

Febrile Respiratory Illness (FRI) Surveillance Update

Operational Infectious Diseases, Naval Health Research Center, San Diego, CA



2016 Week 39 (through 1 October 2016)

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Influenza

NHRC Laboratory-Confirmed Influenza Cases, US Military Basic Trainees

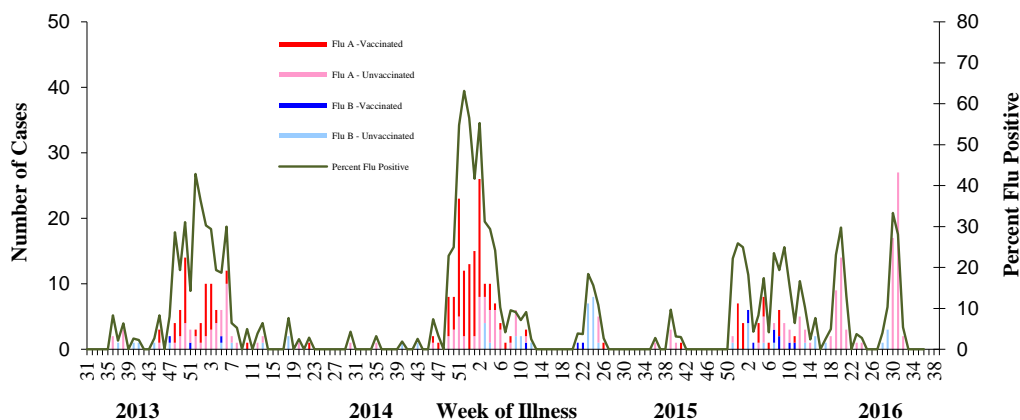
Site	Current Week*				Since Oct.1, 2015				No. Tested
	A/ Untyp.	A/H3	A/H1	B	A/ Untyp.	A/H3	A/H1	B	
Ft. Benning							1	5	207
Ft. Jackson							3		216
Ft. Leonard Wood						1	7	4	172
NRTC Great Lakes							3	1	162
Lackland AFB							1	1	26
MCRD Parris Island						30	6		189
MCRD San Diego						18	1	4	474
CGTC Cape May					2	47	3	9	195
Total	0	0	0	0	2	96	25	24	1641

- NHRC also conducts shipboard FRI surveillance that includes large-deck ships of the US Fleet Forces (Atlantic), 3rd (Pacific), and 7th (Far East) Fleets.
- NHRC conducts FRI surveillance among (non-active duty) DoD beneficiaries in Illinois and San Diego (details on page 7).
- NHRC-CDC-BIDS collaborative border FRI/SARI surveillance program is ongoing at 7 US-Mexico border sites in San Diego (2) and Imperial (5) counties in California. Details on page 8.
- For more information about NHRC FRI surveillance programs, please [contact NHRC](#).

Items of Note

- FRI rates at all basic training centers are at/below expected values
- NHRC is able to test for novel influenza strains, MERS coronavirus, enterovirus EV-68, Ebola virus, and Zika virus

Vaccination Status of Confirmed Influenza Cases Among US Military Basic Trainees, 2013-16

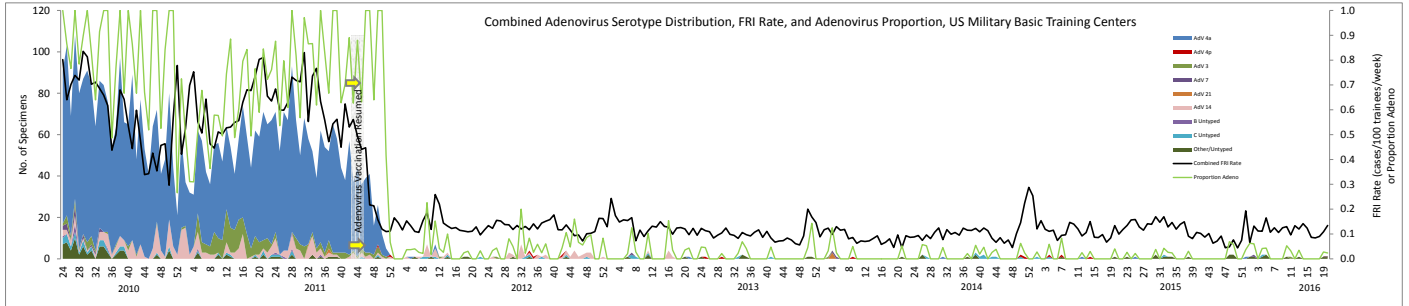


Other Items of Interest

- NHRC is conducting laboratory-based surveillance for meningococcal disease. The program's purpose is to track and characterize meningococcal cases among DoD medical beneficiaries. For more information and the most recent data, [click here](#).

Adenovirus

- Vaccination against types 4 and 7 adenovirus was instituted at all basic training centers by mid-November 2011.
- FRI rates and the proportion of FRI cases positive for adenovirus have decreased markedly since vaccine was reintroduced.
- Sporadic adenovirus cases at basic training centers 2012-16. FRI rates remain low in general.



FRI Rates

- FRI surveillance is ongoing at 8 U.S. military basic training centers, representing all service branches. As each week’s FRI count is reported, [FRI Rate Status](#) is classified into one of 3 categories:
 - At or below expected value (expected value shown as dashed line)
 - Moderately elevated
 - Substantially elevated

Week ending 1 October 2016:

- **At or below expected value:**

[Fort Benning](#)

[Fort Jackson](#)

[Fort Leonard Wood](#)

[Naval Recruit Training Command, Great Lakes](#)

[Marine Corps Recruit Depot, San Diego](#)

[Marine Corps Recruit Depot, Parris Island](#) (data through 24 Sept.)

[Lackland Air Force Base](#) (data through 10 Sept.)

[Coast Guard Training Center, Cape May](#)

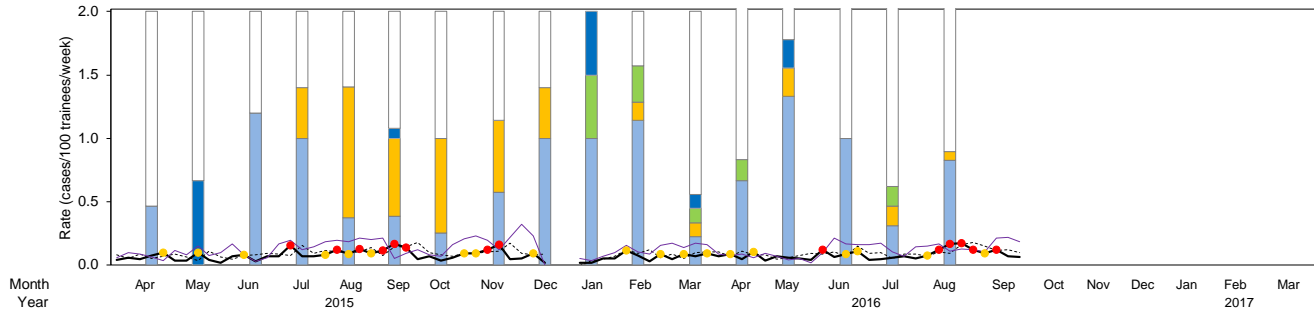
• **Moderately elevated:**

None

• **Substantially elevated:**

None

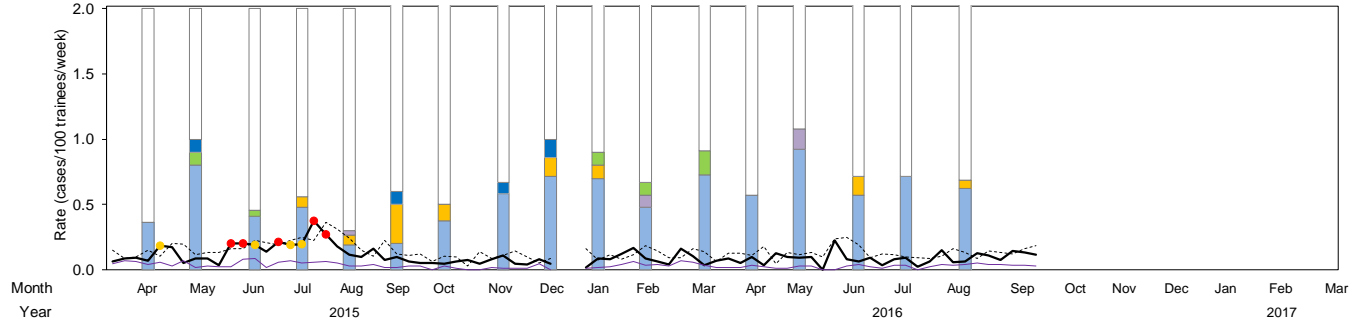
Ft. Benning FRI Rates and Diagnostic Test Results
 Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)



Samples Received		13	6	10	20	27	26	24	35	10	4	14	18	12	9	26	13	29
Adenovirus			33%				4%				25%	6%		11%				
Influenza											25%	14%	6%	8%			8%	
RSV																		
C. pneumo																		
M. pneumo				20%	52%	31%	38%	29%	20%		7%	6%		11%		8%	3%	
Rhinovirus		23%		60%	50%	19%	19%	13%	29%	50%	50%	57%	11%	33%	67%	50%	15%	41%
Influenza Subtype	B										0%	100%	100%	100%			100%	
	A/H3										0%	0%	0%	0%			0%	
	A/pH1										100%	0%	0%	0%			0%	
	Untyped										0%	0%	0%	0%			0%	

[Back to FRI Report](#)

Ft. Jackson FRI Rates and Diagnostic Test Results
 Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)

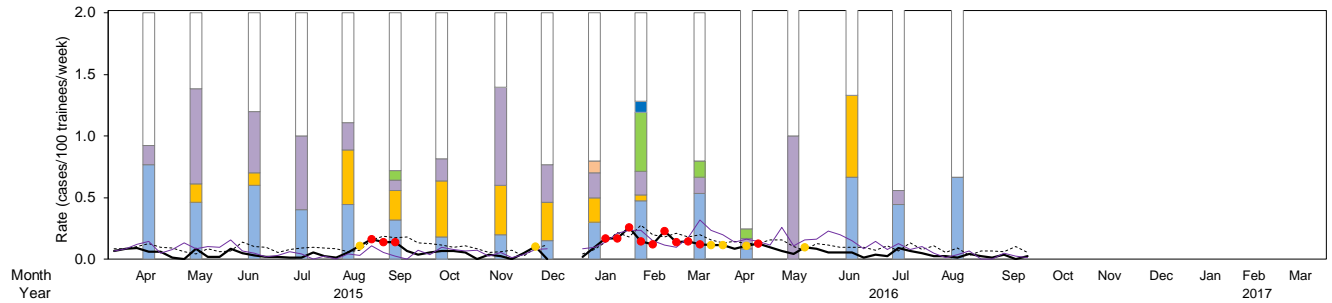


Samples Received		33	20	44	50	53	20	16	24	14	20	21	11	21	13	14	14	32
Adenovirus			5%				5%		4%	7%								
Influenza		5%	2%								5%	5%	9%					
RSV																		
C. pneumo					2%							5%			8%			
M. pneumo				4%	4%	15%	6%		7%	5%						7%	3%	
Rhinovirus		18%	40%	20%	24%	9%	10%	19%	29%	36%	35%	24%	36%	29%	46%	29%	36%	31%
Influenza Subtype	B	100%	100%								0%	0%	0%					
	A/H3	0%	0%								0%	0%	0%					
	A/pH1	0%	0%								100%	100%	100%					
	Untyped	0%	0%								0%	0%	0%					

[Back to FRI Report](#)

— Observed FRI rate (expected rate = dashed line) ● Moderately elevated ● Substantially elevated — Pneumonia rate (incl. afebrile)

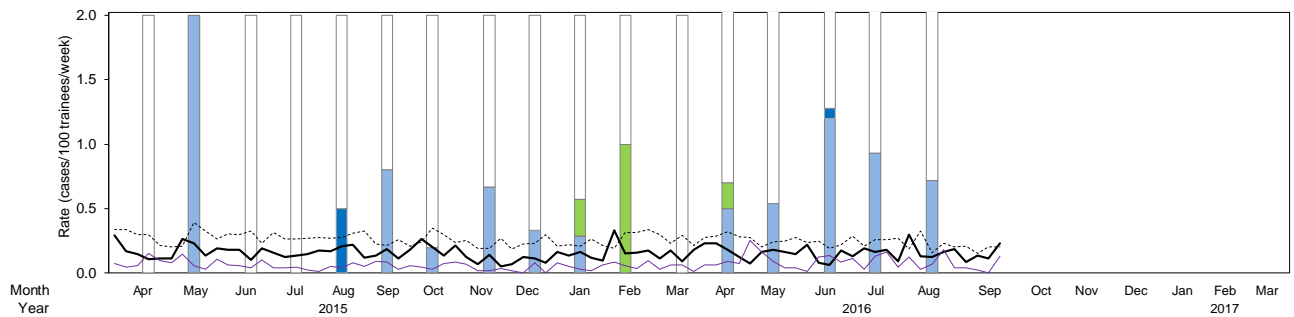
Ft. Leonard Wood FRI Rates and Diagnostic Test Results
 Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)



Samples Received	26	13	20	10	9	25	22	10	13	20	42	15	24	6	3	18	3	
Adenovirus											5%							
Influenza					4%						24%	7%	4%					
RSV										5%								
C. pneumo	8%	38%	25%	30%	11%	4%	9%	40%	15%	10%	10%	7%	4%	50%		6%		
M. pneumo		8%	5%		22%	12%	23%	20%	15%	10%	2%					33%		
Rhinovirus	38%	23%	30%	20%	22%	16%	9%	10%	8%	15%	24%	27%	4%			33%	22%	33%
Influenza Subtype																		
B					0%						20%	100%	100%					
A/H3					100%						10%	0%	0%					
A/pH1					0%						70%	0%	0%					
Untyped					0%						0%	0%	0%					

[Back to FRI Report](#)

Great Lakes FRI Rates and Diagnostic Test Results
 Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)

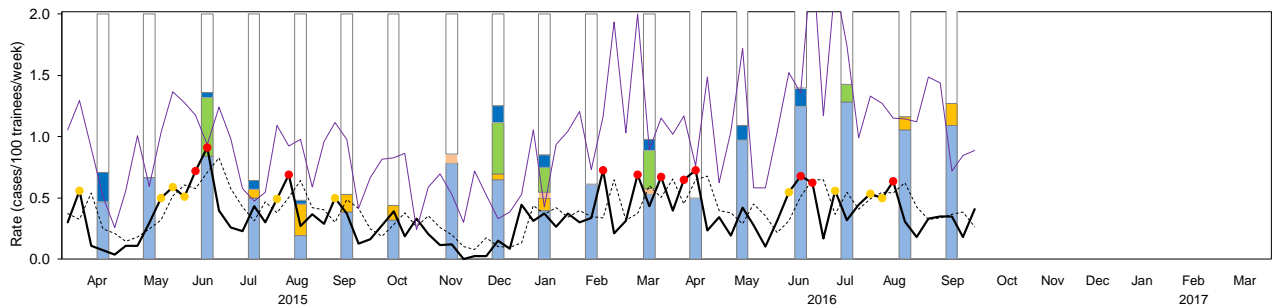


Samples Received	1	1	1	3	4	5	10	3	6	7	2	3	20	26	25	30	25
Adenovirus					25%												
Influenza										14%	50%		10%			4%	
RSV																	
C. pneumo																	
M. pneumo																	
Rhinovirus	100%				40%	10%	33%	17%	14%				25%	27%	60%	47%	36%
Influenza Subtype																	
B											0%	0%	50%				
A/H3											0%	0%	0%				
A/pH1											100%	100%	50%				
Untyped											0%	0%	0%				

[Back to FRI Report](#)

— Observed FRI rate (expected rate = dashed line) ● Moderately elevated ● Substantially elevated — Pneumonia rate (incl. afebrile)

MCRD SD FRI Rates and Diagnostic Test Results
 Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)

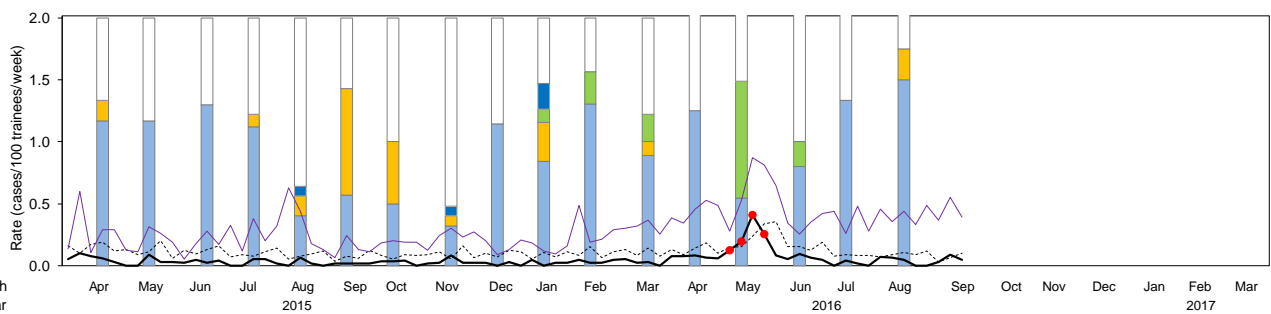


Samples Received	34	42	88	56	62	57	50	28	43	40	13	45	48	33	53	42	55	11
Adenovirus	12%	2%	4%	2%					7%	5%		4%		6%	8%			
Influenza		24%							21%	10%		16%			7%			
RSV								4%		3%		2%						
C. pneumo																		
M. pneumo			4%	13%	7%	6%		2%	5%							5%	9%	
Rhinovirus	24%	33%	42%	25%	10%	19%	16%	39%	33%	20%	31%	27%	25%	48%	62%	64%	53%	55%

Influenza Subtype	B	76%						11%	0%	0%					100%			
A/H3		24%						89%	100%	86%					0%			
A/pH1		0%						0%	0%	14%					0%			
Untyped		0%						0%	0%	0%					0%			

[Back to FRI Report](#)

MCRD PI FRI Rates and Diagnostic Test Results
 Shaded bars represent monthly proportions of each pathogen (clear = no pathogen identified)



Samples Received	12	12	20	41	25	14	4	25	7	19	23	18	8	59	20	6	8
Adenovirus					4%			4%		11%							
Influenza										5%	13%	11%		47%	10%		
RSV																	
C. pneumo																	
M. pneumo	8%		5%	8%	43%	25%	4%		16%		6%						13%
Rhinovirus	58%	58%	65%	56%	20%	29%	25%	16%	57%	42%	65%	44%	63%	27%	40%	67%	75%

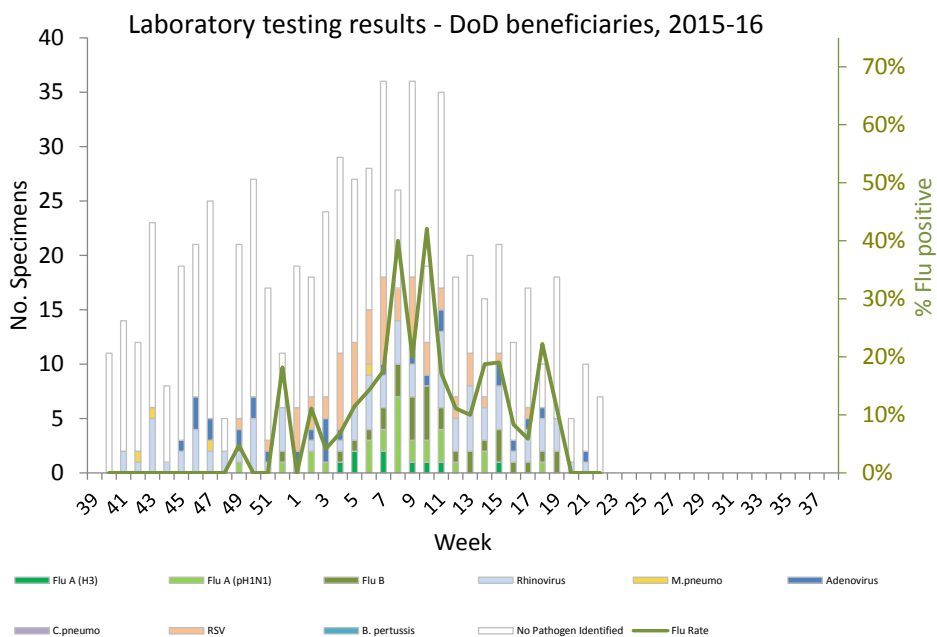
Influenza Subtype	B									0%	0%	0%	0%	0%			
A/H3										0%	0%	0%	100%	100%			
A/pH1										100%	100%	100%	0%	0%			
Untyped										0%	0%	0%	0%	0%			

[Back to FRI Report](#)

— Observed FRI rate (expected rate = dashed line) ● Moderately elevated ● Substantially elevated — Pneumonia rate (incl. afebrile)

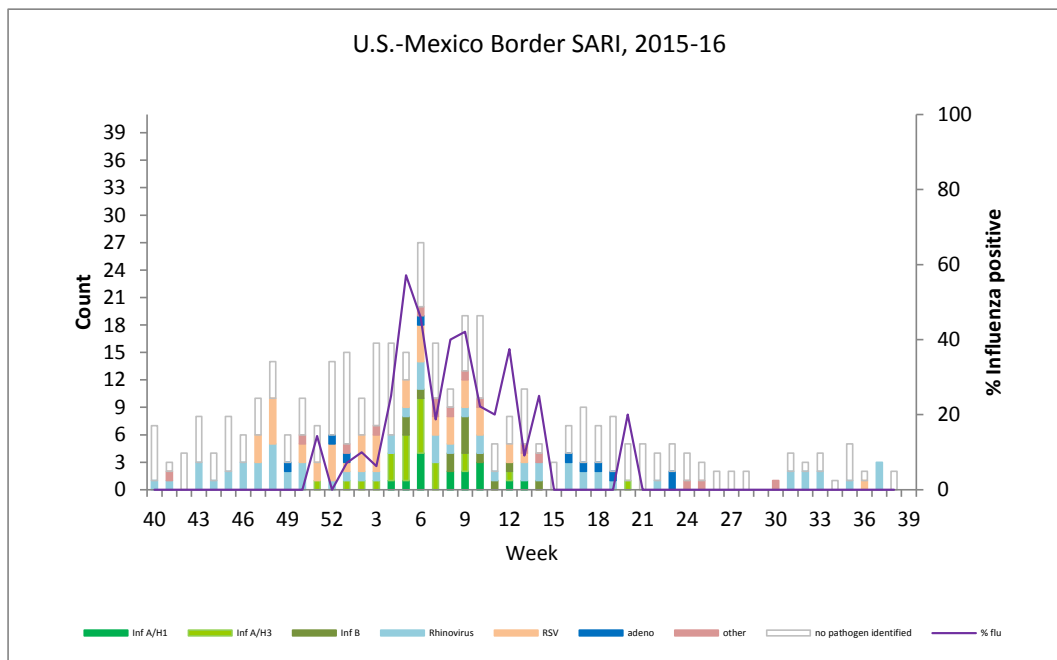
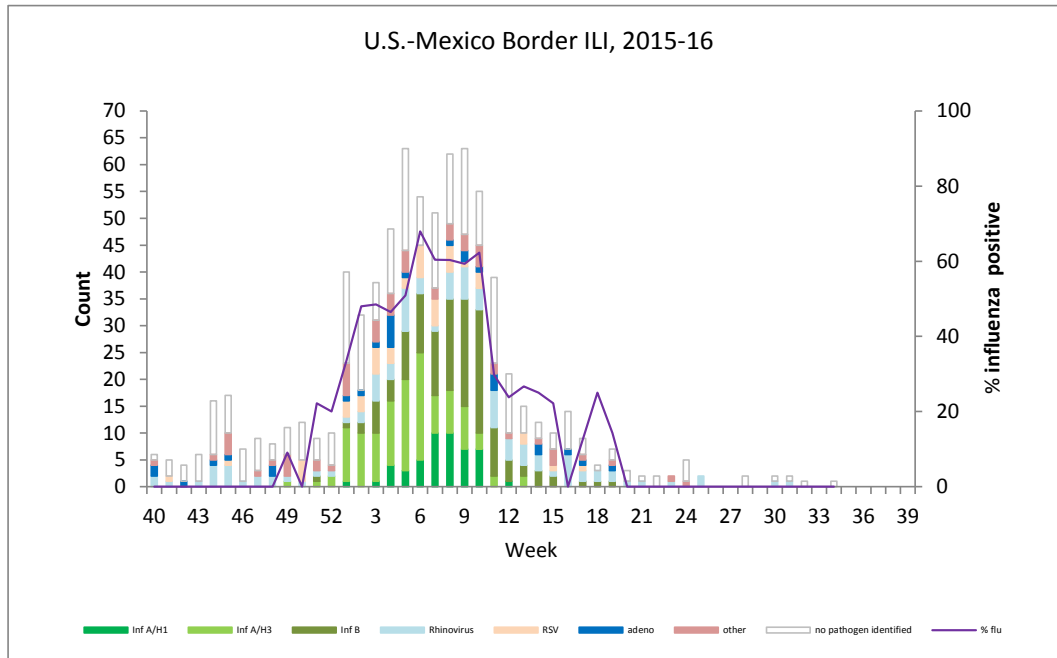
DoD Beneficiary Surveillance

- NHRC conducts FRI surveillance among (non-active duty) DoD beneficiaries at Lovell FHCC (Great Lakes, IL) and in 4 NMC San Diego facilities: the Emergency Department, Pediatric Department, Naval Branch Health Clinic Kearny Mesa, and NH Camp Pendleton.
- For questions regarding surveillance in this population, please contact the principal investigator (Chris Myers, christopher.a.myers48.civ@mail.mil) or the study coordinator (Erin Hansen, erin.a.hansen.ctr@mail.mil).



US-Mexico Border Surveillance

- In collaboration with the CDC Border Infectious Disease Surveillance program and San Diego/Imperial Counties, NHRC performs laboratory testing for FRI cases among civilians near the US-Mexico border. Both outpatient (FRI) and inpatient (Severe Acute Respiratory Illness; SARI) cases are included in the program. Current sites are located in San Diego (2) and Imperial (5) counties in California.



Phylogenetic Comparison of Influenza A-pandemic 2009 H1N1 (pH1N1) HA and NA Protein Sequences

- 47 analyzed Influenza A pH1N1 HA sequences were derived from MDCK isolates and 4 belonged to clade 6B while 43 belonged to the subclade 6B.1, defined by mutations **S84N**, **S162T (ADD GLY)** and **I216T**.
- 46 analyzed Influenza A pH1N1 NA sequences were derived from MDCK isolates.
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown (both HA and NA sequences) are with respect to A/California/07/2009-like virus.

Summary of Influenza A (pH1N1) Protein Homology When Compared to 2015-2016 Vaccine Strain

Segment	No. Isolates	2015-2016 Vaccine Strain	Protein Homology
A/pH1N1 HA	47	A/California/07/2009	97.0-98.0%
A/pH1N1 NA	46	A/California/07/2009	96.1-97.3%

Summary of Influenza A (pH1N1) N-Linked Glycosylation Mutations

- Loss or gain of N-linked glycosylation sites affect host innate immune system recognition and the ability to induce adaptive immune response thus altering its viral antigenicity.¹ Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server <http://www.cbs.dtu.dk/services/NetNGlyc/>

A/pH1N1 Segment	Mutation	
	ADD GLY	LOSS GLY
HA	S162N	
NA	N44S, S70N	N386K

1. Sun X, Jayaraman A, Mainprasad P, Raman R, Houser K, Pappas C, ...Tumpey T. (2013). N-Linked Glycosylation of the Hemagglutinin Protein Influences Virulence and Antigenicity of the 1918 Pandemic and Seasonal H1N1 Influenza A Viruses. *Journal of Virology* 8756-8766.

2. Lee H, Tang J, Kong D, Loh T, Chiang D, Lam T, Koay E. (2013). Comparison of Mutation Patterns in Full-Genome A/H3N2 Influenza Sequences Obtained Directly from Clinical Samples and the Same Samples after a Single MDCK Passage. *PLoS One*.

Phylogenetic Comparison of Influenza A (H3N2) HA and NA Protein Sequences

- **33** analyzed H3N2 HA sequences were derived from MDCK isolates and **5** were derived from clinical specimen.
- **28** analyzed H3N2 NA sequences were derived from MDCK isolates and **5** were derived from clinical specimen.
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown are with respect to 2010 vaccine strain **A/Perth/16/2009-like virus** for HA sequences and **A/Norway/1186/2011** for NA sequences

Summary of Influenza A (H3N2) Protein Homology When Compared to 2015-2016 Vaccine Strain

Segment	No.	2015-2016 Vaccine Strain	Protein Homology
H3N2 HA	38	A/Switzerland/9715293/2013	97.0-99.6%
H3N2 NA	33	A/Switzerland/9715293/2013	97.9-98.6%

Summary of Influenza A (H3N2) N-Linked Glycosylation Mutations

- Loss or gain of N-linked glycosylation sites affect host innate immune system recognition and the ability to induce adaptive immune response thus altering its viral antigenicity.¹ Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server <http://www.cbs.dtu.dk/services/NetNGlyc/>

A/H3N2 Segment	Mutation	
	ADD GLY	LOSS GLY
HA	K160T	S47P N122D T128A N144S N158K N158H T160K T160I
NA	S245N N329I S331R	S247T N329T

1. Sun X, Jayaraman A, Mainprasad P, Raman R, Houser K, Pappas C, ...Tumpey T. (2013). N-Linked Glycosylation of the Hemagglutinin Protein Influences Virulence and Antigenicity of the 1918 Pandemic and Seasonal H1N1 Influenza A Viruses. *Journal of Virology* 8756-8766.

Phylogenetic Comparison of Influenza B (Victoria and Yamagata) HA and NA Protein Sequences

- 50 analyzed Influenza B HA sequences were derived from MDCK isolates. 26 (52%) isolates belonged to the V1A clade of the Victoria Lineage and 24 (48%) belonged to the Y3 clade of the Yamagata lineage.
- 50 analyzed Influenza B NA sequences were derived from MDCK isolates. 26 isolates belonged to the V1A clade of the Victoria Lineage and 24 belonged to the Y3 clade of the Yamagata lineage.
- Phylogenetic trees for both HA and NA protein sequences were generated by Clustal V method using DNASTAR® Lasergene Megalign software.
- Amino acid changes shown (both HA and NA sequences) are with respect to previous vaccine strains **B/Ohio/01/2005-like virus** for B/Victoria specimens and **B/Florida/04/2006-like virus** for B/Yamagata specimens.

Summary of Influenza B Protein Homology When Compared to 2015-2016 Vaccine Strain

Segment	No. Isolates	2015-2016 Vaccine Strain	Protein Homology
B/Victoria HA	26	B/Brisbane/60/2008	99.1-99.5%
B/Victoria NA	26	B/Brisbane/60/2008	98.3-98.54%
B/Yamagata HA	24	B/Phuket/3073/2013	99.1-99.5%
B/Yamagata NA	24	B/Phuket/3073/2013	98.7-100.0%

Summary of Influenza B N-Linked Glycosylation Mutations

- Loss or gain of N-linked glycosylation sites affect host innate immune system recognition and the ability to induce adaptive immune response thus altering its viral antigenicity.¹ Predicted loss or gain of N-linked glycosylation of protein sequences were calculated using CBS NetNGlyc 1.0 Server <http://www.cbs.dtu.dk/services/NetNGlyc/>

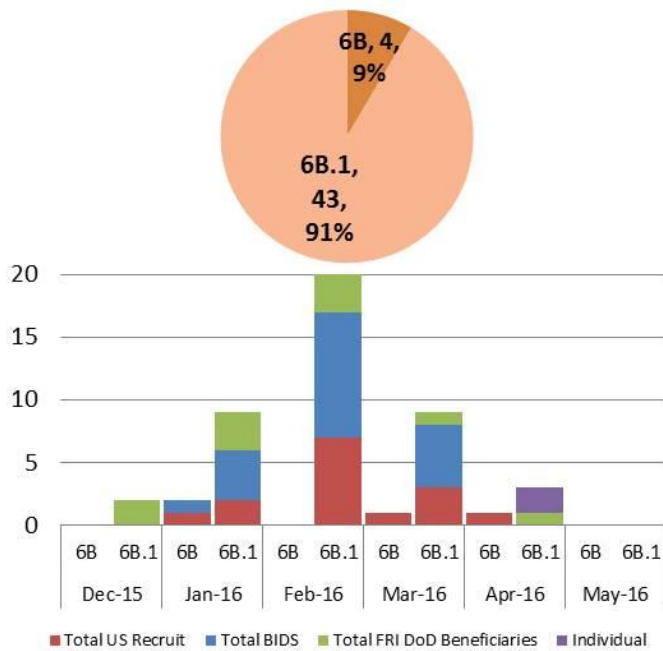
INF B Segment	Mutation	
	ADD GLY	LOSS GLY
HA	A198T	N196D T198N
NA	D463N	

1. Sun X, Jayaraman A, Mainprasad P, Raman R, Houser K, Pappas C, ...Tumpey T. (2013). N-Linked Glycosylation of the Hemagglutinin Protein Influences Virulence and Antigenicity of the 1918 Pandemic and Seasonal H1N1 Influenza A Viruses. *Journal of Virology* 8756-8766.

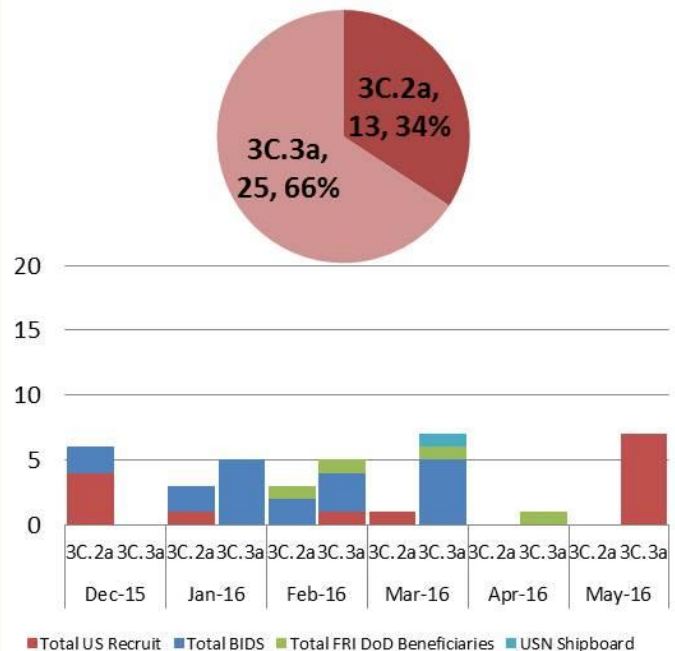
2. Lee H, Tang J, Kong D, Loh T, Chiang D, Lam T, Koay E. (2013). Comparison of Mutation Patterns in Full-Genome A/H3N2 Influenza Sequences Obtained Directly from Clinical Samples and the Same Samples after a Single MDCK Passage. *PLoS One*.

Summary of Influenza A/pH1N1, A/H3N2 and Influenza B Hemagglutinin (HA) Genetic Groups

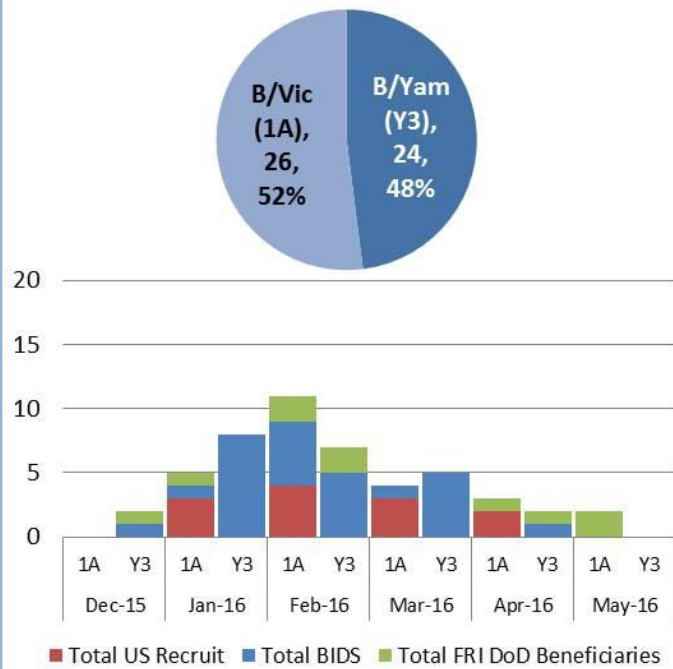
Influenza A/pH1N1



Influenza A/H3N2



Influenza B



Evolutionary Relationships Among Influenza A (pH1N1) Hemagglutinin (HA) Genes 2015-2016 Influenza Season

Vaccine Strain

Reference Strain

2013-2014 consensus*

December 2015

January 2016

February 2016

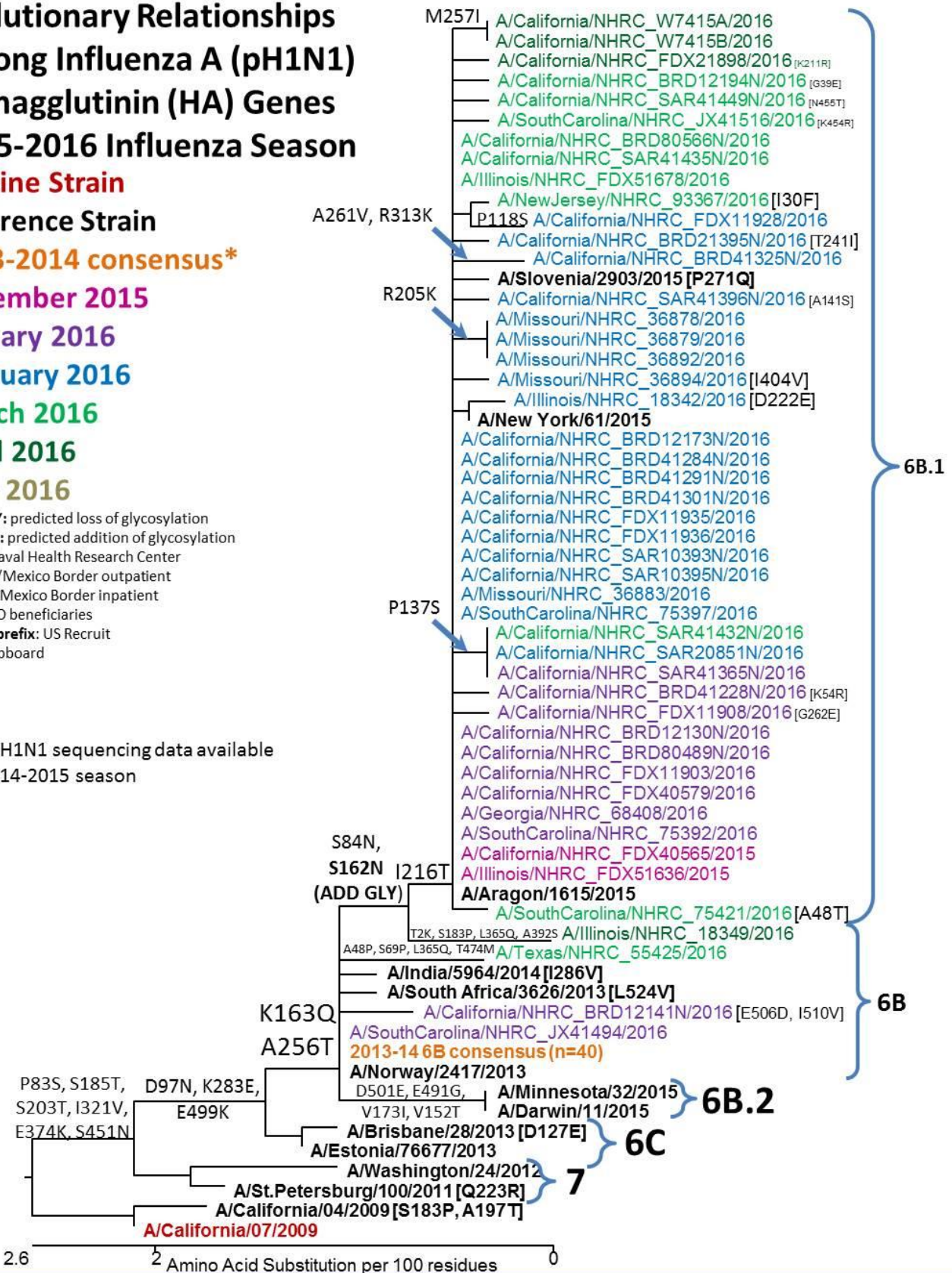
March 2016

April 2016

May 2016

LOSS GLY: predicted loss of glycosylation
ADD GLY: predicted addition of glycosylation
NHRC: Naval Health Research Center
BRD: US/Mexico Border outpatient
SAR: US/Mexico Border inpatient
FDX: DoD beneficiaries
JX or no prefix: US Recruit
Ship: Shipboard

*No pH1N1 sequencing data available for 2014-2015 season



Evolutionary Relationships Among Influenza A (pH1N1) Neuraminidase (NA) Genes 2015-2016 Influenza Season Vaccine Strain

Reference Strain

2013-2014 consensus*

December 2015

January 2016

February 2016

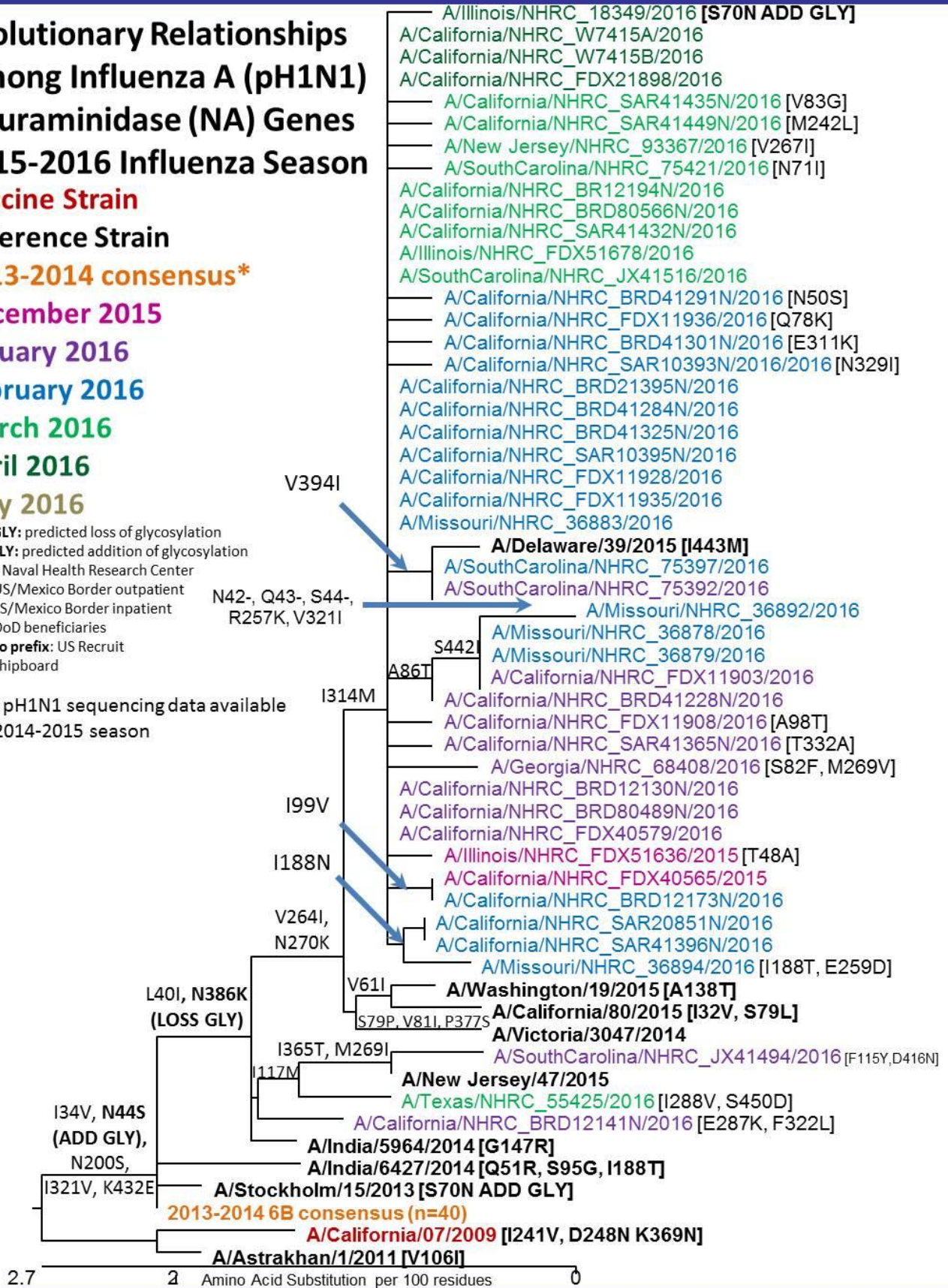
March 2016

April 2016

May 2016

LOSS GLY: predicted loss of glycosylation
ADD GLY: predicted addition of glycosylation
NHRC: Naval Health Research Center
BRD: US/Mexico Border outpatient
SAR: US/Mexico Border inpatient
FDX: DoD beneficiaries
JX or no prefix: US Recruit
Ship: Shipboard

*No pH1N1 sequencing data available for 2014-2015 season



Evolutionary Relationships Among Influenza B Hemagglutinin (HA) Genes 2015-2016 Influenza Season

Vaccine Strain

Reference Strain

2013-2014 consensus

December 2015

January 2016

February 2016

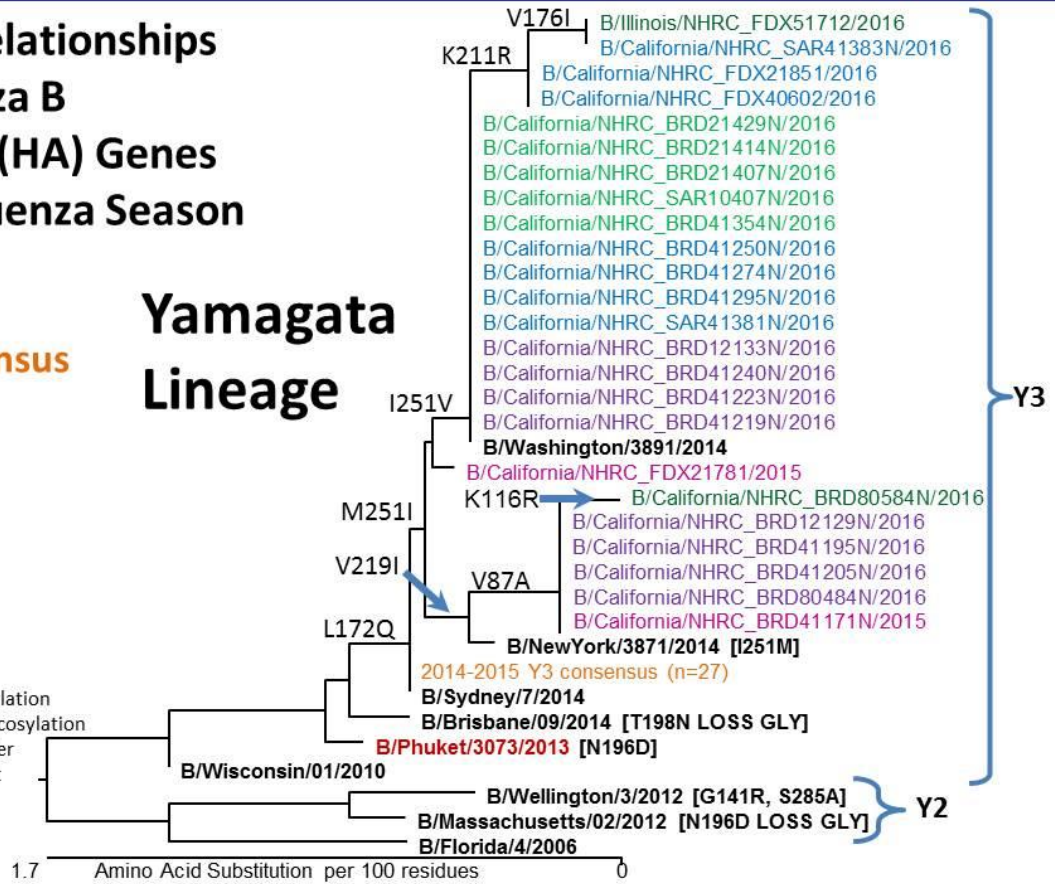
March 2016

April 2016

May 2016

LOSS GLY: predicted loss of glycosylation
 ADD GLY: predicted addition of glycosylation
 NHRC: Naval Health Research Center
 BRD: US/Mexico Border outpatient
 SAR: US/Mexico Border inpatient
 FDX: DoD beneficiaries
 JX or no prefix: US Recruit
 Ship: Shipboard

Yamagata Lineage



Victoria Lineage

