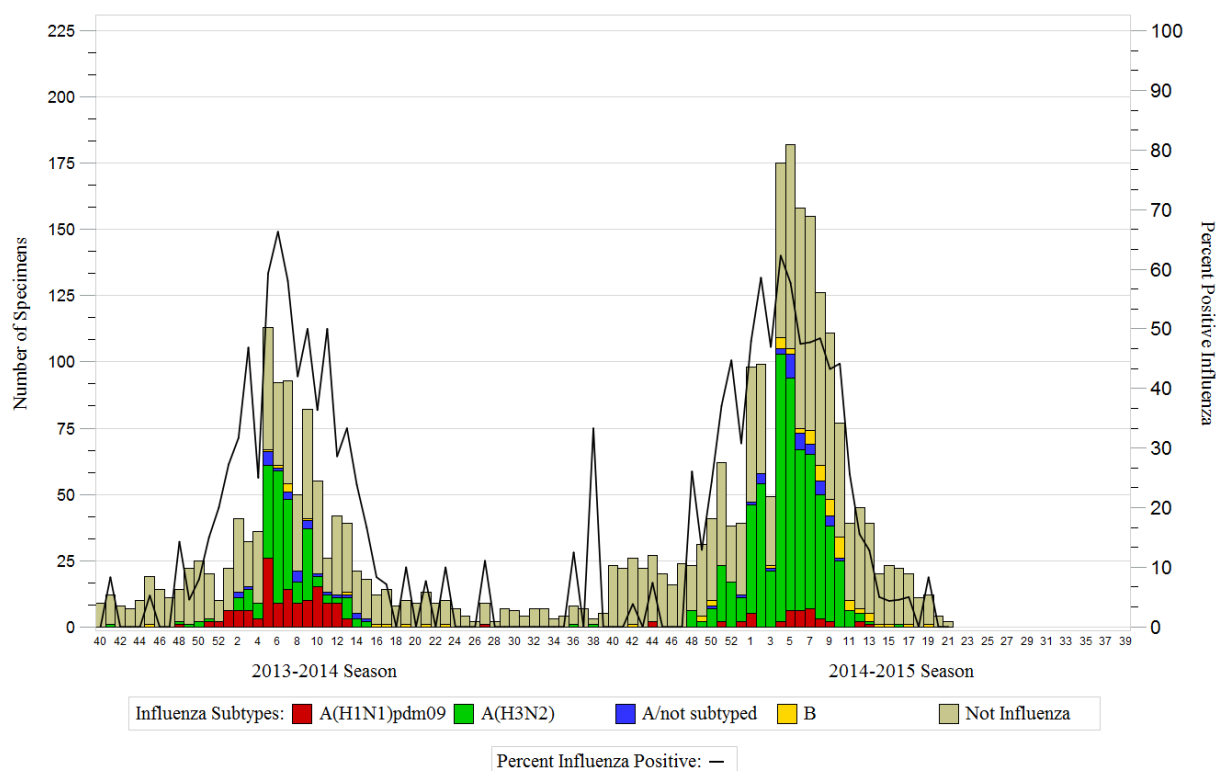
Table 4. Results by region and location for specimens collected and finalized during Weeks 18-21

Region		B	hMNV	Parainfluenza	Rhinovirus/ Enterovirus	hMNV & Rhino/Entero	No Pathogen	Total
Deployed	Country 6, Location A	-	-	-	-	-	2	2
EUCOM	Incirlik AB, Turkey	-	-	1	-	-	1	2
	Landstuhl RMC, Germany	-	-	-	-	-	8	8
	NSA Naples, Italy	-	-	1	-	-	1	2
	RAF Lakenheath, England	1	-	-	1	-	3	5
	Ramstein AB, Germany	-	-	-	-	-	2	2
	USAG Stuttgart, Germany	-	2	-	-	-	-	2
	USAG Vicenza, Italy	-	-	1	-	-	1	2
	Vilseck AHC, Germany	-	-	1	1	1	1	4
Total		1	2	4	2	1	19	29

Table 5. Cumulative results by region and location for specimens collected during the 2014-2015 surveillance year

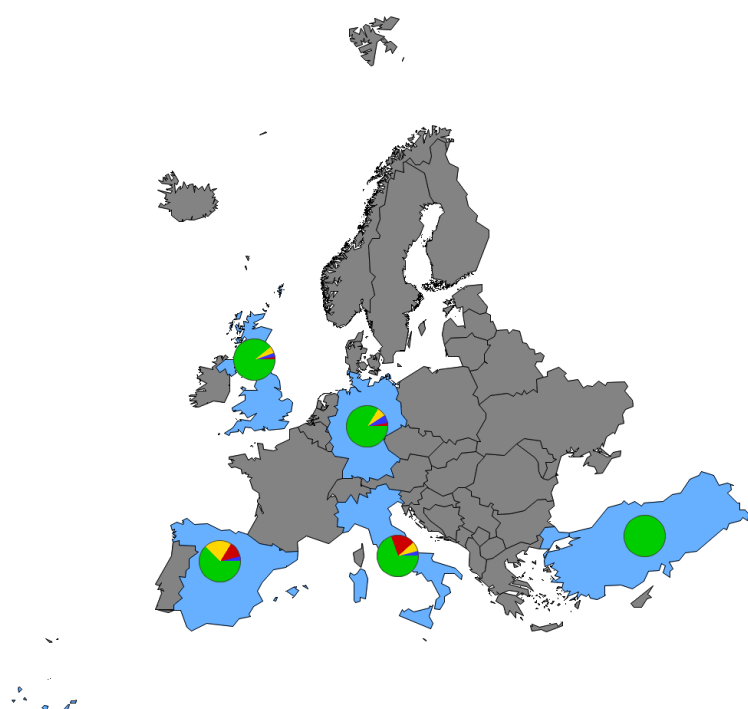
Region		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A/not subtyped & RSV	A/not subtyped & Rhino/Entero	A(H1N1)pdm09 & hMNV	A(H1N1)pdm09 & RSV	A(H3N2) & B	A(H3N2) & hMNV	A(H3N2) & hMNV & Rhino/Entero	A(H3N2) & Para	A(H3N2) & RSV	A(H3N2) & RSV & Rhino/Entero	A(H3N2) & Rhino/Entero	Influenza A & B	B	B & RSV	B & Rhino/Entero	Adenovirus	hMNV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & RSV	Adeno & RSV & Rhino/Entero	Adeno & Rhino/Entero	hMNV & RSV	hMNV & Rhino/Entero	Para & RSV	Para & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total	
Deployed	Country 6, Location A	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	-	-	-	-	33	41	
EUCOM	Aviano AB, Italy	4	12	2	-	-	-	-	1	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	16	38	
	Incirlik AB, Turkey	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	1	2	4	2	3	-	-	1	-	-	-	-	-	13	28
	Landstuhl RMC, Germany	5	108	11	-	1	1	-	-	-	-	-	-	2	-	-	2	10	-	-	1	7	8	46	38	2	1	6	2	-	1	1	7	162	422
	NAS Sigonella, Italy	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	2
	NAVSTA Rota, Spain	3	15	-	1	-	-	-	-	-	-	-	-	-	-	-	-	4	-	1	1	2	-	2	5	-	-	1	-	-	-	-	1	34	70
	NSA Naples, Italy	10	10	1	-	-	-	1	-	-	-	-	-	-	-	-	-	3	-	1	-	1	1	8	9	-	-	-	-	-	-	-	1	27	73
	RAF Lakenheath, England	4	131	3	-	2	-	-	-	-	-	1	3	-	9	-	8	1	-	1	7	6	12	50	-	-	1	-	1	1	3	9	145	398	
	Ramstein AB, Germany	1	59	1	-	1	-	-	-	-	-	-	-	-	2	-	2	-	1	-	4	2	17	18	-	-	1	-	-	-	-	2	1	28	140
	Spangdahlem AB, Germany	1	21	1	1	-	-	-	-	-	1	-	1	-	2	-	1	-	-	1	4	5	13	6	-	-	-	-	-	-	-	-	3	35	96
	USAG Stuttgart, Germany	1	61	7	-	-	-	-	1	-	-	-	1	-	2	-	8	-	-	-	1	4	7	8	15	-	-	-	-	-	-	-	1	76	193
	USAG Vicenza, Italy	6	51	2	-	-	-	-	-	1	-	-	-	-	4	-	-	-	-	1	-	3	2	-	23	-	-	-	-	-	-	-	-	57	150
Vilseck AHC, Germany	1	95	4	-	1	-	2	-	-	-	-	-	4	2	3	-	6	-	2	3	1	3	20	30	-	-	2	-	2	-	-	4	49	234	
Total		36	565	32	2	5	1	3	2	1	1	1	12	2	23	2	45	1	6	9	35	38	128	204	2	1	12	2	3	2	6	27	676	1885	

Graph 5. Percent influenza positive by week: 2013-2014 surveillance year and through Week 21 of the 2014-2015 surveillance year

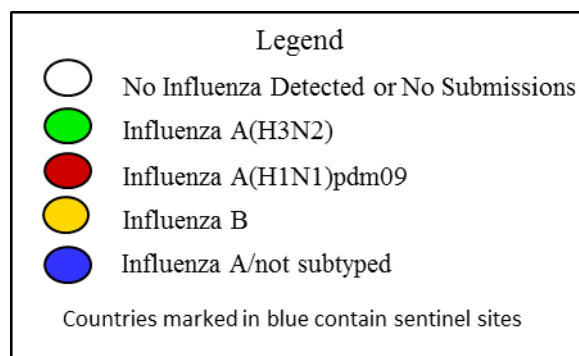


Note: Dual influenza co-infections have been excluded from the graph..

Map 4. Percentage of influenza positive by country for the 2014-15 surveillance year through Week 21 (Europe)



Country	Flu (+)	Flu (-)	% Positive
England	162	236	40.7
Germany	434	648	40.11
Italy	112	150	42.75
Spain	24	46	34.29
Turkey	2	26	7.14



Molecular Sequence Analysis Report USAFSAM Epidemiology Laboratory Service

This is the 10th report for the 2014-2015 season. The sequences reported here are a combination of influenza specimens submitted by USAFSAM sentinel sites and influenza sequence data sent by the Armed Forces Research Institute of Medical Sciences (AFRIMS). There are 32 specimens in this report, collected between 2 February and 21 April 2015 and subsequently analyzed. Of the 32 specimens sequenced, nine (28%) were influenza A(H3N2) viruses (seven were provided by AFRIMS), two (6%) were influenza A (H1N1)pdm09 viruses (both were provided by AFRIMS), 14 (44%) were influenza B/Yamagata viruses (two were provided by AFRIMS), and seven (22%) were influenza B/Victoria virus specimens (three were provided by AFRIMS).

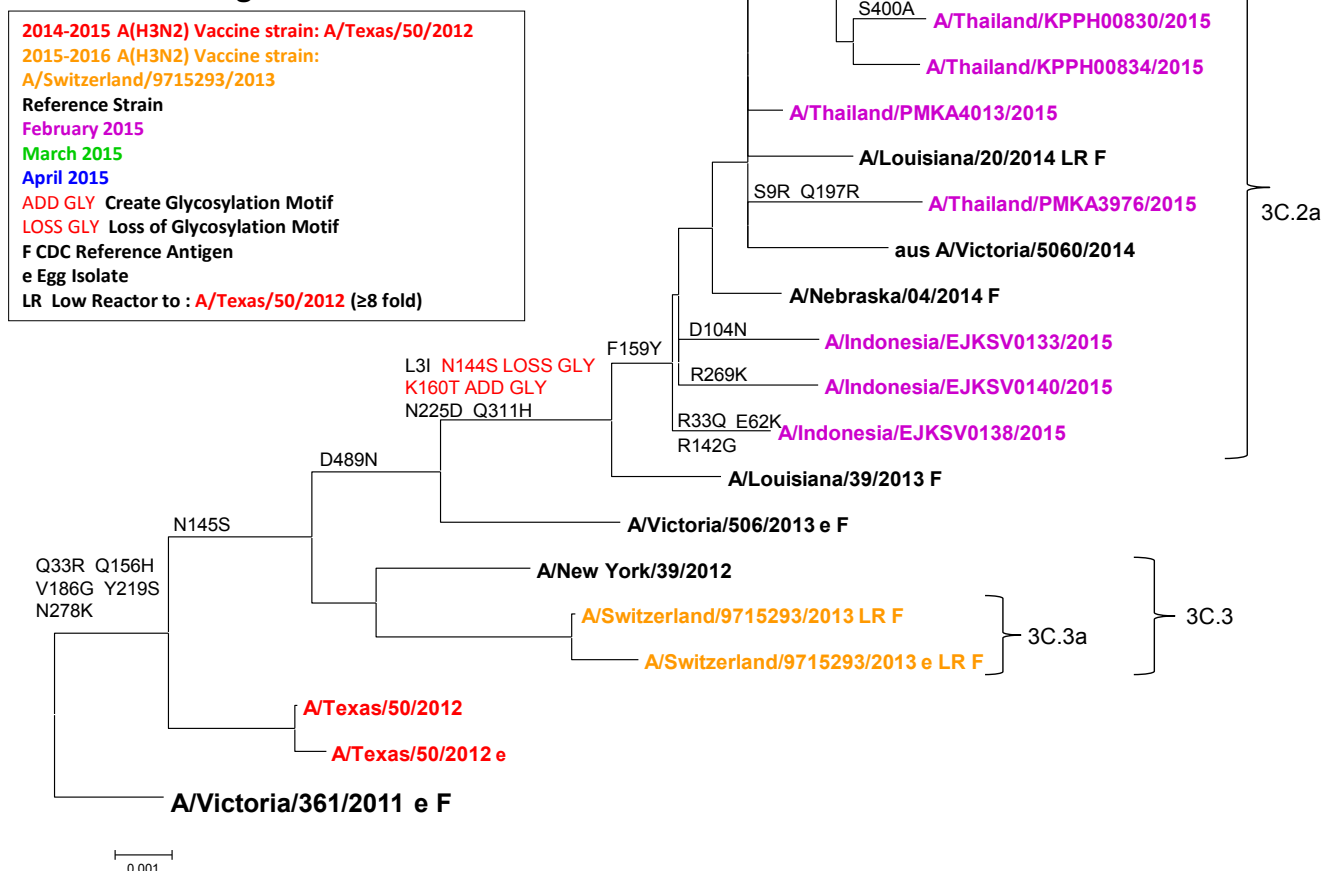
The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously 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)	A(H1N1)pdm09	B/Yamagata	B/Victoria
CONUS	Arizona, Davis-Monthan AFB			1	
	California, Edwards AFB			1	1
	Colorado, Peterson AFB				1
	Connecticut, USCG Academy	1			
	Massachusetts, Hanscom AFB			1	
	Nebraska, Offutt AFB			1	
	Nevada, Nellis AFB				1
	New Jersey, JB McGuire-Dix-Lakehurst			1	
	New York, Ft Drum			1	
	New York, USMA – West Point			2	
	Rhode Island, NHCNE Newport			1	
	South Dakota, Ellsworth AFB			1	
	Utah, Hill AFB			1	
	Washington, Fairchild AFB			1	
	Wyoming, FE Warren AFB				1
OCONUS	Country 3, Location A	1			
	Indonesia, AFRIMS	3	1	1	
	Pakistan, AFRIMS			1	
	Thailand, AFRIMS	4	1		3
TOTAL		9	2	14	7

Influenza A(H3N2)

- Isolates are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the previous vaccine, A/Victoria/361/2011-like virus [Figure 1].
- The influenza A(H3N2) specimens characterized for this report exhibited an overall protein identity of 97.1-97.6% as compared to the influenza A(H3N2) component of the 2013-2014 vaccine formulation, A/Texas/50/2012-like virus.
- Based on the mutations observed, all of the influenza A(H3N2) viruses analyzed belong to clade 3C and can be further classified as clade 3C.2a.
- 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(H3N2) specimens characterized in this report, two mutations: N45D (asparagine to aspartic acid) and N144S (asparagine to serine), 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.

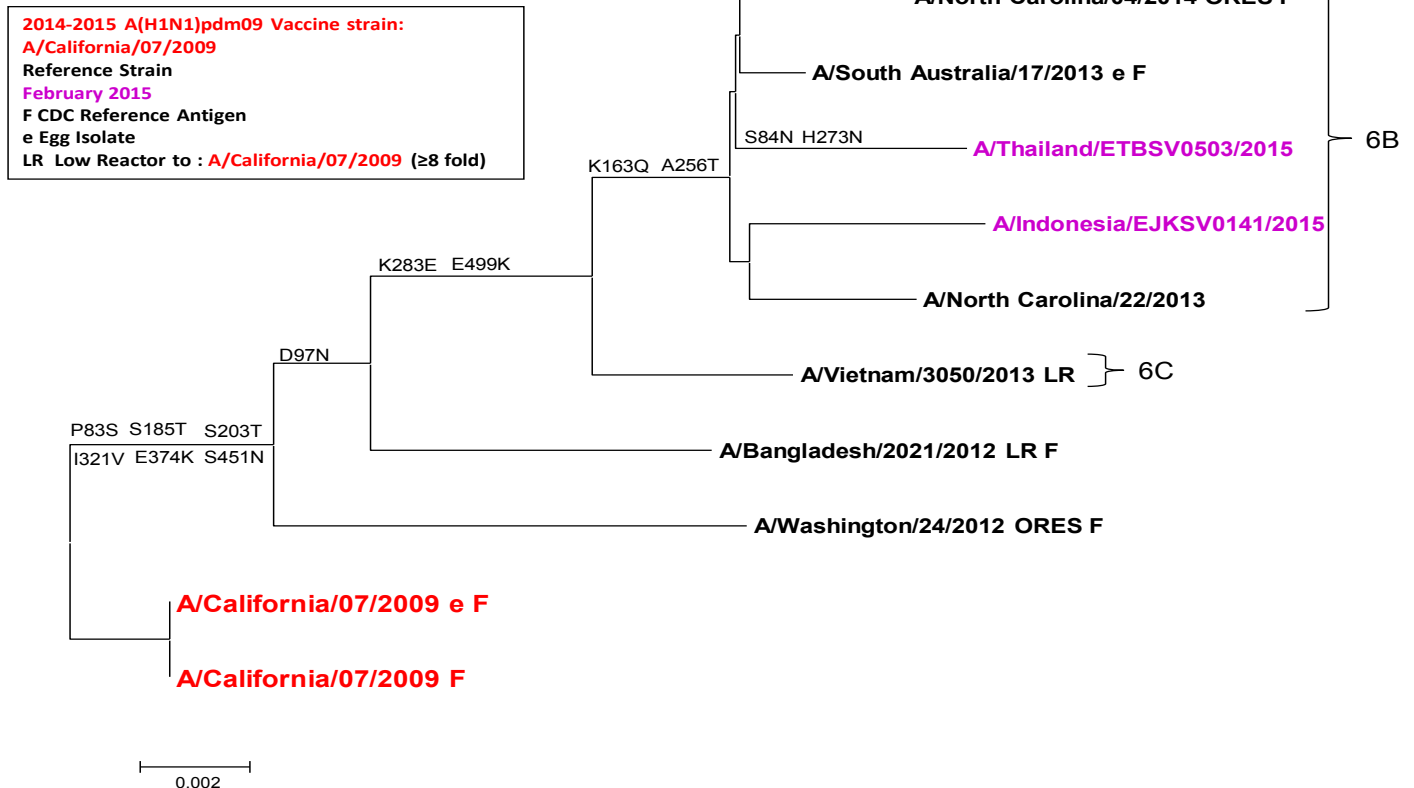
Recent 2014-2015 Influenza A(H3N2) HA Phylogenetic Analysis
Figure 1



Influenza A(H1N1)pdm09

- The 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 influenza A(H1N1)pdm09 specimens characterized for this report exhibited an overall protein identity of 97.1-97.5% compared to A/California/07/2009-like vaccine strain.
- Both of the influenza A(H1N1)pdm09 viruses sequenced for this report, contain mutations consistent with one of the circulating subgroup, referred as group 6B. Isolates of this group share two distinguishing mutations, K163Q (lysine to glutamine), and A256T (alanine to threonine).
- Of the 15 mutations present in the influenza A(H1N1)pdm09 specimens, seven occurred at predicted antigenic sites and three occurred at the receptor binding site. ^{2,5}

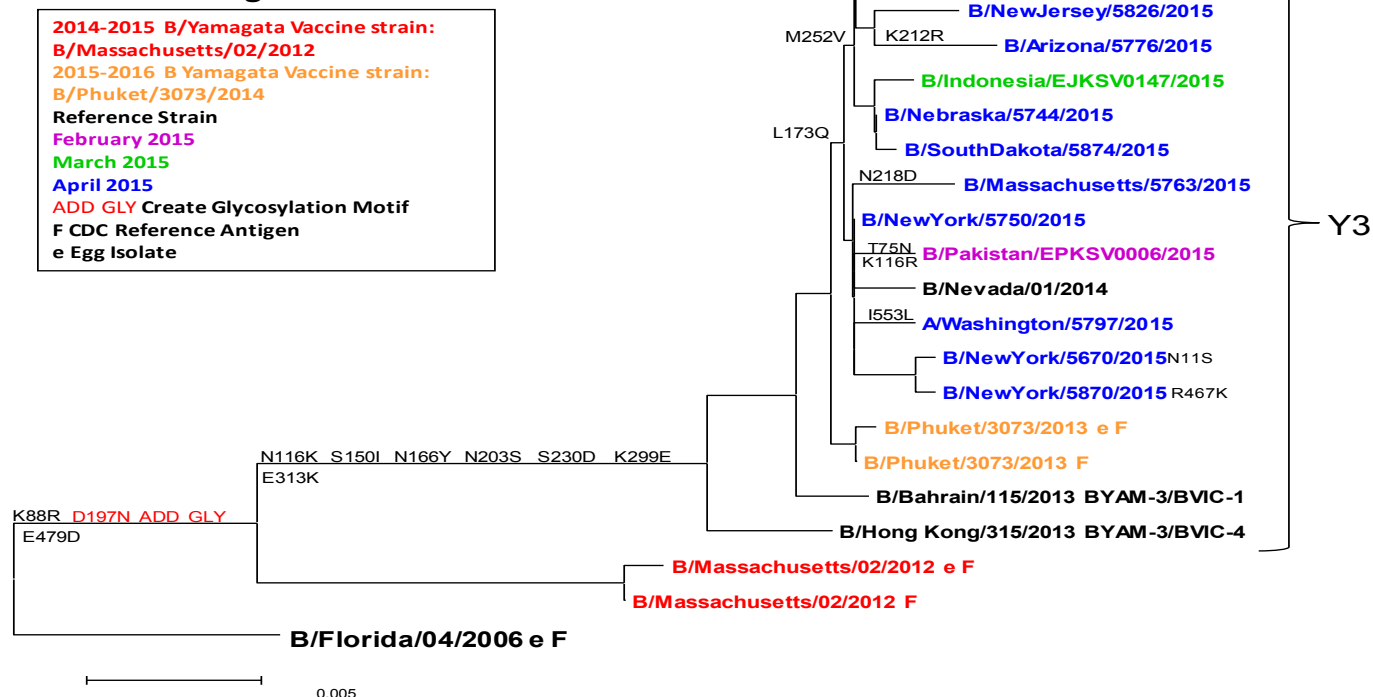
Recent 2014-2015 Influenza A(H1N1)pdm09 HA Phylogenetic Analysis Figure 2



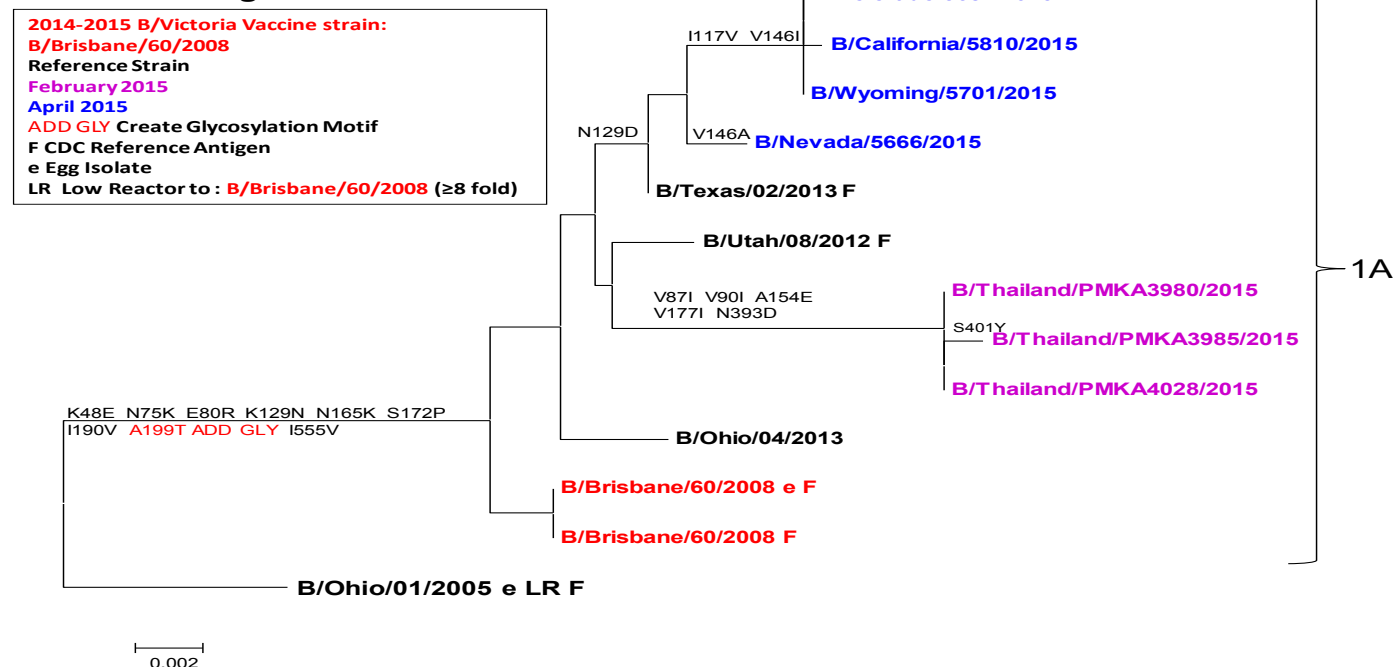
Influenza B

- The influenza B isolates are characterized in lineage specific; neighbor-joining phylogenetic trees with reference strains. The phylogenetic trees are rooted from previous vaccines, B/Florida/04/2006-like virus for Yamagata specimens [Figure 3] and B/Ohio/01/2005-like virus for the Victoria specimen [Figure 4].
- The distinguishing characteristic between the two lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.¹ Fourteen of the influenza B specimens characterized for this report reside within the Yamagata lineage (67%), while seven reside within the Victoria lineage (33%).
- The influenza B/Yamagata specimens characterized for this report exhibited an overall protein identity of 97.2-97.5% 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 98.4-99.3%.
- All 14 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.

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



Recent 2014-2015 Influenza B/Victoria HA Phylogenetic Analysis Figure 4



References:

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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 YI, Viboud C, Holmes EC, Koonin EV, Lipman DJ. Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol Direct*. 2006; 1: 34. Published online 2006 October 26. doi: 10.1186/1745-6150-1-34.

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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)



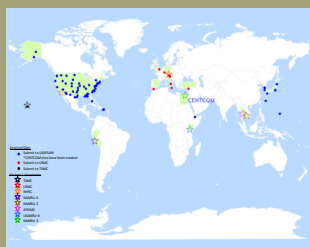
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Contributions to the CDC for National Influenza Surveillance

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)

[https://](https://gumbo2.area52.afnoapps.usaf.mil/epi-consult/influenza)

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.



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