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Respiratory Highlights, 2016-2017 Influenza Season (2 October 2016 – 31 September 2017)

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13. SUPPLEMENTARY NOTES

Cleared, 88PA, Case # 2018-1051, 5 Mar 2018.

14. ABSTRACT

During the 2016-2017 influenza season (2 October 2016 - 30 September 2017), results were finalized for 5,555 specimens from 84 locations. There were 1,833 specimens positive for influenza (29 A(H1N1)pdm09, 1,352 A(H3N2), one influenza A/not subtyped, 443 B, four dual influenza coinfections, and four influenza coinfections with other respiratory pathogens). These results and other respiratory pathogens that were identified can be found in Table 2 on pages 4 & 5. During the 2016-2017 influenza season, influenza A(H3N2) was the predominant strain. Influenza activity peaked at Weeks 7 & 8 and the influenza percent positive for the season was 33%. This is the cumulative report for specimens tested at USAFSAM during the 2016-2017 influenza season.

15. SUBJECT TERMS

Influenza, surveillance, annual report, sentinel sites

16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT	18. NUMBER OF PAGES	19a. NAME OF RESPONSIBLE PERSON
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U	U	U	SAR	31	19b. TELEPHONE NUMBER *(include area code)*

USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

2016-2017

Cumulative Results

Locations	84
Collected	5,618
Tested	5,555

Influenza A	**1,389**
A(H1N1)pdm09	29
A(H1N1)pdm09 & Influenza B	1
A(H3N2)	1,352
A(H3N2) & Influenza B	3
A(H3N2) & Coronavirus & RSV	1
A(H3N2) & RSV	1
A(H3N2) & Rhino/Enterovirus	1
A/not subtyped	1

Influenza B*	**444**
B	443
B & Human Metapneumovirus & Rhino/Enterovirus	1

Other Respiratory Pathogens	**1,236**
Adenovirus	78
Bordetella pertussis	1
Chlamydophila pneumoniae	5
Coronavirus	123
Human Metapneumovirus	95
Mycoplasma pneumoniae	40
Parainfluenza	203
RSV	179
Rhinovirus/Enterovirus	369
Non-influenza Viral Coinfections	135
Non-influenza Bacterial Coinfections	8
-*M. pneumo* coinfections *(8)*	

Results are preliminary and may change as more results are finalized.
**Influenza B lineages and specimens submitted for sequencing only will be reported in the periodic molecular sequencing reports.*

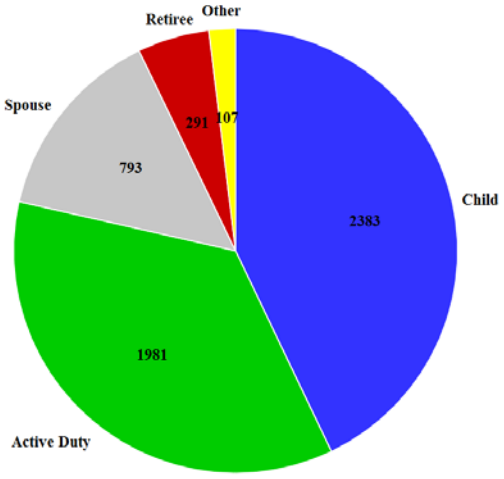
Respiratory Highlights
2016 - 2017 Influenza Season (2 October 2016 - 30 September 2017)

- During the 2016-2017 influenza season (2 October 2016 - 30 September 2017), results were finalized for 5,555 specimens from 84 locations. There were 1,833 specimens positive for influenza (29 A(H1N1)pdm09, 1,352 A(H3N2), one influenza A/not subtyped, 443 B, four dual influenza coinfections, and four influenza coinfections with other respiratory pathogens). These results and other respiratory pathogens that were identified can be found in Table 2 on pages 4 & 5.
- During the 2016-2017 influenza season, influenza A(H3N2) was the predominant strain. Influenza activity peaked at Weeks 7 & 8 and the influenza percent positive for the season was 33%.
- This is the cumulative report for specimens tested at USAFSAM during the 2016-2017 influenza season.

Table 1. ILI by age group for the 2016-2017 surveillance year

Age Group	Frequency	Percent
0-5	1245	22.41
6-9	495	8.91
10-17	652	11.74
18-24	780	14.04
25-44	1725	31.05
45-64	533	9.59
65+	125	2.25

Graph 1. ILI by beneficiary status for the 2016-2017 surveillance year



Demographic Summary

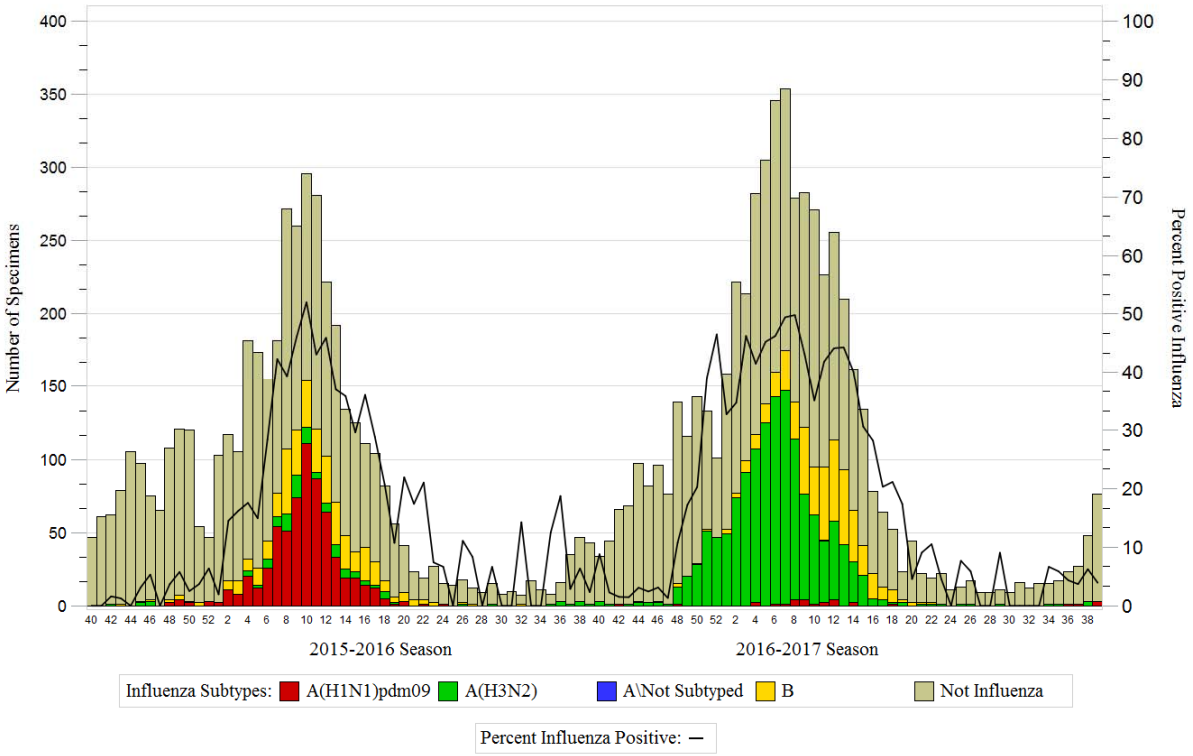
Of 5,555 ILI cases, 1,981 are service members (35.6%), 2,383 are children (42.9%), 793 are spouses (14.3%), and 398 (7.2%) are retirees and other beneficiaries. The median age of ILI cases with known age (n=5,555) is 21 (range 0, 96).

Table of Contents

Cleared, 88PA, Case # 2018-1051, 5 Mar 2018.

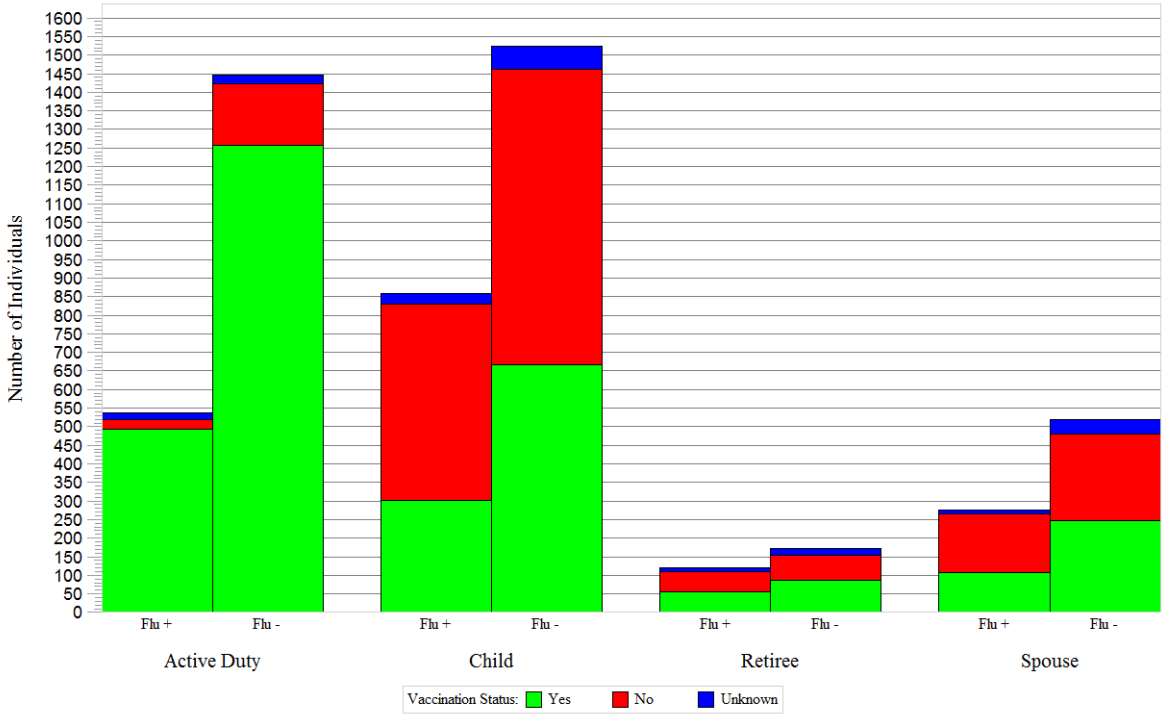
Laboratory Results - Cumulative for Season

Graph 2. Percent influenza positive by week: 2015-2016 and 2016-2017 surveillance years



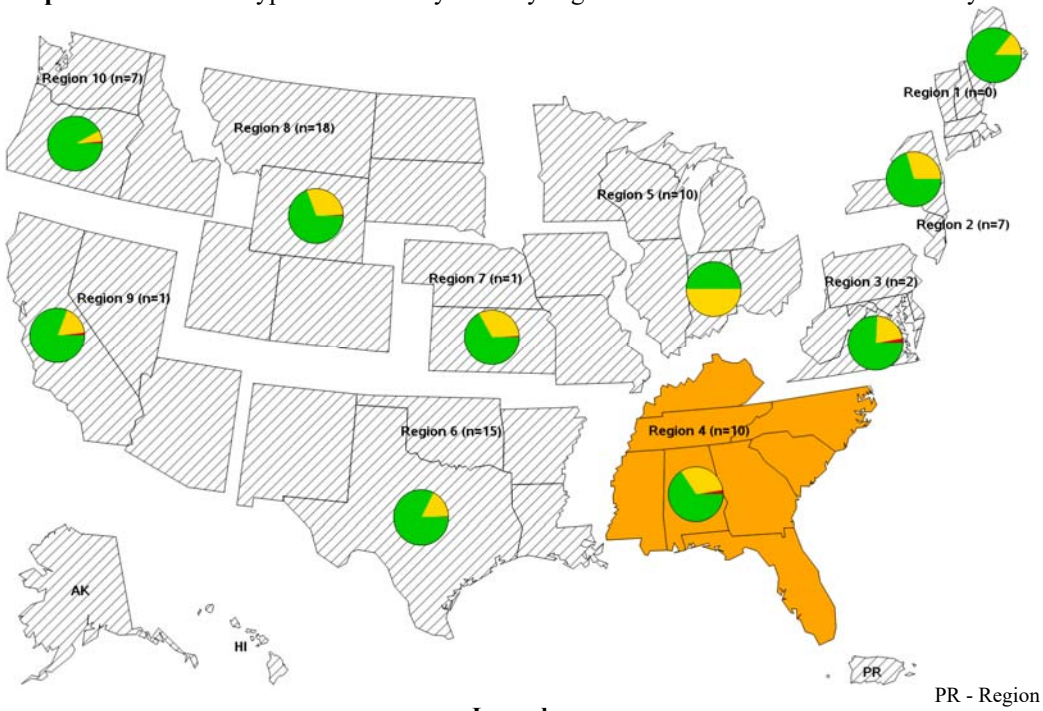
Note: Dual influenza coinfections are excluded from this graph. Specimens with pending results are used in the denominator to calculate percent positive, but are not displayed in the graph.

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



DoD Global, Laboratory-Based, Influenza Surveillance Program

Map 1. Influenza subtypes and activity level by region for the 2016-2017 surveillance year



HI - Region 9

AK - Region 10

PR - Region 2

Legend

Influenza Activity - Weeks 38 - 39

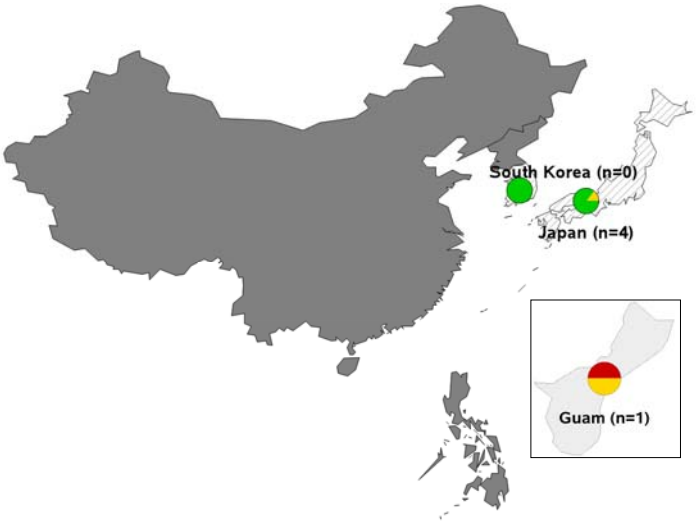
(n = # of finalized results)

- No activity (0% +) or no submissions
- Low (<25% +)
- Moderate (25-49% +)
- High (>50% +)

Influenza Results - Cumulative

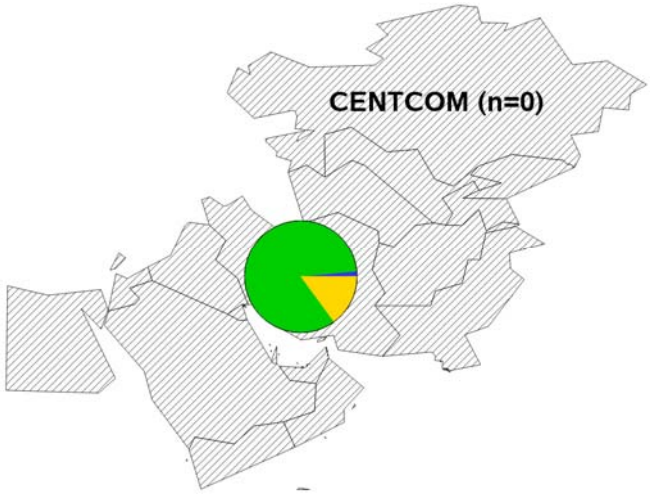
- Influenza A(H3N2)
- Influenza A(H1N1)pdm09
- Influenza B
- Influenza A/not subtyped

Map 2. Influenza subtypes by country for the 2016-2017 surveillance year (Pacific)



Note: Sentinel sites are not present in gray areas within the map.

Map 3. Influenza subtypes for CENTCOM for the 2016-2017 surveillance year



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

Cleared, 88PA, Case # 2018-1051, 5 Mar 2018.

Laboratory Results

Table 2. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & hMNV & Rhino/Entero	Adenovirus	*B. pertussis*	*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	-	14	-	-	-	-	-	-	9	-	-	-	-	2	-	-	-	1	2	1	-	11	40
	Country 1, Location D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Country 2, Location A	-	33	1	-	-	-	-	1	1	-	-	-	-	6	-	-	-	-	8	2	-	16	68
EUCOM	Incirlik AB, Turkey	-	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	3	5
PACOM	CFA Okinawa, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	5
	JR Marianas - Andersen AFB, Guam	1	-	-	-	-	-	-	-	1	-	2	-	-	-	-	1	1	-	-	-	-	8	14
	Kadena AB, Japan	-	4	-	-	-	-	-	-	1	-	-	-	-	-	1	-	3	-	3	1	1	24	38
	Kunsan AB, South Korea	-	2	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	1	5
	Misawa AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	NH Okinawa, Japan	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Osan AB, South Korea		4													1							9	14
	Tripler AMC, HI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3
	Yokota AB, Japan	-	36	-	-	-	-	-	-	6	-	1	-	-	3	1	2	4	2	12	5	-	76	148
Region 1	Hanscom AFB, MA	-	3	-	-	-	-	-	-	1	-	1	-	-	-	-	1	2	-	-	1	-	4	13
	USCG Academy, CT	-	9	-	-	-	-	-	-	1	-	-	-	-	1	1	1	-	-	3	-	2	6	24
Region 2	CGAS Borinquen, PR	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Ft Drum, NY	1	49	-	-	1	-	-	-	62	-	7	-	1	5	10	1	9	8	11	6	-	101	272
	JB McGuire-Dix-Lakehurst, NJ	-	54	-	-	-	-	-	-	2	-	3	-	-	6	9	2	10	6	13	5	-	87	197
	USMA - West Point, NY	-	86	-	-	-	-	-	-	15	-	12	-	-	5	7	3	11	13	20	9	-	167	348
Region 3	Dover AFB, DE	-	19	-	-	-	-	-	-	11	-	2	-	-	2	1	1	1	1	7	-	-	52	97
	JB Anacostia-Bolling, DC	-	14	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	1	-	-	-	-	19
	JB Andrews, MD	2	23	-	-	-	-	-	-	12	-	-	-	-	2	1	-	3	2	1	2	-	44	92
	JB Langley-Eustis, VA	6	149	-	1	1	-	-	-	31	-	1	-	-	4	10	2	12	21	38	11	-	262	549
	NCRM - Walter Reed NMMC, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	3
	NMC Portsmouth, VA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	3
	US Naval Academy, MD	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Region 4	CGS Mobile, AL	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
	Columbus AFB, MS	-	5	-	-	-	-	-	-	1	-	-	-	-	2	-	-	-	-	2	-	-	21	31
	Eglin AFB, FL	1	15	-	-	-	-	-	-	5	-	7	-	-	2	2	2	2	5	12	6	-	49	108
	Ft Bragg, NC	2	8	-	-	-	-	-	-	6	-	-	-	-	1	1	1	3	2	7	4	3	40	78
	Ft Campbell, KY	1	15	-	-	-	-	-	-	9	1	2	-	-	-	1	-	-	3	-	4	-	17	53
	Hurlburt Field, FL	3	19	-	-	-	-	-	-	6	-	3	-	-	1	-	1	1	2	5	1	-	30	72
	JB Charleston (AF), SC	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	19
	JB Charleston (Navy), SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Keesler AFB, MS	-	2	-	-	-	1	-	-	-	-	-	-	-	-	1	-	3	3	8	3	-	22	43
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	1	-	-	8	11
	Maxwell AFB, AL	-	10	-	-	-	-	-	-	2	-	-	-	-	-	1	-	2	-	2	-	-	15	32
	Moody AFB, GA	-	36	-	-	-	-	-	-	45	-	1	-	-	2	7	1	15	9	18	14	1	97	246
	NH Beaufort, SC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	5	7
	NH Camp Lejeune, NC	-	2	-	-	1	-	-	-	-	-	-	-	-	-	-	-	2	-	2	1	-	12	20
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	4	6
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Robins AFB, GA	-	25	-	-	-	-	-	-	8	-	-	-	-	-	-	2	1	3	3	-	-	34	76
	Seymour Johnson AFB, NC	3	17	-	-	-	-	-	-	1	-	2	-	-	-	-	1	1	2	1	-	-	24	52
	Shaw AFB, SC	-	71	-	-	-	-	-	-	34	-	1	-	1	7	5	1	6	1	13	2	-	73	215
	Tyndall AFB, FL	-	11	-	-	-	-	-	-	5	-	1	-	-	-	-	-	-	-	-	-	-	1	18

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

(Cont'd on page 5)

Cleared, 88PA, Case # 2018-1051, 5 Mar 2018.

Laboratory Results

Table 2. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

(Cont'd from page 4)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H1N1)pdm09 & B	A(H3N2) & B	A(H3N2) & Corona & RSV	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	B & hMNV & Rhino/Entero	Adenovirus	*B. pertussis*	*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	-	-	-	-	-	-	3	-	-	-	-	-	-	1	3	1	1	-	1	9	22
	Wright-Patterson AFB, OH	-	10	-	-	-	-	-	-	10	-	-	-	-	2	1	1	3	-	5	2	-	49	83
Region 6	Altus AFB, OK	-	7	-	-	-	-	-	-	1	-	2	-	-	1	1	-	1	5	8	4	-	41	71
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	2	-	2	-	-	8	13
	Cannon AFB, NM	-	13	-	-	-	-	-	-	4	-	-	-	-	2	-	1	3	-	5	1	-	42	71
	Ft Polk, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	3
	JBSA Lackland, TX	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1
	Kirtland AFB, NM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Laughlin AFB, TX	1	-	-	-	-	-	-	-	1	-	-	-	-	1	2	-	-	-	1	-	-	7	13
	Little Rock AFB, AR	-	12	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	13	26
	Sheppard AFB, TX	-	60	-	-	-	-	-	-	9	-	1	-	-	10	6	1	7	2	13	-	-	98	207
	Tinker AFB, OK	1	99	-	-	-	-	1	-	25	-	2	-	-	10	4	1	9	7	15	6	-	154	334
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	16	17
Region 7	McConnell AFB, KS	-	25	-	-	-	-	-	-	18	-	1	-	-	4	-	1	4	5	9	3	-	37	107
	Offutt AFB, NE	1	32	-	-	-	-	-	-	9	-	1	-	-	6	2	-	2	1	13	1	-	63	131
Region 8	Ellsworth AFB, SD	-	15	-	-	-	-	-	-	15	-	-	-	-	3	-	-	3	1	4	-	-	42	83
	FE Warren AFB, WY	-	36	-	-	-	-	-	-	7	-	3	-	-	4	1	2	5	6	5	-	-	59	128
	Hill AFB, UT	-	30	-	-	-	-	-	-	5	-	-	-	-	3	1	1	8	4	9	2	-	52	115
	Malmstrom AFB, MT	-	7	-	-	-	-	-	-	3	-	-	-	-	-	-	1	-	-	1	-	-	9	21
	Minot AFB, ND	1	25	-	-	-	-	-	-	15	-	-	-	-	3	2	1	1	6	10	3	-	50	117
	Peterson AFB, CO	1	19	-	-	-	-	-	-	12	-	-	1	-	3	-	-	5	11	6	4	-	38	100
	USAF Academy, CO	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	1	2	1	-	5	11
Region 9	Beale AFB, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5
	Davis-Monthan AFB, AZ	1	16	-	-	-	-	-	-	4	-	-	-	-	-	2	-	5	1	8	5	-	46	88
	Edwards AFB, CA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Los Angeles AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Luke AFB, AZ	-	-	-	-	-	-	-	-	5	-	1	-	-	2	-	-	1	3	3	1	-	23	39
	Nellis AFB, NV	1	3	-	-	-	-	-	-	4	-	3	-	-	1	-	-	5	4	6	7	-	35	69
	Travis AFB, CA	-	58	-	-	-	-	-	-	5	-	1	-	1	6	8	-	7	13	17	5	-	51	172
	Vandenberg AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	7
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	4
	Eielson AFB, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	-	-	2	-	7	12
	Fairchild AFB, WA	2	17	-	-	-	-	-	-	2	-	5	-	-	3	-	1	5	2	6	-	-	56	99
	JB Elmendorf-Richardson, AK	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	4	6
	JB Lewis-McChord, WA	-	2	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	3
	Mt Home AFB, ID	-	23	-	-	-	-	-	-	1	-	1	-	1	1	-	1	23	12	12	5	-	81	161
	NH Bremerton, WA	-	67	-	-	-	-	-	-	5	-	9	-	1	3	1	2	8	7	12	4	-	30	149
Total		29	1352	1	1	3	1	1	1	443	1	78	1	5	123	95	40	203	179	369	135	8	2486	5555

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

Cleared, 88PA, Case # 2018-1051, 5 Mar 2018.

EUCOM Respiratory Surveillance Supplemental Report
2016-2017 Season

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

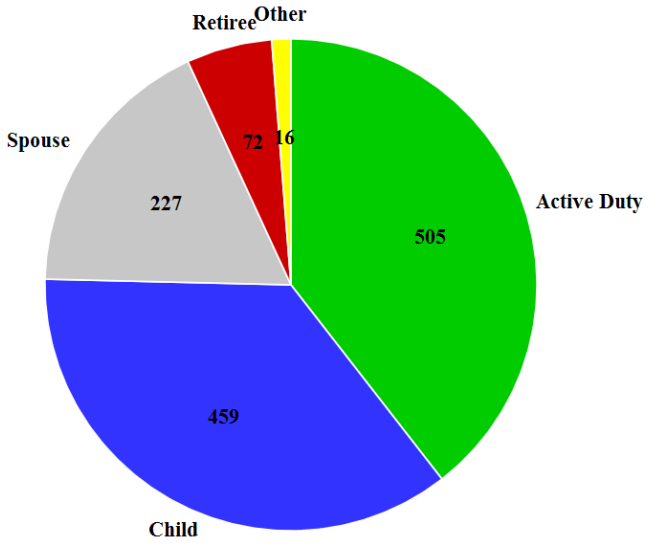
Table 3. Cumulative results by region and location for specimens collected during the 2016-2017 surveillance year

Region		A(H1N1)pdm09	A(H3N2)	A/not subtyped	A(H3N2) & Adeno	A(H3N2) & hMNV & Rhino/Entero	A(H3N2) & RSV	A(H3N2) & Rhino/Entero	B	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 2, Location A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2
	Country 6, Location A	-	3	-	-	-	-	2	-	-	-	-	-	-	4	-	-	-	-	-	-	-	20	29
EUCOM	Aviano AB, Italy	-	-	-	-	-	-	-	2	-	-	-	-	-	2	-	-	-	-	-	-	-	11	15
	Landstuhl RM C, Germany	1	58	-	-	-	2	1	7	-	2	12	12	17	46	1	-	3	-	1	1	-	3	190	357
	NAS Sigonella, Italy	-	6	-	-	-	-	-	-	-	-	1	-	3	4	-	-	-	-	-	-	-	5	19
	NAVSTA Rota, Spain	-	2	1	-	-	-	-	-	-	-	2	4	5	11	-	-	-	-	-	-	-	35	60
	NSA Naples, Italy	-	10	-	-	-	-	1	-	-	-	2	5	4	12	-	-	-	-	-	-	-	34	68
	RAF Lakenheath, England	-	24	-	-	-	-	1	2	-	3	11	5	14	29	-	1	1	-	1	-	-	95	189
	Ramstein AB, Germany	-	24	1	-	-	-	-	3	-	1	8	3	12	24	-	-	1	-	-	-	1	-	63	141
	Spangdahlem AB, Germany	-	1	-	-	-	-	1	-	-	-	-	-	1	2	-	-	-	-	-	-	-	-	6	11
	USAG Stuttgart, Germany	-	17	-	-	-	-	-	1	1	-	5	3	7	20	-	-	-	-	-	-	-	-	35	89
	USAG Vicenza, Italy	-	14	1	2	-	-	-	-	-	-	3	1	2	4	-	-	-	-	-	-	1	-	30	58
	Vilseck AHC, Germany	-	41	-	-	1	-	-	4	-	1	14	16	31	31	-	-	1	1	-	2	3	-	95	241
Total		1	209	3	2	1	2	6	19	1	7	56	49	96	189	1	1	6	1	2	3	5	5	621	1279

Table 4. ILI by age group for the 2016-2017 surveillance year

Age Group	Frequency	Percent
0-5	346	27.05
6-9	58	4.53
10-17	56	4.38
18-24	158	12.35
25-44	473	36.98
45-64	141	11.02
65+	47	3.67

Graph 4. ILI by beneficiary status for the 2016-2017 surveillance year



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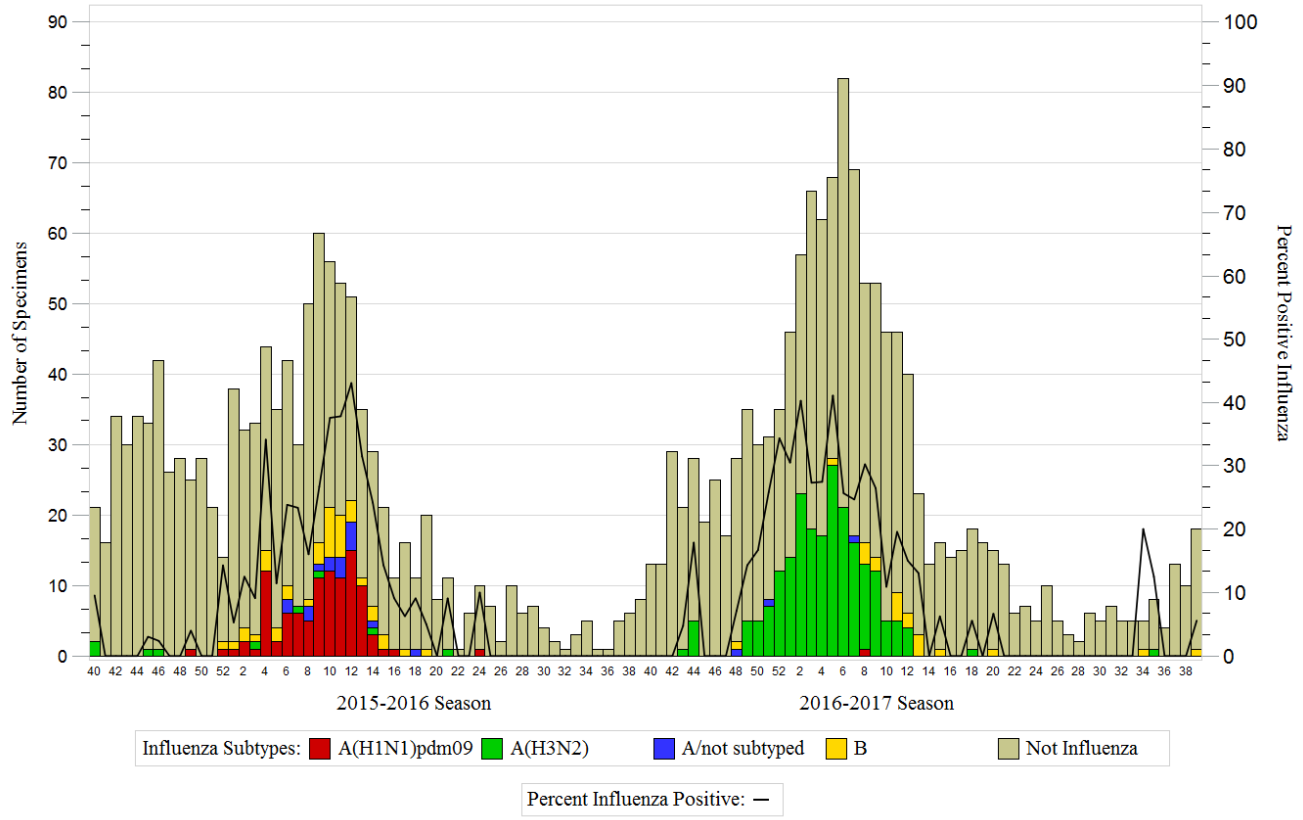
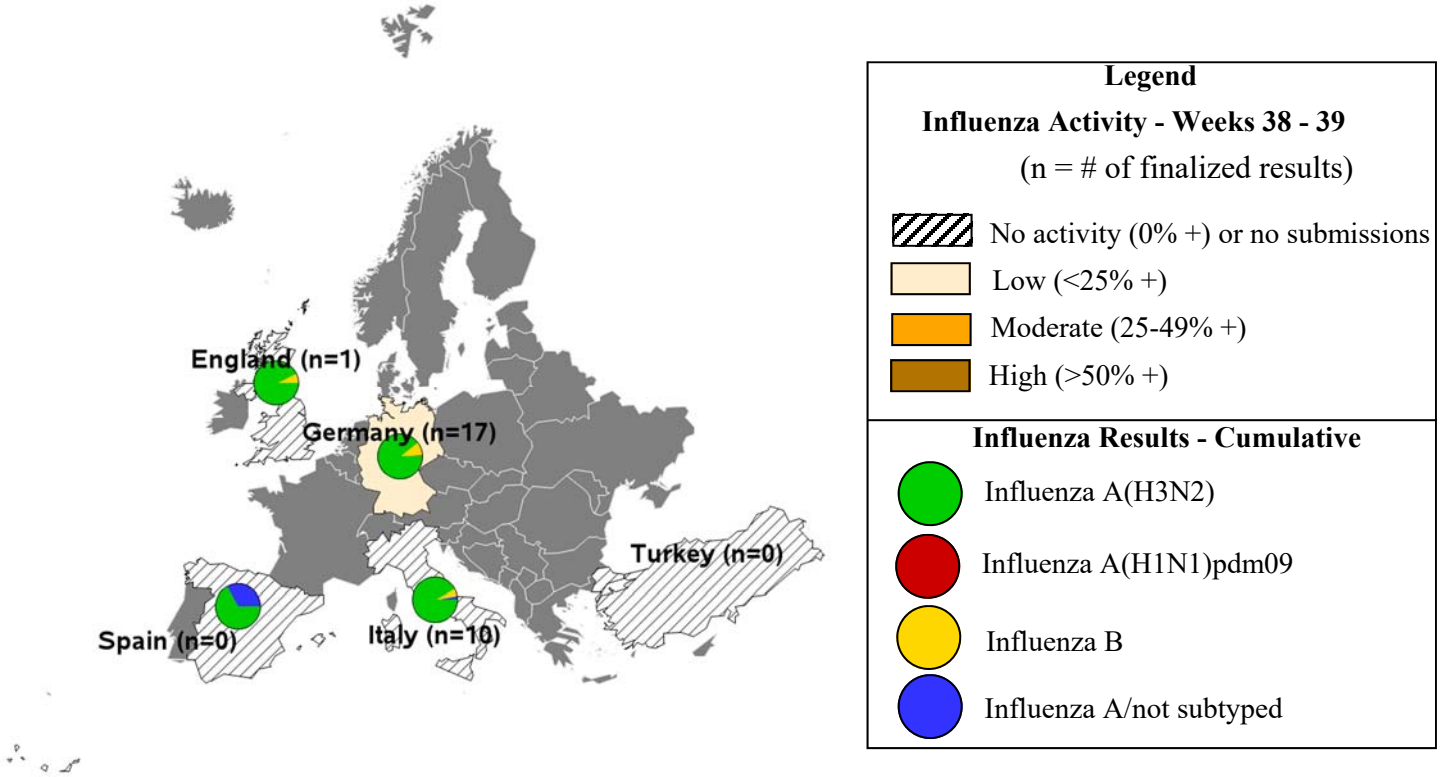
Graph 5. Percent influenza positive by week: 2015-2016 and 2016-2017 surveillance years (EUCOM)



Map 4. Influenza subtypes and activity level by country for the 2016-2017 surveillance year (Europe)



2016-2017 Season Influenza Hemagglutinin Gene Sequence Analysis Report

This report is a summary of the influenza hemagglutinin (HA) gene sequences analyzed and reported by USAFSAM throughout the 2016-2017 influenza season as part of the DoD Global Respiratory Pathogen Surveillance Program. Several HA sequences from August-September 2016 were included for a pre-season snapshot of circulating influenza viruses leading up to the 2017-2017 season. The 2016-2017 influenza season was dominated by A(H3N2) viruses with a low prevalence (<5%) of the A(H1N1)pdm09 virus and a moderate prevalence (>20%) of influenza B virus that was roughly a 45/55% split between the B/Victoria and B/Yamagata lineages, respectively. One influenza A(H3N2) variant virus [A(H3N2)v] was identified as a swine origin influenza from an infected child with a history of swine contact at an agricultural event in Texas. The HA gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the HA gene. Antigenic sites, receptor binding sites, and glycosylation motifs are predicated upon correlations with previously published experimental evidence.[1-3] Sequence data were constructed and analyzed using multiple software programs. Genetic and predicted antigenic information that resulted from this analysis is shared with the U.S. Centers for Disease Control and Prevention and the World Health Organization (WHO) and contribute to the seasonal Northern and Southern Hemisphere vaccine component selections.

In total, 1,142 influenza sequences were analyzed and reported by USAFSAM during the 2016-2017 season, including 50 (4.4%) A(H1N1)pdm09, 824 (72.2%) A(H3N2), 121 (10.6%) B/Victoria, and 146 (12.8%) B/Yamagata, in addition to the single A(H3N2)v sequence. The majority of the influenza HA sequences were generated at USAFSAM using Sanger sequencing, while additional HA sequences were provided to USAFSAM from Global Emerging Infections Surveillance and Response System (GEIS) partner laboratories, which include the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Thailand, Navy Medical Research Unit Two (NAMRU-2) in Cambodia, NAMRU-6 in Peru, the Naval Health Research Center (NHRC) in San Diego, California, the U.S. Army Medical Research Directorate – Kenya (USAMRD-K), and the Walter Reed Army Institute of Research (WRAIR) in Silver Spring, Maryland. The distribution of 2016-2017 influenza HA sequences analyzed by USAFSAM spans 39 states and 17 countries and covers 6 of the global U.S. Combatant Commands. Eight hundred and forty-nine (74.3%) of the HA sequences are from within the contiguous United States (CONUS) and the remaining 293 (25.7%) are from outside the contiguous United States (OCONUS). Tables 5 and 7 show the distribution of influenza A subtype and B lineage HA sequences contributed by all partner laboratories and sentinel sites, respectively. Figures 1 and 2 detail the specimen and sequence coverage across U.S. Combatant Commands and CONUS/OCONUS sites. Table 6 displays the combined protein homology range and average of 2016-2017 HA sequences to that of the 2016-2017 influenza vaccine strains.

Highlights from the 2016-2017 influenza season included a change of the influenza A(H1N1)pdm09 vaccine component for the 2017-2018 season, continued dominance of the A(H3N2) subclade 3C.2a1, several appearances of a 6 base pair deletion in the HA gene of B/Victoria specimens, and the single appearance of 3 base pair deletion in the HA gene of a B/Yamagata specimen.

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In September 2016, WHO recommended to change the Southern Hemisphere influenza vaccine A(H1N1)pdm09 component from A/California/07/2009-like virus to A/Michigan/45/2015-like virus for the 2017 Southern Hemisphere influenza season due to a better antigenic response by the Michigan strain. The A/Michigan/45/2015 virus is in the same 6B.1 subclade that the majority of the 2016-2017 influenza A(H1N1)pdm09 specimens reside. Based on the Southern Hemisphere decision, the 2017 Vaccines and Related Biological Products Advisory Committee (VRBPAC) followed suit by selecting the A/Michigan/45/2015-like virus for the 2017-2018 influenza vaccine A(H1N1)pdm09 component for the Northern Hemisphere vaccine.

Within the A(H3N2) subtype, the prevalence of subclade 3C.2a1 increased dramatically during the 2015-2016 season and remained as the prominent A(H3N2) subclade throughout the 2016-2017 season. The mutation N121K, which was present in 83 of the other 3C.2a specimens (32.0%), was shown in a majority (423, 86.5%) of 3C.2a1 specimens. The mutation T135K was also present in 164 (33.5%) of the 3C.2a1 specimens and often coincided with the N121K mutation. These mutations increased in frequency during the season in the USAFSAM surveillance system as well as in other reported sources and may contribute largely to the reduced effectiveness of the egg-propagated A/Hong Kong/4801/2014-like virus vaccine component.[4,5]

As a surprising development in the 2016-2017 influenza B/Victoria HA sequences, a specimen collected in December 2016 at Moody AFB, Georgia, was found to contain a 6 base pair deletion resulting in the loss of 2 amino acids at positions 162-163, which falls in the same region as the single amino acid deletion at 162 observed in Yamagata lineage specimens. At the time of this discovery, only one B/Victoria HA sequence containing this deletion was found in GenBank, which was collected November 2016 in New York. Specimens containing this 6 base pair deletion continued to show up in the 2016-2017 USAFSAM influenza surveillance; these at first were concentrated to Georgia and other Southeastern U.S. states, but by the end of the season they were identified in other states such as California, Illinois, and Colorado. In March 2017, a B/Yamagata specimen collected at Vilseck AHC, Germany, was found to contain an additional 3 base pair deletion resulting in the loss of a single amino acid at position 527 that had not been previously seen in USAFSAM surveillance specimens. One B/Yamagata HA sequence in GenBank, collected in Alberta, Canada, shares this deletion. Insertions and deletions have historically been an adaptive strategy of influenza B viruses, but have not been observed with much frequency for many years.[6] Antigenic characterization studies have shown that the currently used influenza B/Victoria vaccine component, B/Brisbane/60/2008-like virus, has reduced protection against the B/Victoria deletion strains.[7]

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Table 5. Influenza A(H1N1)pdm09, A(H3N2), A(H3N2)v, B/Victoria, B/Yamagata specimens and sequences contributed by partner laboratories during the 2016-2017 influenza season

	A(H1N1)pdm09	A(H3N2)	A(H3N2)v	B/Victoria	B/Yamagata	Total
AFRIMS	3	3		4		10
LRMC	2	101		1	6	110
NAMRU-2	9	5		19	1	34
NAMRU-6	1	2				3
NHRC	9	74		7	9	99
USAFSAM	24	615	1	84	130	854
USAMRD-K	2	21		6		29
WRAIR		3				3
Total	**50**	**824**	**1**	**121**	**146**	**1142**

Table 6. Protein homologies (percent amino acid match) of circulating 2016-2017 influenza strains relative to vaccine strains. Prior to B/Phuket/3073/2013-like virus being used as the B/Yamagata portion of the vaccine, B/Wisconsin/01/2010-like virus was used in the 2012-2013 season and B/Massachusetts/02/2012-like virus was used from 2013-2015. Use of the quadrivalent vaccine, which contains strains from each of the influenza B lineages in addition to one A(H1N1)pdm09 and one A(H3N2) virus, began in 2013 for the 2013-2014 influenza season.

Subtype or Lineage	Season(s) Component Used	Vaccine Component	Min	Max	Average
A(H1N1)pdm09	2010-2017	A/California/07/2009-like	96.5%	97.6%	97.2%
A(H1N1)pdm09	2017-2018	A/Michigan/45/2015-like	98.9%	99.8%	99.5%
A(H3N2)	2016-2018	A/Hong Kong/4801/2014-like	96.9%	99.3%	98.3%
B/Victoria	2009-2012 and 2013-2018	B/Brisbane/60/2008-like*	98.4%	99.5%	99.1%
B/Yamagata	2015-2018	B/Phuket/3073/2013-like**	98.8%	99.3%	99.2%

*Quadrivalent only during the 2013-2016 seasons.
**Quadrivalent only during the 2016-2018 seasons.

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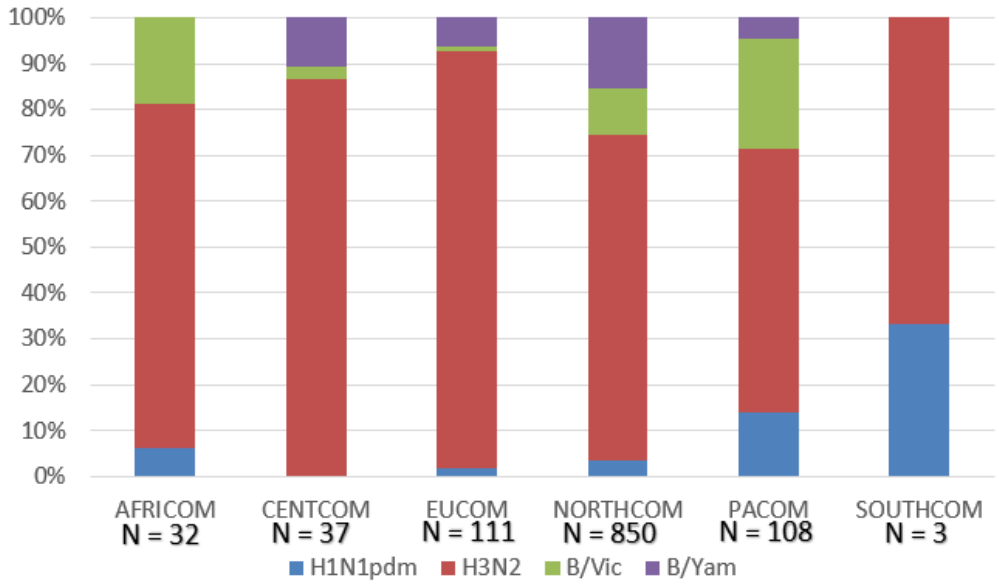

Figure 1. The proportion of HA sequences for influenza A(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata from each of the United States Combatant Commands during the 2016-2017 season. The number of total sequences from each U.S. Combatant Command are shown below each bar. The A(H3N2)v specimen, from NORTHCOM, was excluded because it would not have been distinguishable.

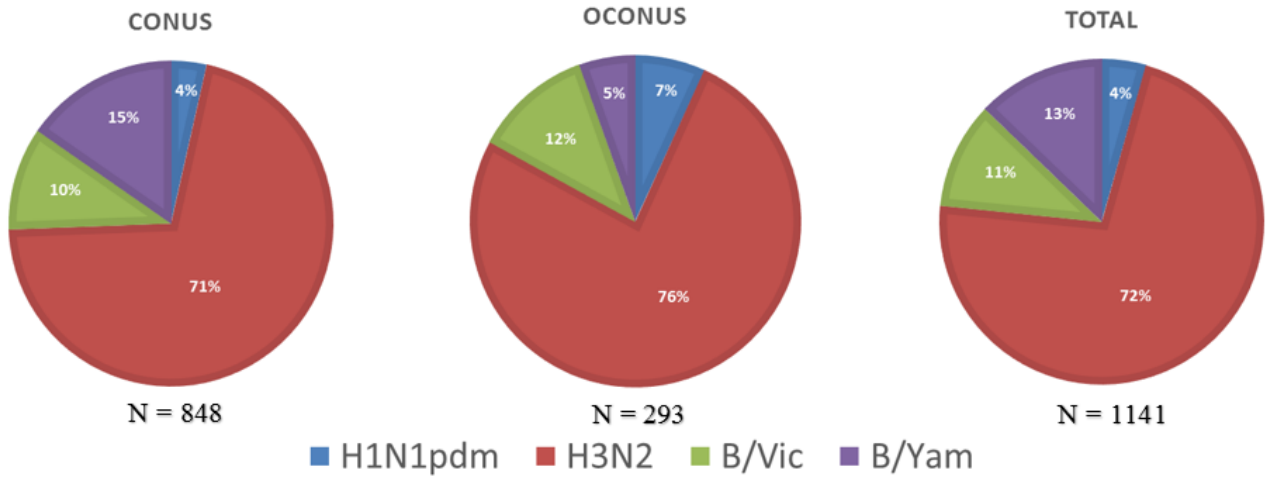

Figure 2. The proportion of influenza A(H1N1)pdm09, A(H3N2), B/Victoria, B/Yamagata specimens and sequences submitted from CONUS/OCONUS sites, and all sites during the 2016-2017 season. The number of total sequences represented are shown below each pie chart. The A(H3N2)v specimen, from CONUS, was excluded because it would not have been distinguishable.

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Table 7. List of CONUS and OCONUS sentinel site contributions of influenzaA(H1N1)pdm09, A(H3N2), B/Victoria, and B/Yamagata specimens or sequences during the 2016-2017 influenza season

	A(H1N1)pdm09	A(H3N2)	A(H3N2)v	B/Victoria	B/Yamagata	Total
CONUS						
Alabama						
Maxwell AFB		5				5
Arizona						
Davis-Monthan AFB		8		1		9
Luke AFB				2	1	3
Arkansas						
Little Rock AFB		6				6
California						
Beale AFB		4				4
NHRC	8	37		2	4	51
Travis AFB		23			1	24
Vandenberg AFB		2				2
Colorado						
Peterson AFB		10		2	6	18
USAF Academy		1				1
Connecticut						
USCG Academy		6			1	7
Delaware						
Dover AFB		3		1	1	5
District of Columbia						
JB Anacostia-Bolling		6			1	7
Florida						
Eglin AFB		7		2	1	10
Hurlburt Field		8		3		11
Tyndall AFB		3		1	2	6
Georgia						
Moody AFB		9		27	7	43
NHRC		5				5
Robins AFB		10		1	3	14
Idaho						
Mt Home AFB		13				13
Illinois						
NHRC		6		5	3	14
Scott AFB		1				1
Kansas						
McConnell AFB		15			4	19
Kentucky						
Ft Campbell		10		2	2	14

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	A(H1N1)pdm09	A(H3N2)	A(H3N2)v	B/Victoria	B/Yamagata	Total
Louisiana						
Ft Polk		1				1
Maryland						
JB Andrews	2	6			3	11
NCRM - Walter Reed NMMC		3				3
US Naval Academy		1				1
Massachusetts						
Hanscom AFB		3			1	4
Mississippi						
Columbus AFB		3				3
Keesler AFB	2	15		4	6	27
Missouri						
NHRC	1	5				6
Montana						
Malmstrom AFB		3			3	6
Nebraska						
Offutt AFB	1	12			1	14
Nevada						
Nellis AFB		3		1	1	5
New Jersey						
JB McGuire-Dix-Lakehurst		19		1		20
NHRC		3				3
New Mexico						
Cannon AFB		7		1	1	9
New York						
Ft Drum	1	15		1	22	39
USMA - West Point		28		3	2	33
North Carolina						
Ft Bragg	1	3		2	1	7
NH Camp Lejeune	1	9			1	11
Seymour Johnson AFB		4			1	5
North Dakota						
Minot AFB	1	8			5	14
Ohio						
Wright-Patterson AFB	1	22		3	8	34
Oklahoma						
Altus AFB		4				4
Tinker AFB	1	40			11	52
Oregon						
CGS North Bend		1				1
South Carolina						
JB Charleston (AF)		6				6

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	A(H1N1)pdm09	A(H3N2)	A(H3N2)v	B/Victoria	B/Yamagata	Total
South Carolina						
NHRC		16			2	18
Shaw AFB		13		10	2	25
South Dakota						
Ellsworth AFB		3		1	2	6
Texas						
Ft Bliss	1	2				3
Ft Hood		1				1
Laughlin AFB					1	1
SAMMC	5	26	1	4	8	44
Sheppard AFB		34			7	41
Utah						
Hill AFB		17			1	18
Virginia						
JB Langley-Eustis	2	11		2	3	18
NMC Portsmouth	1			1		2
Washington						
Fairchild AFB	1	8		1		10
JB Lewis-McChord		2				2
NH Bremerton		31		3		34
Wyoming						
FE Warren AFB		15				15
OCONUS						
Alaska						
Eielson AFB		1				1
Elmendorf AFB		1				1
Belgium						
SHAPE		3				3
Cambodia						
NAMRU-2	9	5		19	1	34
Country 1						
Location A		2				2
Location B		10		1	4	15
Country 2						
Location A		18				18
Country 6						
Location A		2				2
Germany						
Landstuhl RMC	1	33		1	3	38
Ramstein AB		8				8
USAG Baumholder		1			1	2
USAG Grafenwoehr		5				5

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	A(H1N1)pdm09	A(H3N2)	A(H3N2)v	B/Victoria	B/Yamagata	Total
Germany						
USAG Stuttgart		4				4
USAG Wiesbaden	1	8				9
Vilseck AHC		12			1	13
Geilenkirchen NATO AB		1				1
Guam						
JB Marianas - Andersen AFB	1			1		2
Hawaii						
Tripler AMC	2	11		1		14
Italy						
Aviano AB					1	1
NAS Sigonella		3				3
NSA Naples		4				4
USAG Vicenza		19				19
Japan						
Kadena AB		4		1		5
NH Okinawa		1				1
NHRC		2				2
Yokota AB		17			3	20
Kenya						
USAMRD-K	2	21		6		29
Nigeria						
WRAIR		3				3
Paraguay						
NAMRU-6	1					1
Peru						
NAMRU-6		2				2
South Korea						
Brian Allgood ACH		14			1	15
Kunsan AB		2				2
Osan AB		3				3
Thailand						
AFRIMS	3	3		4		10
Turkey						
Incirlik AB					1	1
Grand Total	**50**	**824**	**1**	**121**	**146**	**1142**

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Influenza A(H1N1)pdm09

- Among the 874 influenza A isolates, 50 (5.7% of A, 4.4% of total influenza) 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 2016-2017 influenza vaccine strain, A/California/07/2009-like virus [Figure 3].
- The influenza A(H1N1)pdm09 isolates characterized for this report exhibited an overall protein homology of 96.5 – 97.6% (average 97.2%) compared to the 2016-2017 influenza vaccine component, A/California/07/2009-like virus, and 98.9 – 99.8% (average 99.5%) compared to the 2017-2018 influenza vaccine component, A/Michigan/45/2015-like virus [Table 2]. Only full-length coding HA sequences were used for protein homology calculations; therefore, nine truncated sequences were omitted.
- All influenza A(H1N1)pdm09 HA sequences contained mutations consistent with the dominating subgroup referred to as clade 6B, and 46 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 the 2016-2017 season, one mutation, S162N (serine to asparagine), was observed that caused the gain of a glycosylation motif.
- Among the 49 amino acid residues that showed substitutions in the 2016-2017 influenza A(H1N1) pdm09 isolates, 19 occurred at predicted antigenic sites (1 at site A, 3 at site B, 1 at sites A and B, 3 at site C, 4 at site D, and 7 at site E) and 3 occurred at the receptor binding sites.[8,9]
- Two of the sequenced influenza A(H1N1)pdm09 specimens were isolated from hospitalized patients.

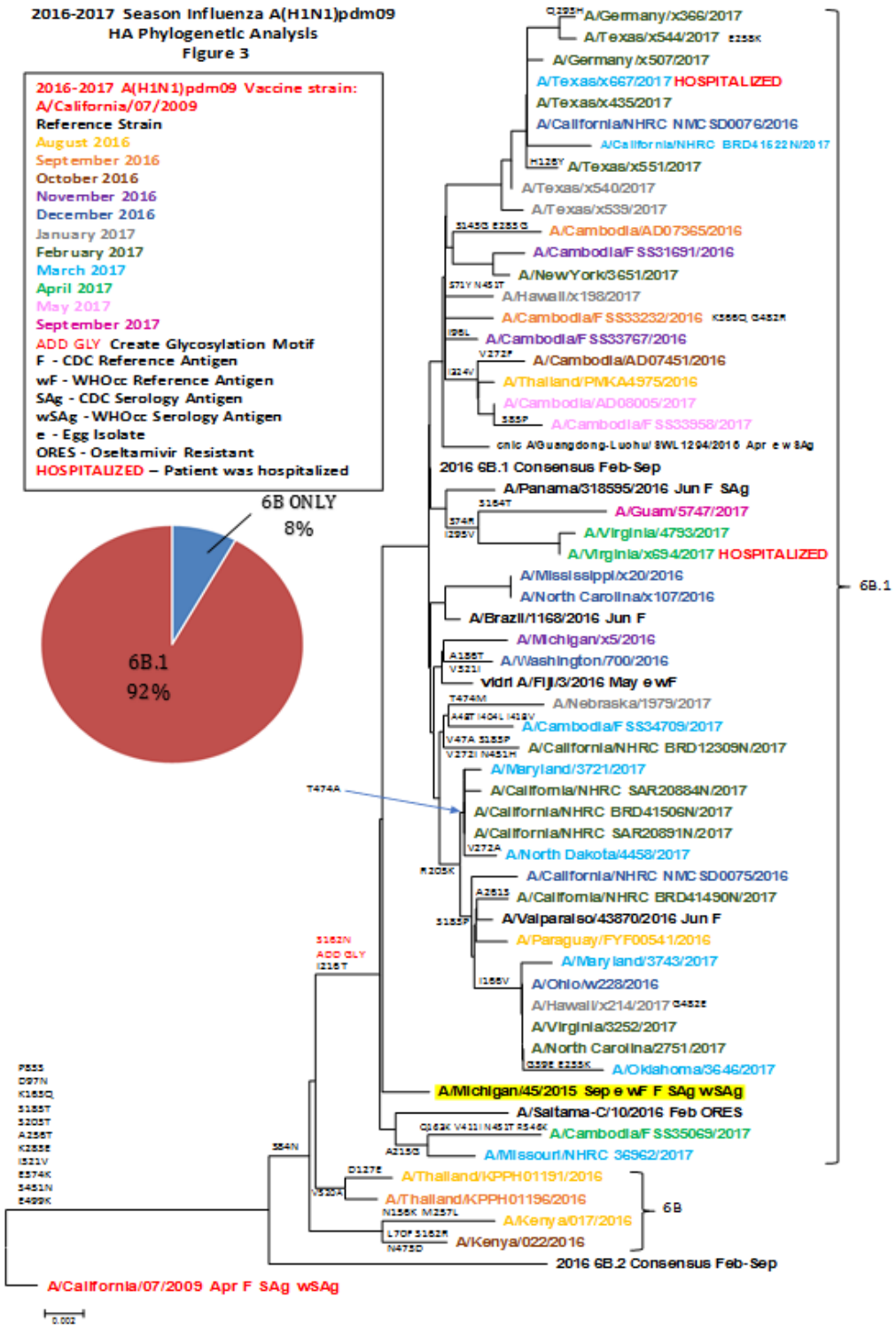

Figure 3. 2016-2017 season influenza A(H1N1)pdm09 HA phylogenetic analysis. Fifty influenza A(H1N1)pdm09 sequences collected between 2 August 2016 and 7 September 2017 were analyzed and all resided in clade 6B, with 46 (92.0%) in subclade 6B.1. The 6B.1 isolates all shared the addition of a single glycosylation motif. The influenza vaccine A(H1N1)pdm09 component for the 2016-2017 season was A/California/07/2009-like virus but was changed to A/Michigan/45/2015-like virus (highlighted in yellow) for the 2017-2018 season.

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Influenza A(H3N2)

- Among the 874 influenza A isolates, 824 (94.3% of A, 72.2% of total influenza) were influenza A(H3N2). The 2016-2017 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 4].

- The influenza A(H3N2) isolates characterized for this report exhibited an overall protein homology of 96.9-99.3% (average 98.3%) compared to the 2016-2017 influenza vaccine component, A/Hong Kong/4801/2014-like virus [Table 6]. Only full-length coding HA sequences were used for protein homology calculations; therefore, 19 truncated sequences were omitted.

- All of the influenza A(H3N2) isolates sequenced for this report were in clade 3C, with 76 (9.2%) in clade 3C.3a and 748 (90.8%) in clade 3C.2a. Of the 3C.2a clade sequences, 489 (65.4%) further classified as the subclade 3C.2a1. The mutation N121K was present in 423 (86.5%) of the 3C.2a1 isolates and 506 (61.4%) of the total influenza A(H3N2) isolates. The mutation T135K was present in 165 isolates (33.5%) of the 3C.2a1 isolates and 20.0% of the total A(H3N2) isolates.

- Among the influenza A(H3N2) isolates characterized in this report, 21 mutations—T10M (3), N122K (1), N45S (1), N122D (2), S124G (1), S124N (2), T128N (2), T135A (1), T135K (7), N144S (1), N144K (2), N158D (1), N158H (1), N158K (2), T160A (2), T160I (3), T160K (14), N246S (4), N246T (1), T248A (1), and T248P (1)—were observed that caused the loss of a glycosylation motif. Four other mutations—D122N (1), N128T (1), S144N (1), and K160T (1)—were observed that caused the gain of a glycosylation motif. The numbers in parentheses indicate the likely number of separate instances for each mutation occurring.

- Among the 167 amino acid residues that showed substitutions in the 2016-2017 influenza A(H3N2) specimens, 34 occurred at predicted antigenic sites (7 at site A, 5 at site B, 6 at site C, 7 at site D, and 9 at site E) and 5 occurred at the receptor binding site.[8,9]

- Eleven of the sequenced influenza A(H3N2) specimens were isolated from hospitalized patients and two were from patients identified with a co-infection of influenza A(H3N2) and influenza B.

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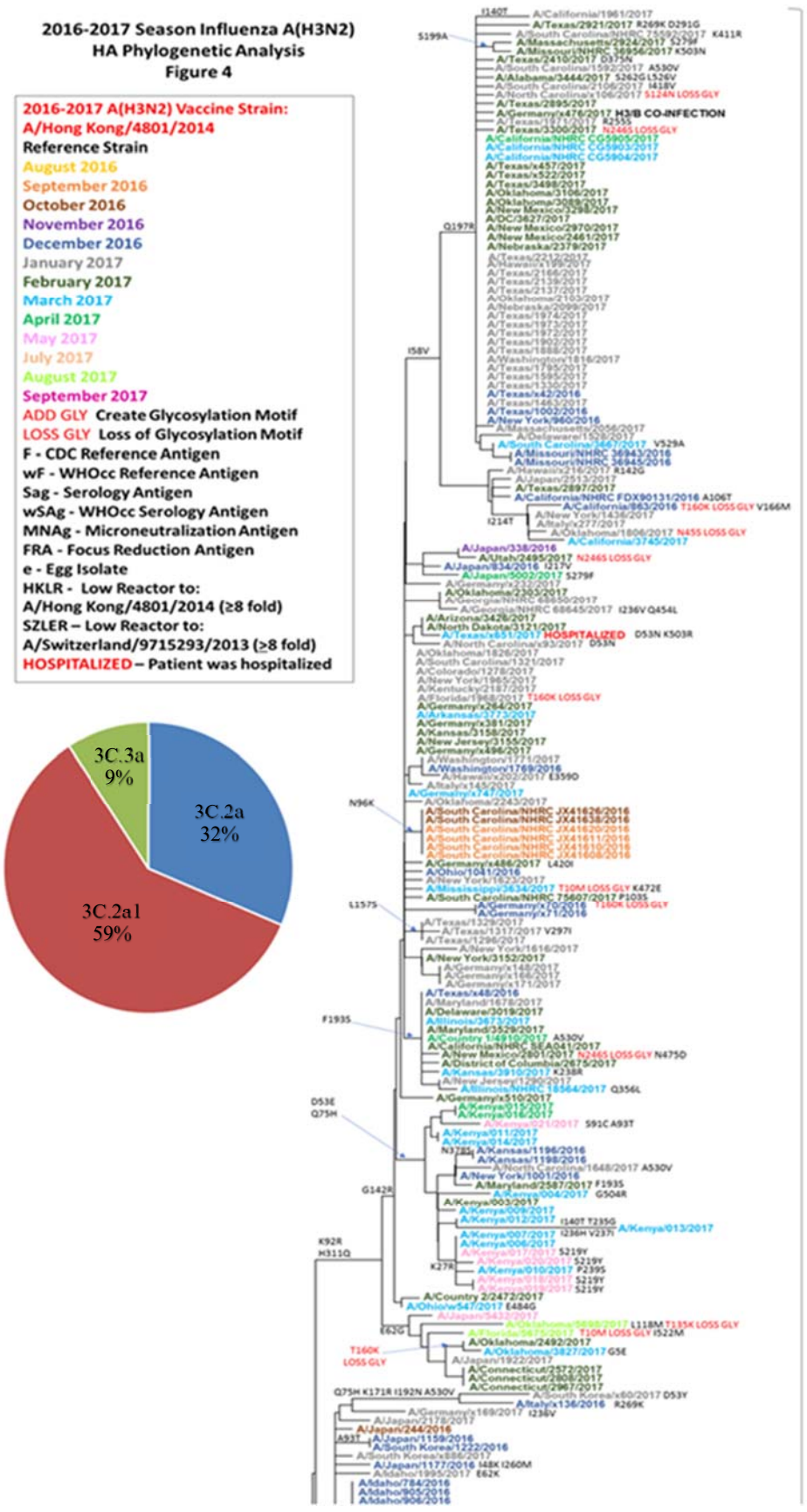

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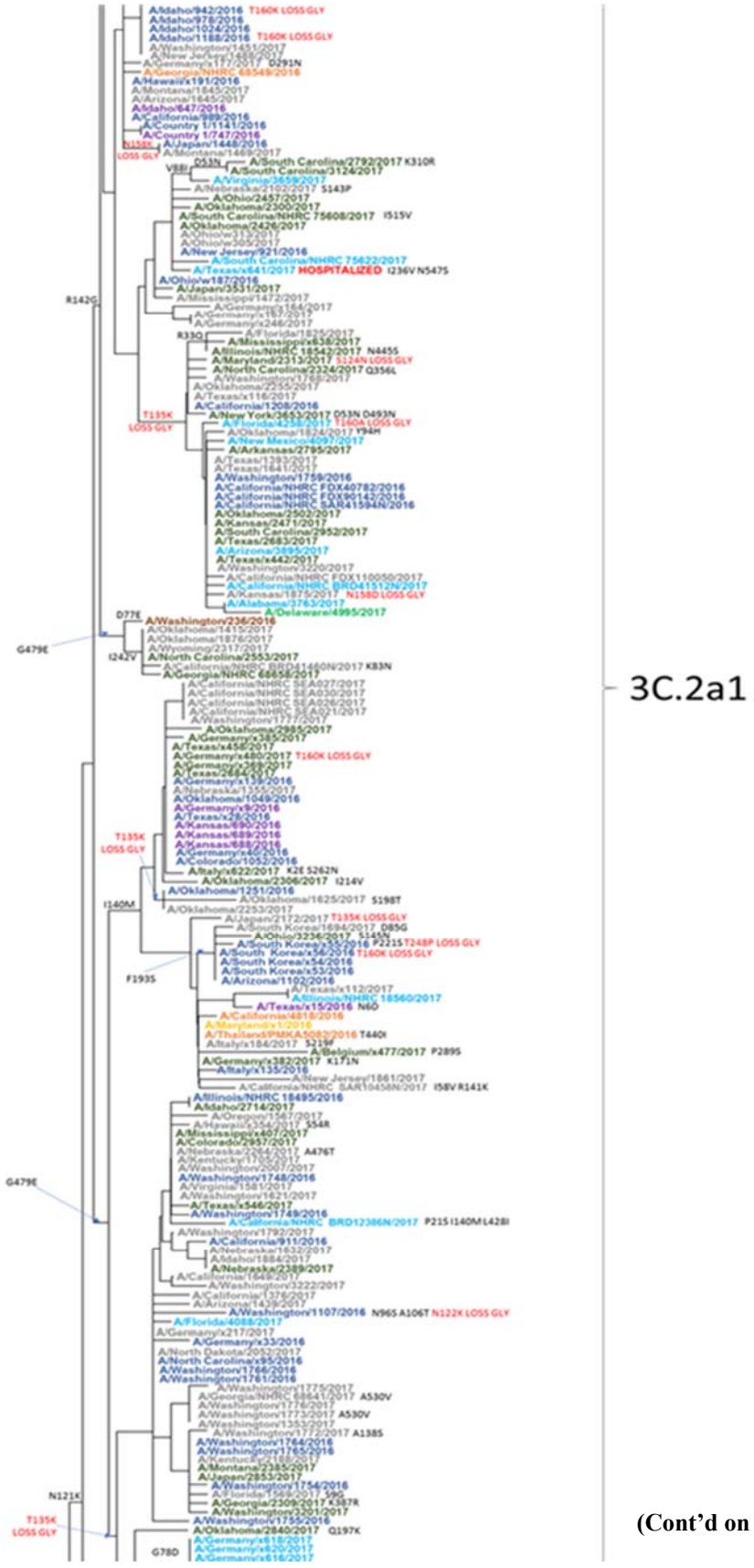

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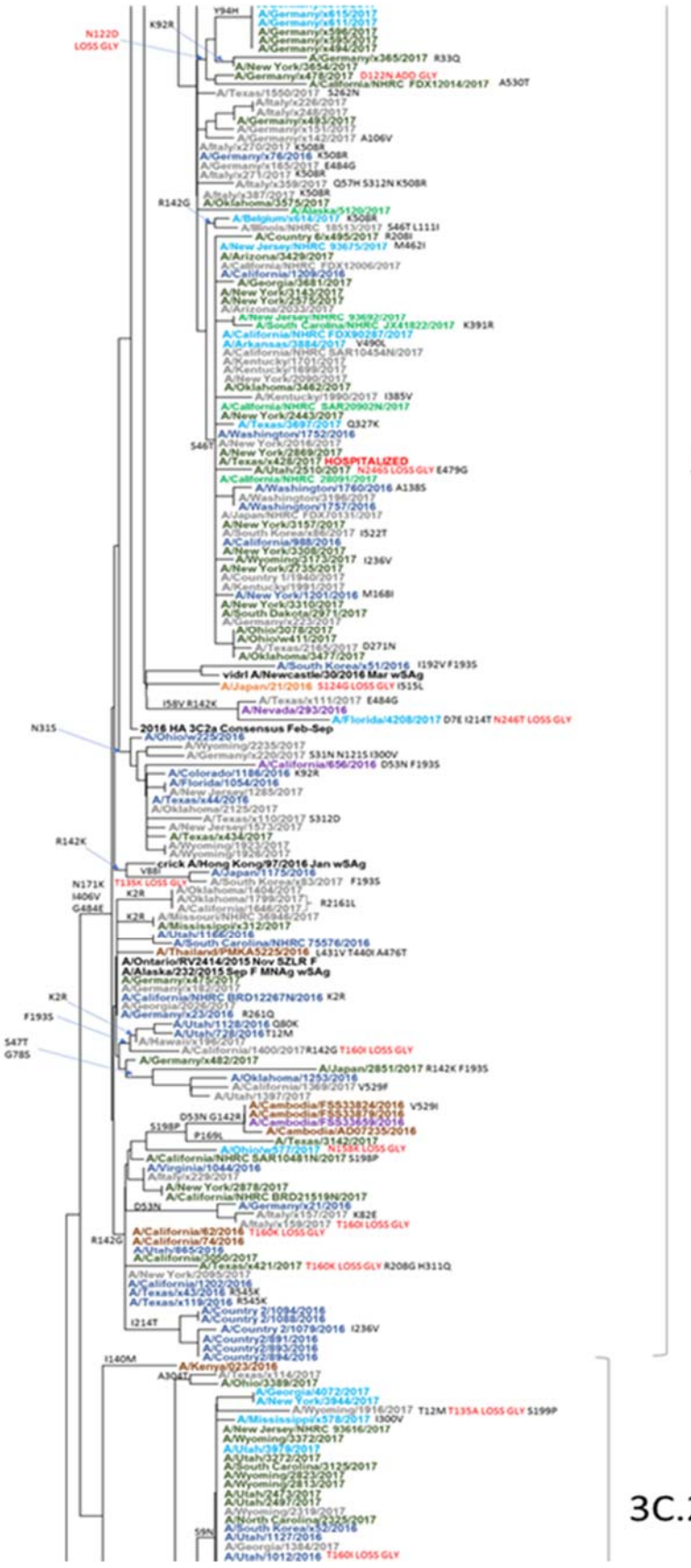

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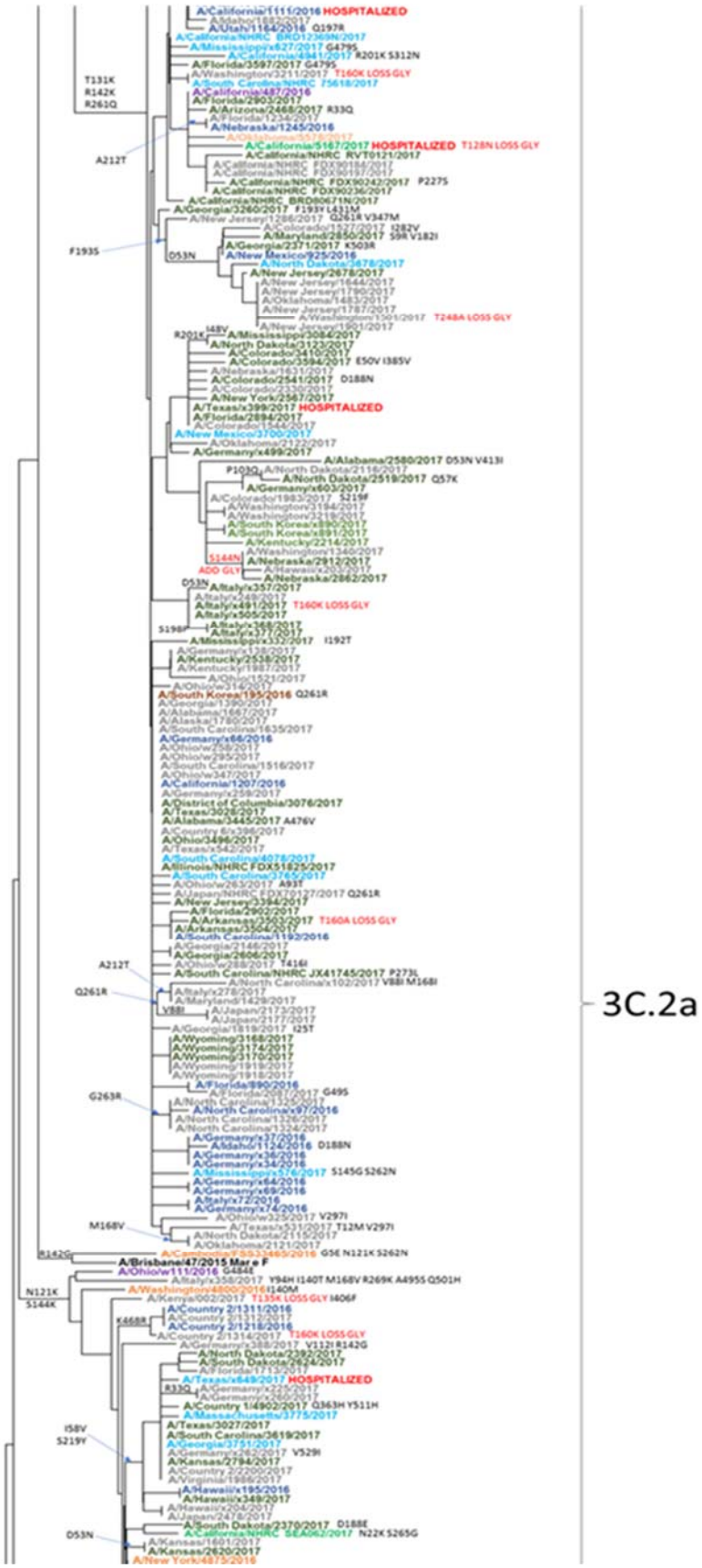

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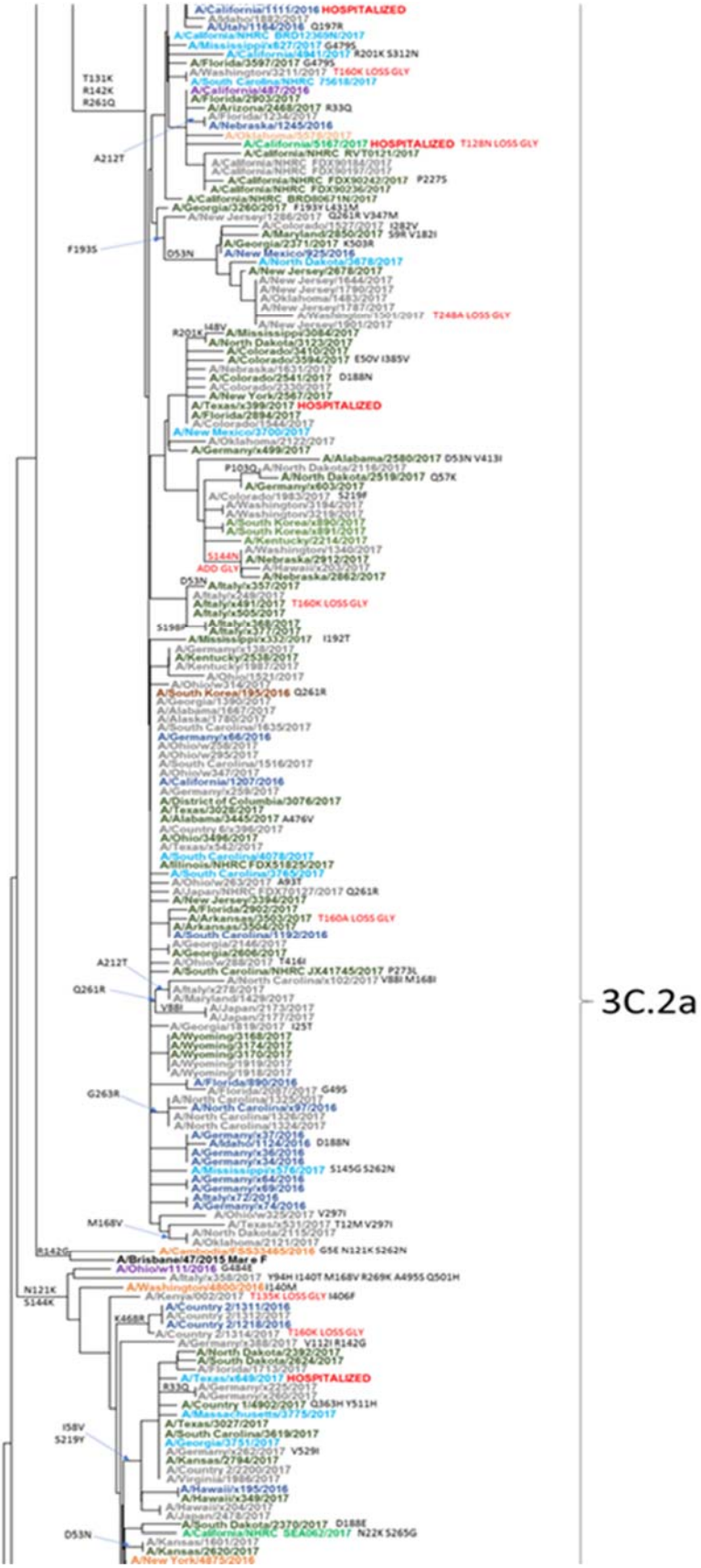

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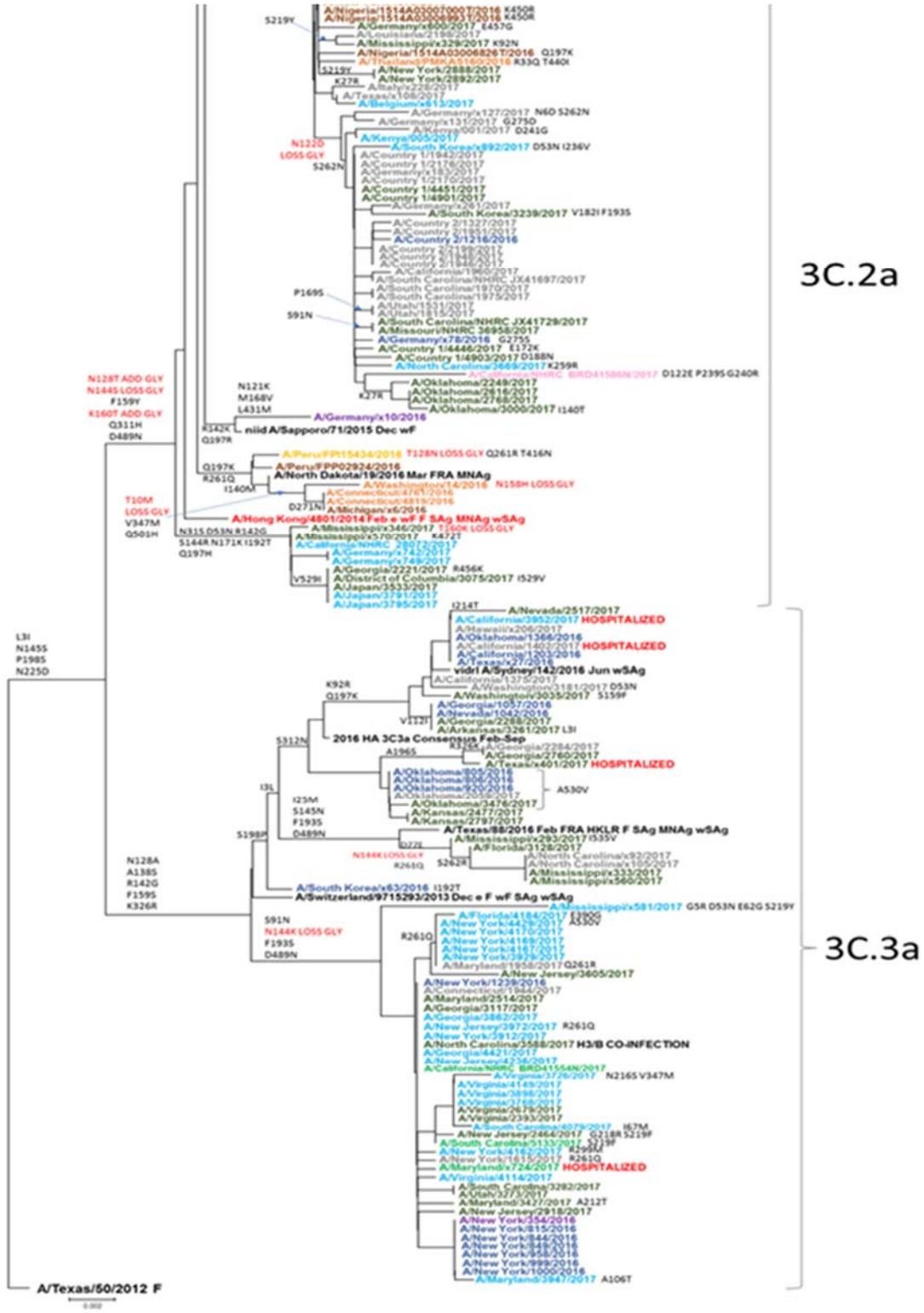

Figure 4. 2016-2017 season influenza A(H3N2) HA phylogenetic analysis. Eight hundred twenty-four influenza A (H3N2) sequences collected between 13 August 2016 and 30 August 2017 were analyzed, of which the majority resided in subclade 3C.2a1 (59.3%), followed by 3C.2a (31.4%) and 3C.3a (9.2%). Twenty-one mutations caused the loss of glycosylation motifs, while four mutations caused the gain of glycosylation motifs.

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Influenza A(H3N2)v

- During the 2016-2017 season, one isolate was identified as a variant influenza A(H3N2)v. A variant is an influenza strain that typically circulates in swine, but has been found to infect a human and contains segments of swine H3N2 lineage as well as the matrix protein of the A(H1N1)pdm09 virus. This particular variant was collected from a 1-year-old female in Texas. Further investigation revealed that the child had attended an agricultural event with her family and was in contact with a swine litter. No other cases of a H3N2v were identified in close contacts or other attendees. The H3N2v HA sequence was characterized phylogenetically with swine H3N2 and human H3N2v references with a midpoint root from other circulating 2017 swine H3N2 viruses [Figure 5]. Reference strains that include "swine" in the nomenclature were isolated from swine and are considered zoonotic. The Ohio strain that does not include "swine" was an A(H3N2)v virus that was identified at USAFSAM during the summer of the 2013-2014 season.

- The A(H3N2)v isolate exhibited a protein homology of 86.9% compared to the rooted strain A/swine/Iowa/A01667096/2017, 94% compared to the previous USAFSAM H3N2v isolate A/Ohio/4319/2014, and 99.5% compared to its nearest neighbor A/swine/Indiana/15TOSU8898/2015.

- The influenza A(H3N2)v isolate characterized in this report contained one mutation, N122Q (asparagine to glutamine), that caused the loss of a glycosylation motif and one mutation, E165N (glutamic acid to asparagine), that added a glycosylation motif, relative to the basal strains.

- Of the 72 mutations present in the A(H3N2)v specimen relative to the rooted 2017 swine H3N2 strains, 21 occurred at predicted antigenic sites (5 at site A, 5 at site B, 3 at site C, 3 at site D, and 5 at site E) and 4 occurred at the receptor binding site.[2,5]

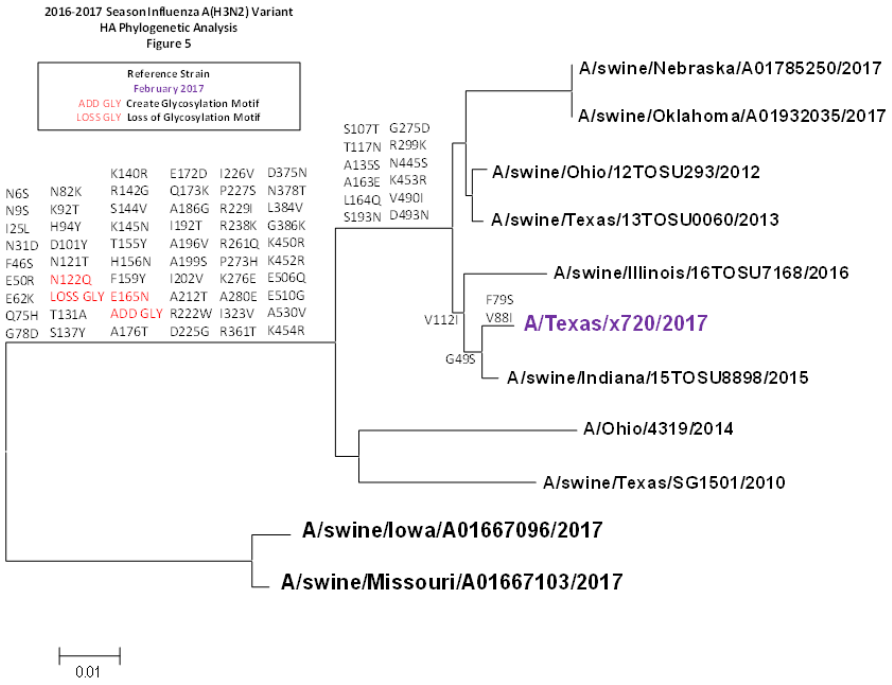

Figure 5. A single influenza A(H3N2)v was identified at USAFSAM from a child in Texas who had attended an agricultural event. The A(H3N2)v virus HA sequence is shown here in comparison to swine H3N2 viruses circulating in the 2016-2017 and previous seasons, as well as an A(H3N2)v virus previously identified at USAFSAM during the 2013-2014 season, A/Ohio/4319/2014.

Influenza B

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees and are rooted from the reference strain B/Ohio/01/2005 for the B/Victoria isolates [Figure 6] and from the previous vaccine strain B/Massachusetts/02/2012-like virus for the B/Yamagata isolates [Figure 7].
- The distinguishing characteristic between the two influenza B lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the B/Yamagata lineage.[1] Of the 267 influenza B isolates sequenced during the 2016-2017 season, 121 (45.3% of influenza B, 10.6% of total influenza) fell into the B/Victoria lineage and 146 (54.7% of influenza B, 12.8% of total influenza) fell into the B/Yamagata lineage.
- Of interest, 39 (32.2%) of the influenza B/Victoria sequences contained a 6 base pair deletion causing a double amino acid deletion (positions K162 – N163), which falls in the same region as the single amino acid deletion at position 162 observed in Yamagata lineage specimens. All of these B/Victoria deletion specimens also shared the mutations I180V and R498K, and 32 (82.1%) shared the mutation D129G.
- Additionally, one B/Yamagata lineage isolate showed a 3 base pair deletion causing a single amino acid deletion at position D527.
- The influenza B/Victoria isolates characterized for this report exhibited a protein homology from 98.4 – 99.5% (average 99.1%) when compared to the 2016-2017 B/Victoria vaccine component, B/Brisbane/60/2008-like virus [Table 6]. Only full-length HA coding sequences were included in protein homology calculations; therefore, three truncated B/Victoria sequences were omitted.
- The influenza B/Yamagata isolates characterized for this report exhibited a protein homology of 98.8 – 99.3% (average 99.2%) when compared to the 2016-2017 B/Yamagata vaccine component, B/Phuket/3073/2013-like virus [Table 6]. All B/Yamagata sequences were full-length HA coding sequences; therefore, none were omitted for protein homology calculations.
- 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), added a glycosylation motif, while two mutations, N145D (asparagine to aspartic acid) and N197S (asparagine to serine), caused the loss of glycosylation motifs relative to the root strain B/Ohio/01/2005. For the B/Yamagata isolates, no mutations were present that caused any changes to glycosylation motifs relative to the root strain B/Massachusetts/02/2012.
- One B/Victoria specimen was collected from a patient who was hospitalized.
- One B/Yamagata specimen was collected from a patient who was hospitalized, and two were collected from patients with A(H3N2)/B co-infections.

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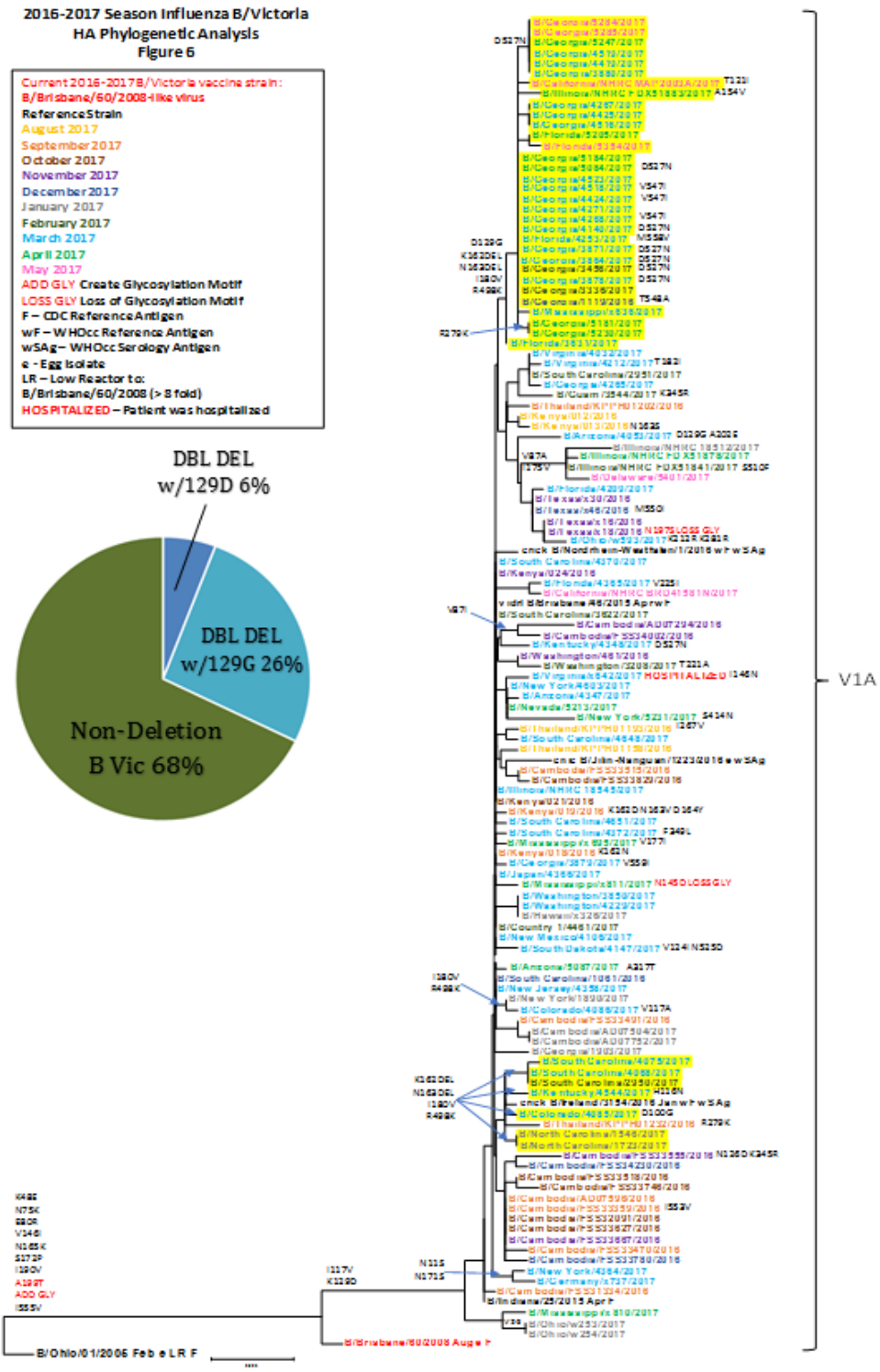

Figure 6. 2016-2017 season influenza B/Victoria HA phylogenetic analysis. One hundred twenty-one influenza B/Victoria sequences collected between 1 August 2016 and 18 May 2017 were analyzed and all resided in clade V1A, with one shared addition of a glycosylation motif and two individual losses of glycosylation motifs. Thirty-nine (32.2%) of these sequences had a double deletion (DBL DEL) at amino acid positions 162-163 and shared the mutations I180V and R498K, while an additional 32 (82.1%) of these shared the mutation D129G. All DBL DEL sequences are highlighted in yellow.

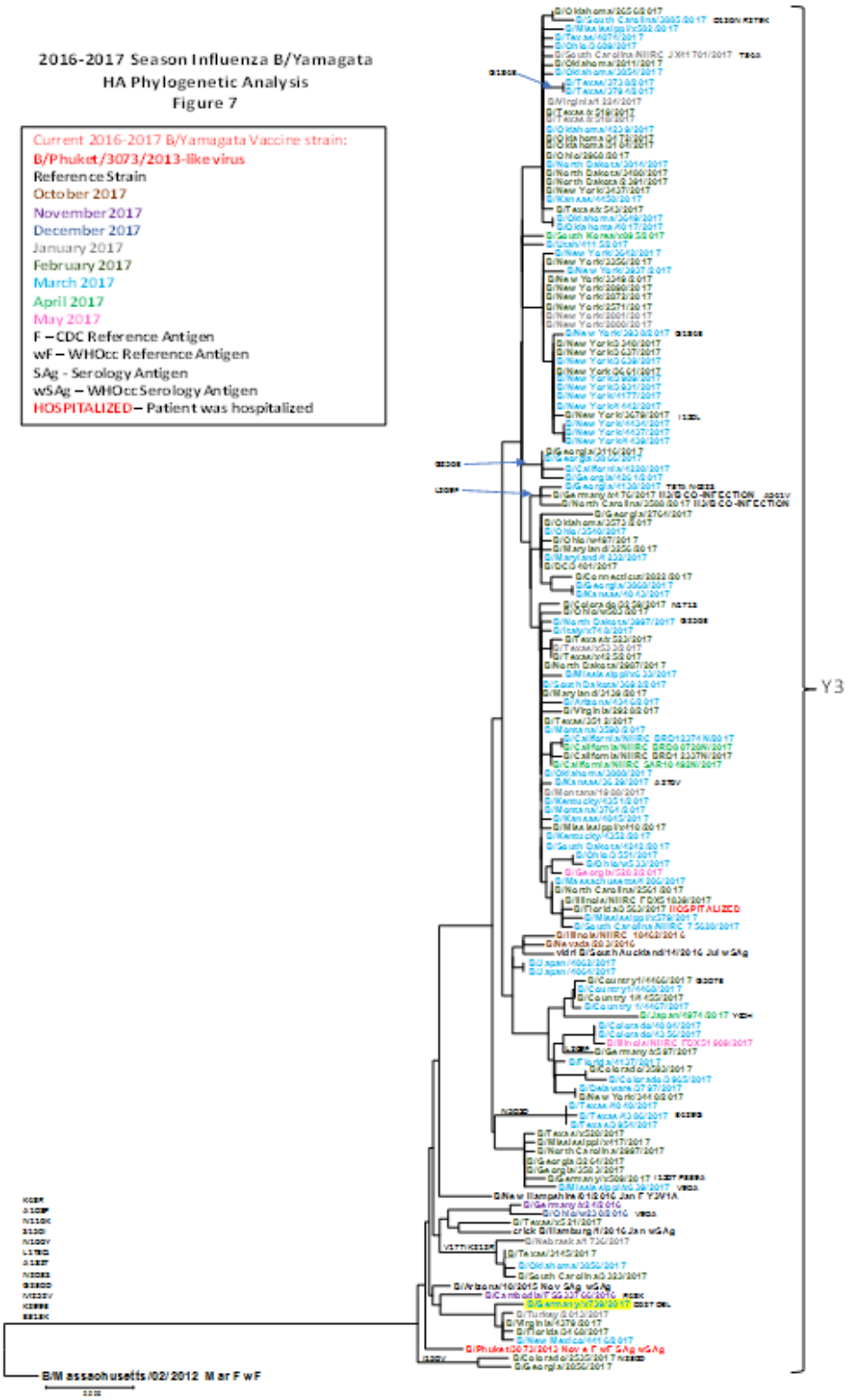

Figure 7. 2016-2017 season USAFSAM influenza B/Yamagata HA phylogenetic analysis. One hundred forty-six influenza B/Yamagata sequences collected between 3 October 2016 and 19 May 2017 were analyzed and all resided in clade Y3, with no observed changes to glycosylation motifs. One isolate, highlighted in yellow, had a deletion at amino acid position 527 (D527 DEL).

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Cleared, 88PA, Case # 2018-1051, 5 Mar 2018.

USAF School of Aerospace Medicine & Defense Health Agency

DoD Global, Laboratory-Based, Influenza Surveillance Program

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:

DoD Global Respiratory Pathogen Surveillance Program
https://gumbo2.wpafb.af.mil/epi-consult/influenza/welcome/

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.

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