Individuals using assistive technology may not be able to fully access the information contained in this file. For assistance, please call 800-835-4709 or 240-402-8010, extension 1. CBER Consumer Affairs Branch or send an e-mail to: ocod@fda.hhs.gov and include 508 Accommodation and the title of the document in the subject line of your e-mail.

DoD Influenza Surveillance and Mid-Season Vaccine Effectiveness

Presentation to the Vaccines and Related Biological Products Advisory Committee (VRBPAC) – 5 March 2024

Anthony C. Fries, PhD**

****Representing the DoD CONUS and OCONUS lab-based influenza surveillance activities**

Armed Forces Health Surveillance Division (AFHSD)
Naval Health Research Center (NHRC)
Naval Medical Research Command (NMRC)
United States Air Force School of Aerospace Medicine (USAFSAM)
DoD Global Respiratory Pathogen Surveillance Program Partners

Briefing Outline

- Purpose: To provide an update to the VRBPAC on DoD influenza surveillance activities for 2023-2024
  - Program Descriptions
  - Vaccine Effectiveness in DoD Populations
    - ✓ DoD Beneficiaries
    - ✓ DoD Active Component Service Members
  - DoD Phylogenetic Analyses
  - DoD Antigenic Characterization

Influenza Surveillance in the DoD: Overview

- Global Influenza Surveillance
  - Approximately 400 locations in over 30 countries
    - ✓ Military, local government/academic
  - Extensive characterization capabilities within the DoD
    - ✓ Culture, PCR, sequencing, serology
  - Rapid sharing of results with CDC and/or regional WHO reference centers

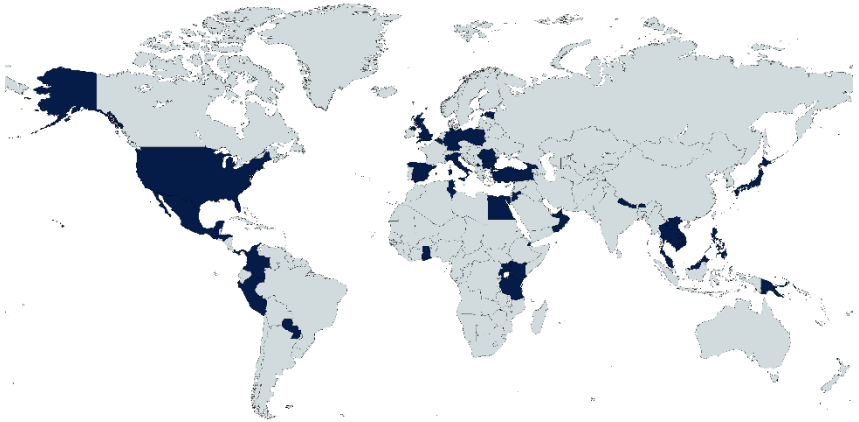
- Comprehensive Epidemiology and Analysis Capabilities
  - Over 12 million Active Component records (health care utilization, immunizations, deployment, reportable diseases, etc.)
    - ✓ Produce Medical Surveillance Monthly Report (MSMR), ad-hoc requests, studies/analyses
    - ✓ Weekly influenza reports
    - ✓ Vaccine safety and effectiveness studies

Influenza Surveillance in the DoD: GEIS

- The Global Emerging Infectious Surveillance (GEIS) partner laboratories form a wide-reaching network across the globe

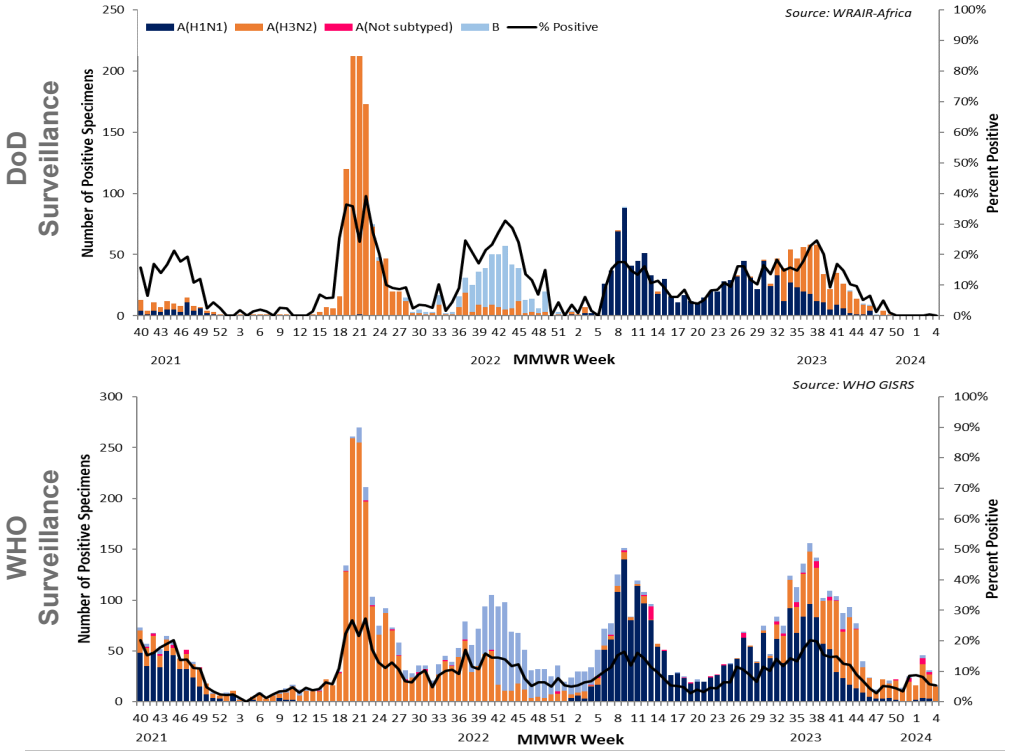
- Influenza surveillance activities in the DoD complement existing WHO efforts
  - Can surveil some locations where data does not otherwise exist (e.g., Djibouti, Tanzania)
  - Surveil Service Members and their beneficiaries, U.S. civilians, and foreign national populations
  - The DoD Service Member population is highly vaccinated and widely distributed across the globe

GEIS-Funded Laboratory Influenza Surveillance Footprint



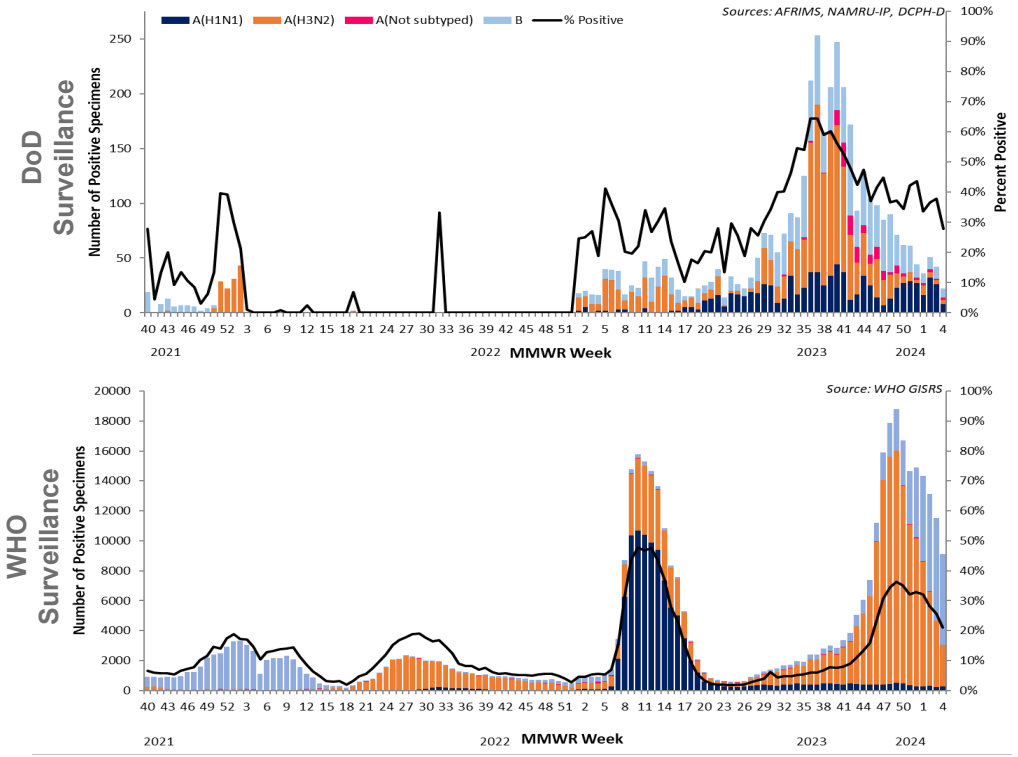
Influenza Surveillance: Subtype Circulation – W. Africa

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data



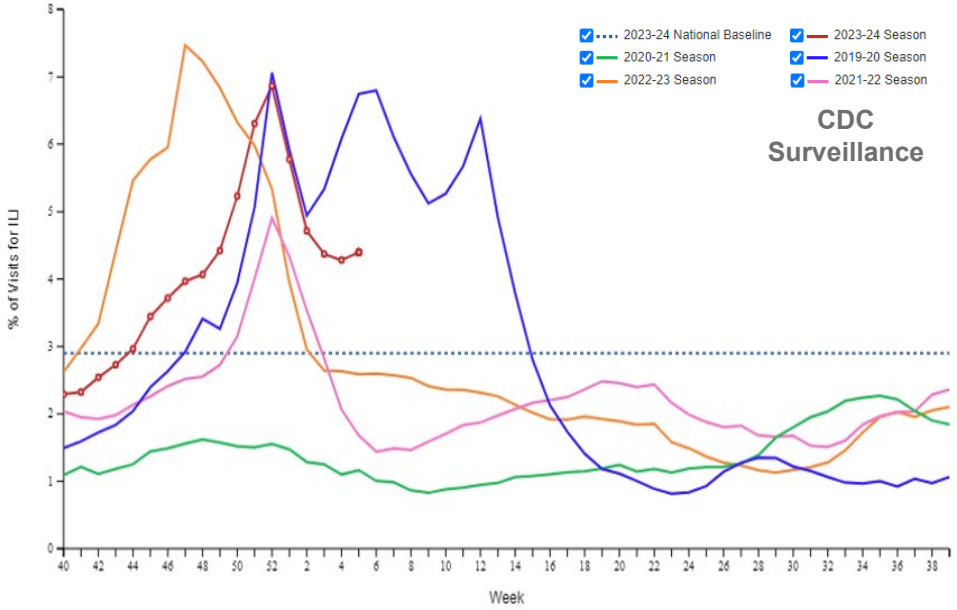
Influenza Surveillance: Subtype Circulation – Asia

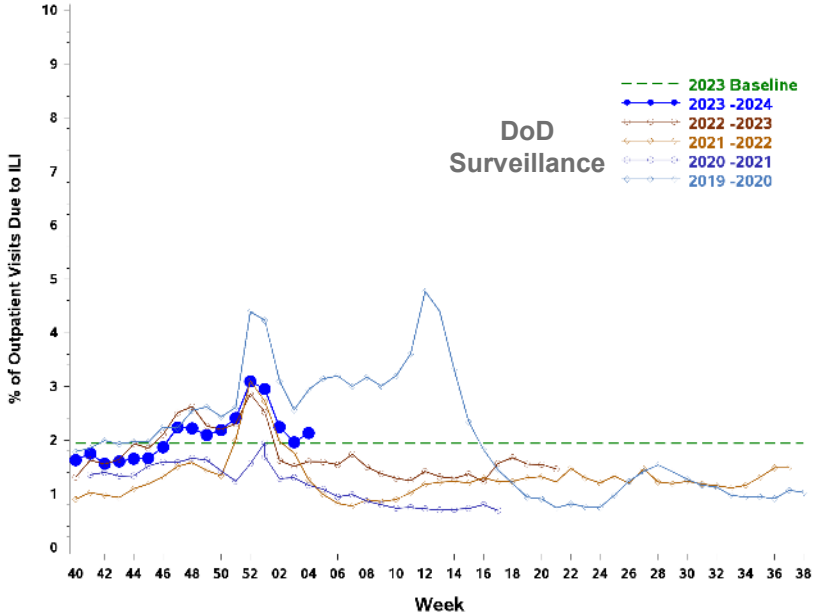
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization



Influenza Surveillance in the DoD: MHS vs. CDC

- Even more broadly, data collected across the Military Health System (MHS) typically mirrors trends observed by CDC





DoD Influenza Mid-Season Vaccine Effectiveness (1)

Matched Case-Control Study DoD TRICARE Beneficiaries

Beneficiary VE: Study Design and Case Definition

- Case, test-negative control study design
  - Population: DoD TRICARE beneficiaries, excluding Service Members
  - VE against medically-attended (outpatient), influenza-like illness (ILI) laboratory-confirmed influenza cases
  - Time period: October 1, 2023 – February 17, 2024 (Weeks 40-07)

- Influenza-like illness case definition:
  - Fever (≥100.4°F) and cough or
  - Fever (≥100.4°F) and 2 or more additional symptoms (fatigue, body aches, sore throat, headache, sinus congestion, shortness of breath, chills, runny nose, loss of taste or smell, acute respiratory distress) or
  - Physician diagnosed ILI

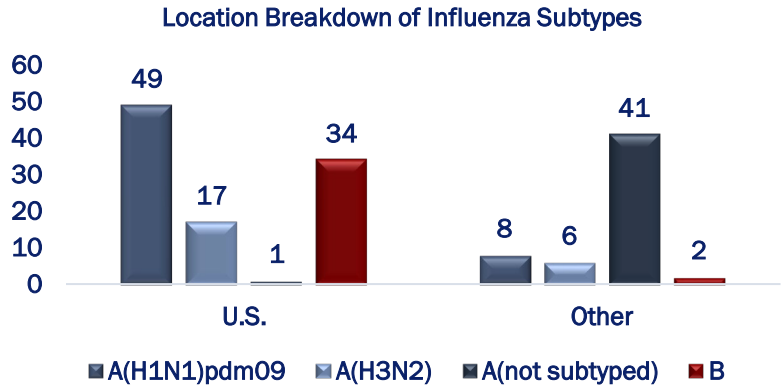
Beneficiary VE: Analyses

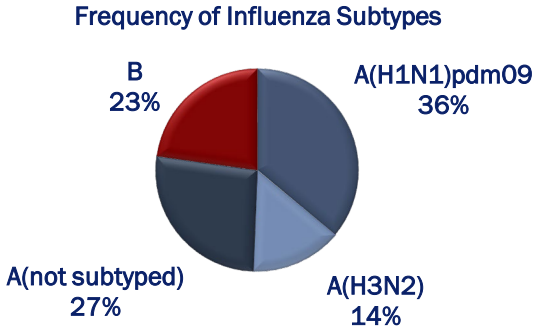
- Controls matched to cases by specimen collection time period
  - Matched 1 case to 4 controls for all analyses

- Analyses by:
  - Influenza (overall) all dependents
  - Influenza (overall) children (2-17 years)
  - Influenza (overall) adults (18-64 years)
  - Influenza A (overall) all dependents
  - Influenza A (H1N1)pdm09 all dependents
  - Influenza A(H3N2) all dependents
  - Influenza B all dependents

Breakdown of Data for VE analyses

- Laboratories contributing to analyses:
  - USAFSAM: n=492 (77%)
  - Landstuhl Regional Medical Center (LRMC): n=145 (23%)
- Cases: n=158 (25%)
  - 83 (53%) vaccinated
  - 75 (47%) unvaccinated
- Controls: n=479 (75%)
  - 289 (60%) vaccinated
  - 190 (40%) unvaccinated





Beneficiary VE: Case/Control Characteristics (1)

Characteristic		Cases n= 158 No. (%)	Controls n= 479 No. (%)	p-Value
Gender	Male	66 (41.77)	190 (39.66)	0.6396
	Female	92 (58.22)	289 (60.33)	
Age	2-5	24 (15.18)	130 (27.13)	0.0006
	6-9	39 (24.68)	62 (12.94)	
	10-17	35 (22.15)	77 (16.07)	
	18-24	5 (3.16)	19 (3.97)	
	25-44	28 (17.72)	112 (23.38)	
	45-64	27 (17.08)	79 (16.49)	
Beneficiary Category	Child (2-17)	98 (62.02)	269 (56.15)	0.1957
	Adult (18-64)	60 (37.97)	210 (43.84)	
Month of Illness	October	9 (5.67)	39 (8.141)	0.0584
	November	10 (6.33)	60 (12.52)	
	December	40 (25.31)	136 (28.39)	
	January	65 (41.13)	170 (35.49)	
	February	34 (21.51)	74 (15.44)	

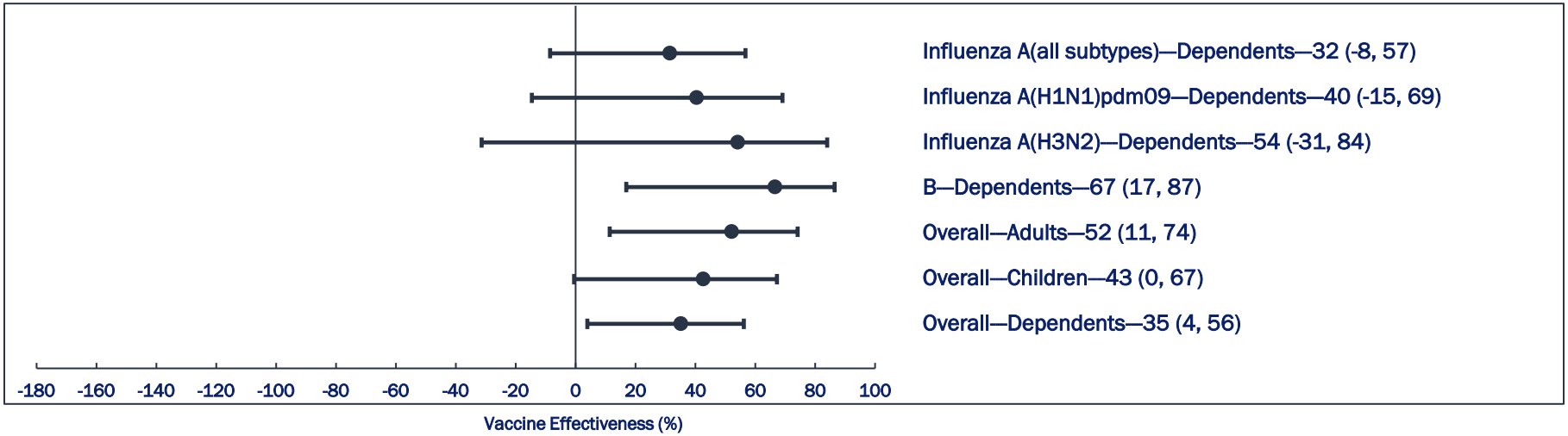
Beneficiary VE: Case/Control Characteristics (2)

Characteristic		Cases n= 122 No. (%)	Controls n= 385 No. (%)	p-Value
Geographic Region	Eastern U.S.	52 (32.91)	151 (31.52)	0.6695
	Western U.S.	49 (31.01)	167 (34.86)	
	Other	57 (36.07)	161 (33.61)	
Vaccination Status	Vaccinated	83 (52.53)	289 (60.33)	0.0845
	Unvaccinated	75 (47.46)	190 (39.66)	
Influenza Status	Influenza A(H1N1)pdm09	57 (36.07)	0 (0)	<0.0001
	Influenza A(H3N2)	23 (14.55)	0 (0)	
	Influenza A/not subtyped	42 (26.58)	0 (0)	
	Influenza B	36 (22.78)	0 (0)	
	Not Influenza	0 (0)	479 (100)	

Beneficiary VE: 2023-2024 Mid-Season Influenza Estimates (1)

Type	Population	Vaccine Status	Cases (%)	Controls (%)	Crude VE (95% CI)	Adjusted VE (95% CI)
A	Dependents	Yes No	73 (13) 49 (8)	287 (50) 168 (29)	16 (-28, 45)	32 (-8, 57)
A(H1N1)pdm09	Dependents	Yes No	22 (8) 35 (12)	130 (46) 98 (34)	56 (18, 76)	40 (-15, 69)
A(H3N2)	Dependents	Yes No	11 (10) 12 (10)	51 (44) 41 (36)	28 (-86, 72)	54 (-31, 84)
B	Dependents	Yes No	10 (6) 26 (14)	96 (53) 48 (27)	82 (59, 92)	67 (17, 87)
Overall	Adults	Yes No	30 (11) 30 (11)	131 (50) 71 (27)	47 (5, 70)	52 (11, 74)
Overall	Children	Yes No	53 (14) 45 (12)	170 (45) 107 (29)	41 (2, 64)	43 (0, 67)
Overall	Dependents	Yes No	83 (13) 75 (12)	289 (45) 190 (30)	37 (8, 57)	35 (4, 56)

Beneficiary VE: 2023-2024 Mid-Season Influenza Estimates (2)



- Overall Influenza: VE was moderately protective and significant among dependents (35%) and adults (52%)
  - Among children, VE was moderate (43%), but not significant
- A(H1N1)pdm09: VE was moderately protective but not significant among dependents (40%)
- A(H3N2): VE was moderate (54%) but not significant, and had very wide confidence intervals and a small sample size
- VE was highest among the B analysis at 67% and significant

DoD Influenza Mid-Season Vaccine Effectiveness (2)

Case Test-Negative Control Design: Ambulatory Care
U.S. Active Component Service Members

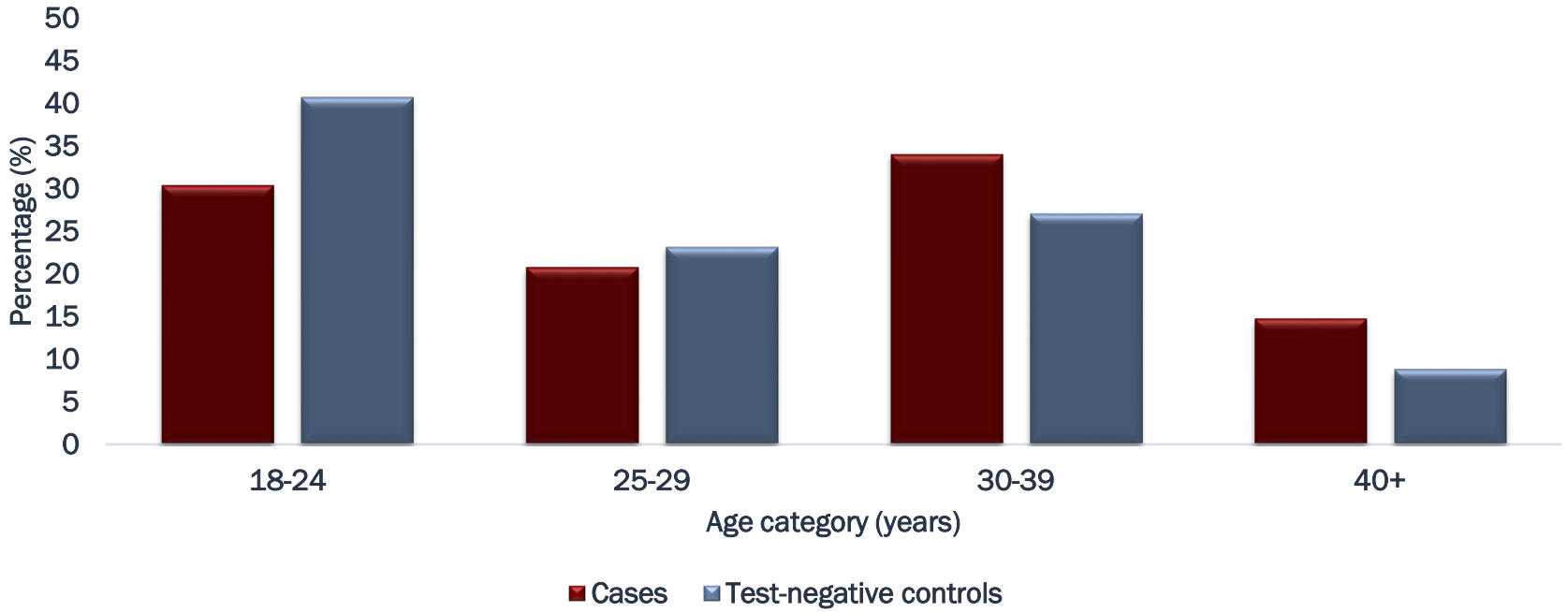
U.S. Service Members VE: Study Design (Ambulatory)

- Case test-negative control design (ambulatory subjects only)
- Population: Active component Service Members
- Army, Navy, Air Force, Marine Corps, Coast Guard, and Space Force
- Time Period: December 1, 2023 – February 23, 2024
- Lab-confirmed flu cases: positive by rapid, RT-PCR, or culture assays
- Test-negative Controls: negative by RT-PCR or culture assays (subjects with negative rapid excluded)
- Models adjusted for sex, age category, prior vaccination (yes or no in previous 5 years), and month of diagnosis

U.S. Service Members VE: Vaccination & Cases (Ambulatory)

- Vaccination
  - Quadrivalent inactivated influenza vaccine was the only vaccine type among the study subjects
  - 92% of subjects had prior flu vaccine in previous 5 years
- Cases
  - Influenza A (any subtype) = 2,794
  - Influenza A(H3N2) = 246
  - Influenza A(H1N1)pdm09 = 119
  - Influenza B = 751

U.S. Service Members VE: Age Breakdown (Ambulatory)



U.S. Service Members VE: Interim Estimates (Ambulatory)

Influenza Type	Vaccination Status	Cases No. (%)	Controls No. (%)	Crude VE (95% CI)	Adjusted VE (95% CI)*
A	Vaccinated	2,271 (81)	14,013 (85)	26 (18, 33)	26 (18, 34)
	Unvaccinated	523 (19)	2,398 (15)		
A(H1N1)pdm09	Vaccinated	96 (81)	14,013 (85)	29 (-13, 55)	23 (-23, 51)
	Unvaccinated	23 (19)	2,398 (15)		
A(H3N2)	Vaccinated	204 (83)	14,013 (85)	17 (-16, 51)	28 (-1, 49)
	Unvaccinated	42 (17)	2,398 (15)		
B	Vaccinated	652 (87)	14,013 (85)	-13 (-40, 9)	-5 (-30, 16)
	Unvaccinated	99 (13)	2,398 (15)		

*Adjusted for sex, age category, 5-year prior vaccination (Y/N), and month of diagnosis

DoD Influenza Mid-Season Vaccine Effectiveness (3)

Cohort Study Design – Hospitalizations U.S. Active Component Service Members

U.S. Service Members VE: Cohort Study Design (Hospitalization)

- Cohort study design (hospitalizations only)
- Population: Active component Service Members
- Army, Navy, Air Force, Marine Corps, Coast Guard, and Space Force
- Time Period: September 1, 2023 – February 14, 2024
- Outcome definition:
  - Lab-confirmed flu case (rapid/RT-PCR/culture) indicating hospitalization AND/OR
  - Hospitalization record with 1st or 2nd diagnostic ICD-10 code for influenza (J09-J11)

U.S. Service Members VE: Vaccination & Cases (Hospitalization)

- Vaccination status
  - Unvaccinated: any person-time and cases prior to vaccination and up to 13 days post-vaccination
  - Vaccinated: any person-time and cases at least 14 days after vaccination
- Crude and adjusted incidence rate ratios (IRR) and VE calculated
- Models adjusted for sex, age category, prior vaccination, and month of diagnosis

U.S. Service Members VE: Estimates (Hospitalizations)

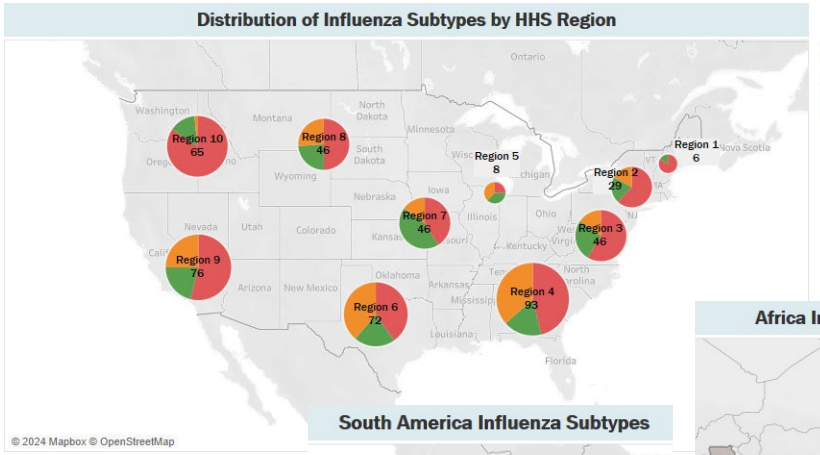
Outcome	Vaccination Status	Case No. (%)	Person-Years (PY)	Incidence Rate per 10,000 PY	Adjusted IRR (95% CI)*	Adjusted VE (95% CI)*
Lab-confirmed only	Vaccinated	17 (66)	321,131	0.05	0.54 (0.30, 0.98)	46 (2, 70)
	Unvaccinated	30 (34)	307,610	0.10		
Lab-confirmed & hospitalized flu encounter	Vaccinated	21 (33)	321,129	0.07	0.46 (0.28, 0.78)	54 (12, 72)
	Unvaccinated	43 (67)	307,607	0.14		

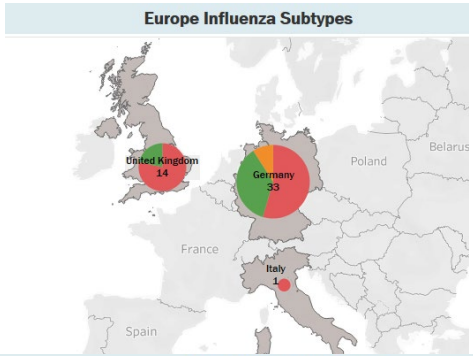
*Adjusted for sex, age category, 5-year prior vaccination (Y/N), and month of diagnosis

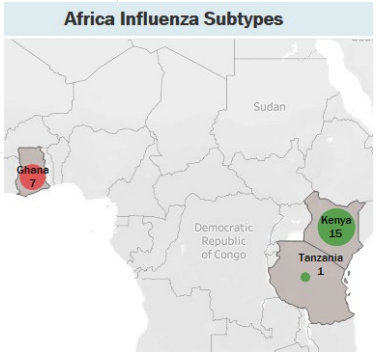
DoD Phylogenetic Analyses - Outline

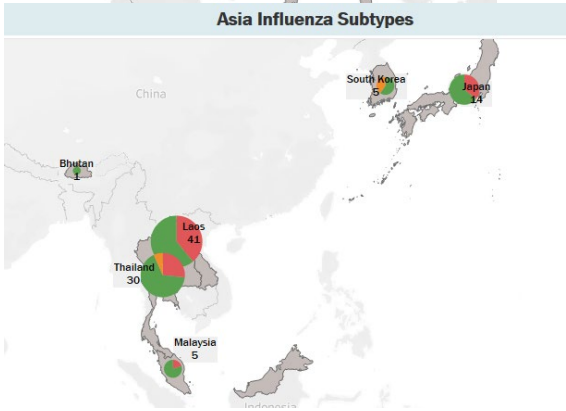
- Geographical distribution of all influenza viruses characterized for the DoD
- Influenza A(H1N1)pdm09 clade proportions and phylogeny
- Influenza A(H3N2) clade proportions and phylogeny
- Influenza B phylogeny
- Summary

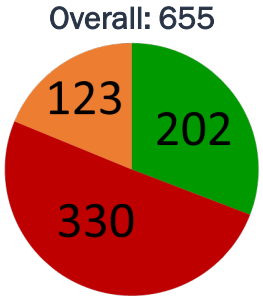
Geographical Distribution of 2023-2024 DoD Influenza Sequence Data



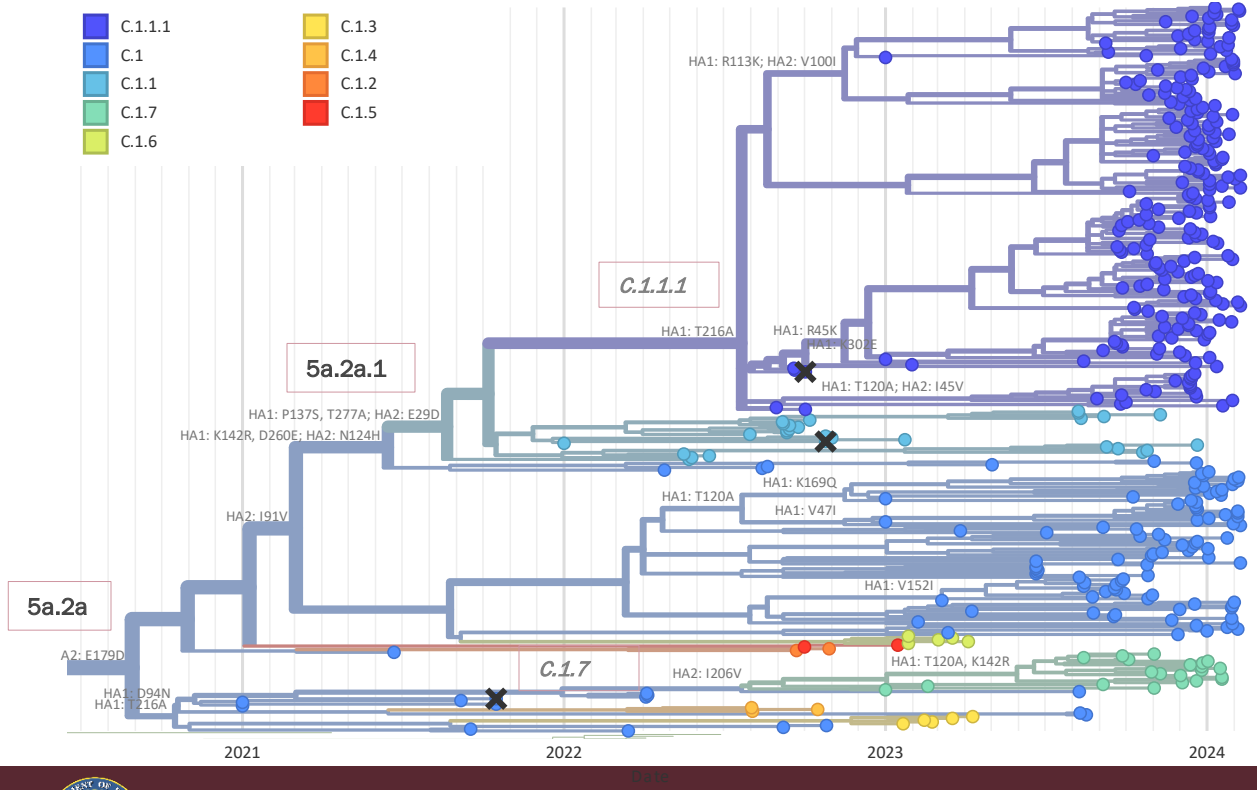






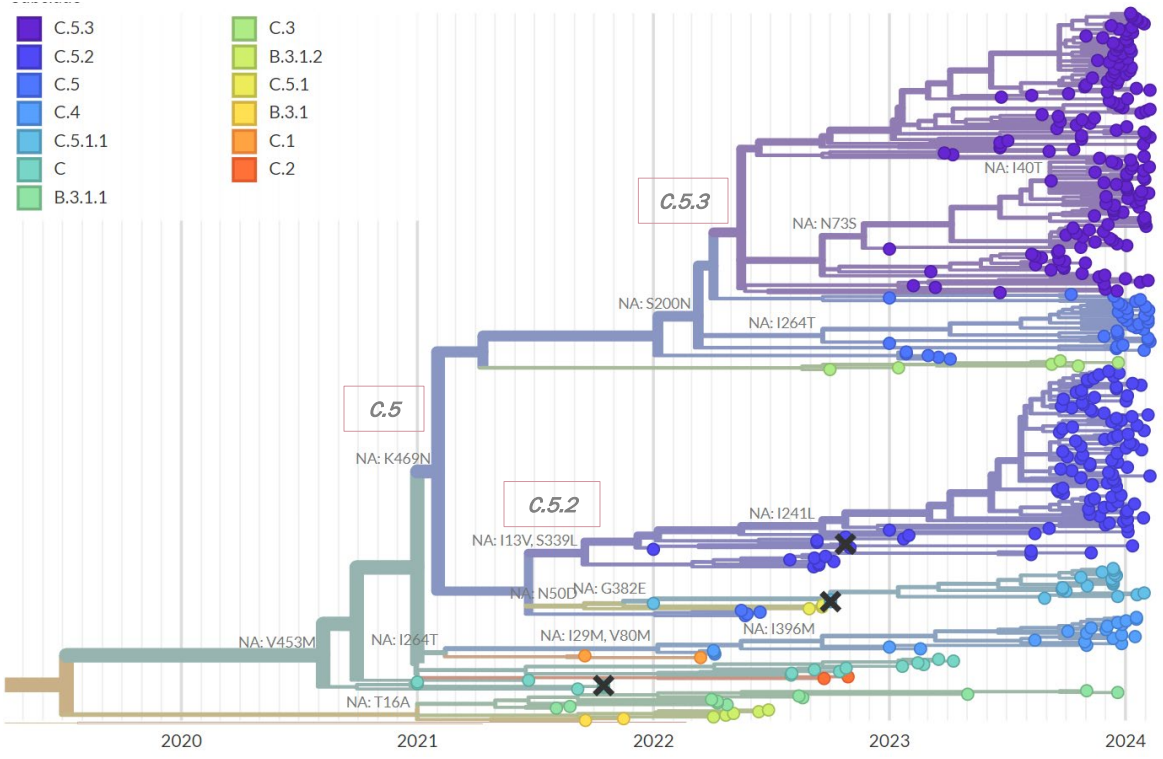


DoD Phylogenetic Analyses – A(H1N1)pdm09 HA



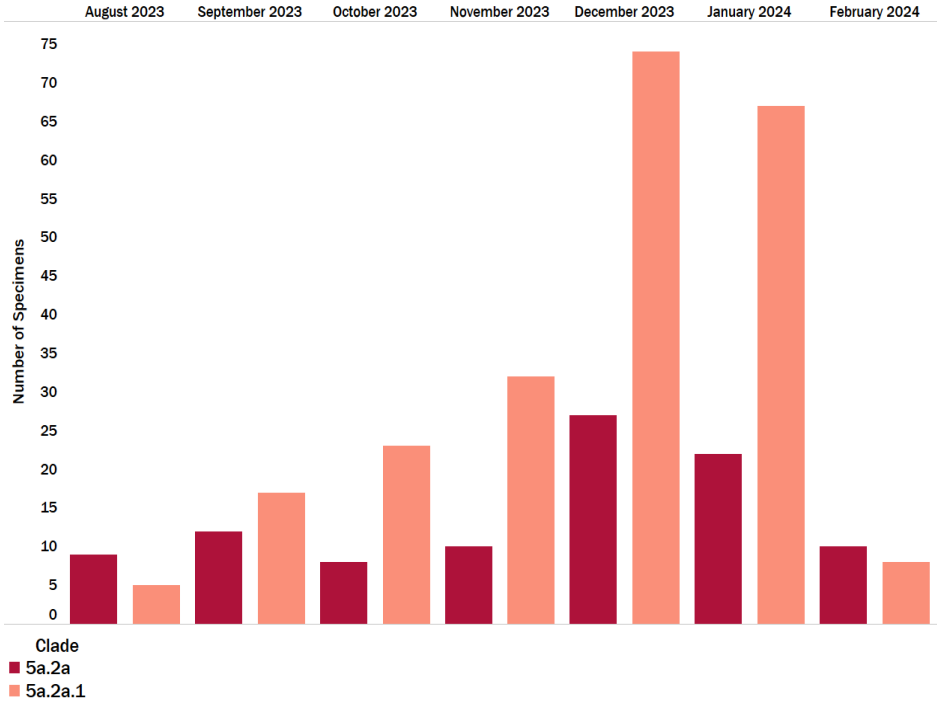
Clade/Subclade	No.	%
5a.2a	104	31.5%
C.1	86	26.1%
C.1.7	18	5.5%
5a.2a.1	226	68.5%
C.1.1	10	3.0%
C.1.1.1	216	65.5%

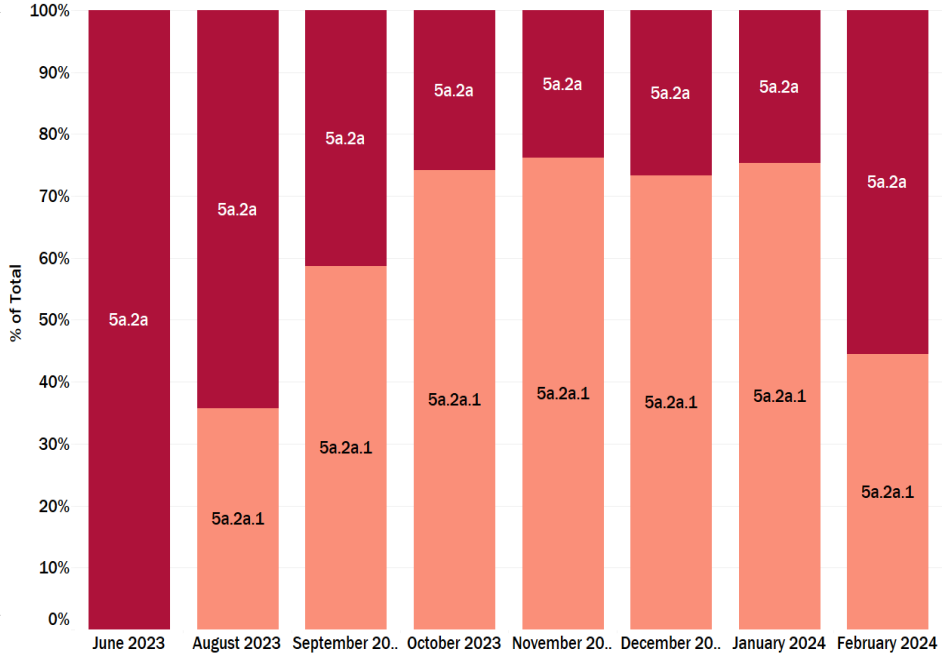
DoD Phylogenetic Analyses – A(H1N1)pdm09 NA



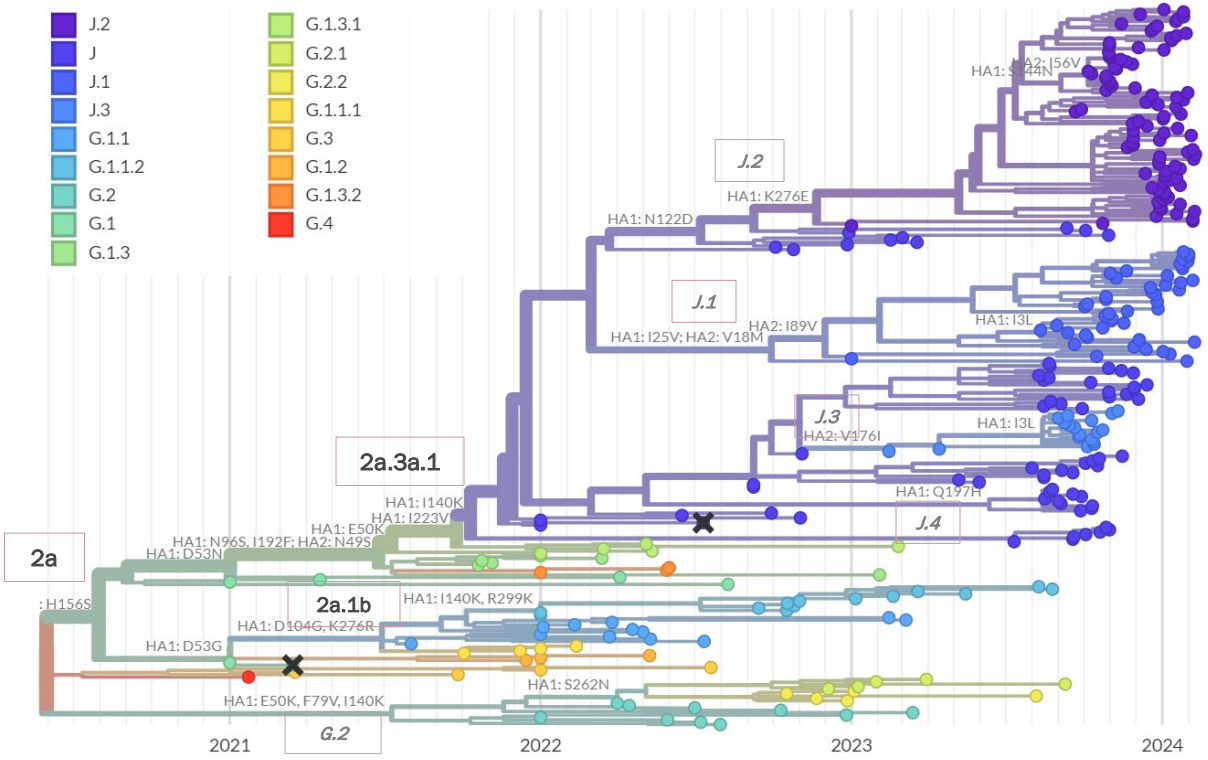
Clade	No.	%
B.3.1.1	2	0.6%
C.3	4	1.3%
C.4	15	4.7%
C.5	28	8.8%
C.5.1.1	18	5.7%
C.5.2	96	30.2%
C.5.3	155	48.7%

A(H1N1)pdm09 Clade Dynamics



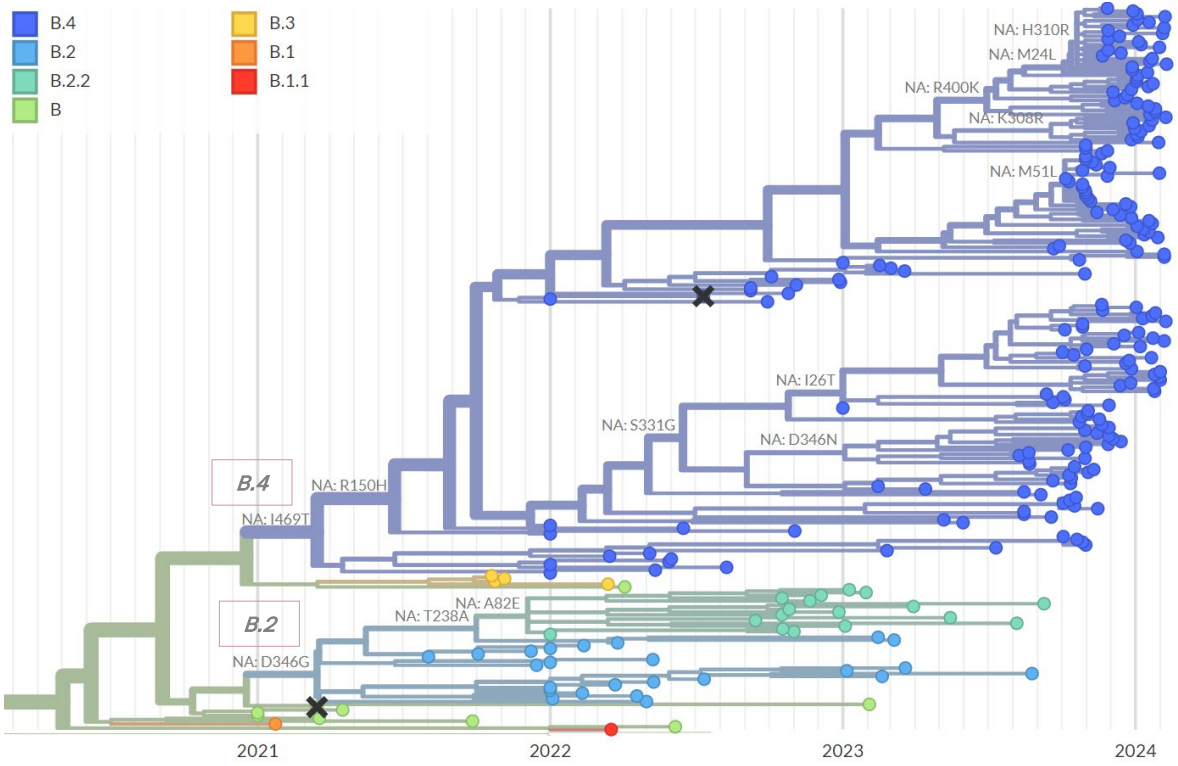


DoD Phylogenetic Analyses – A(H3N2) HA



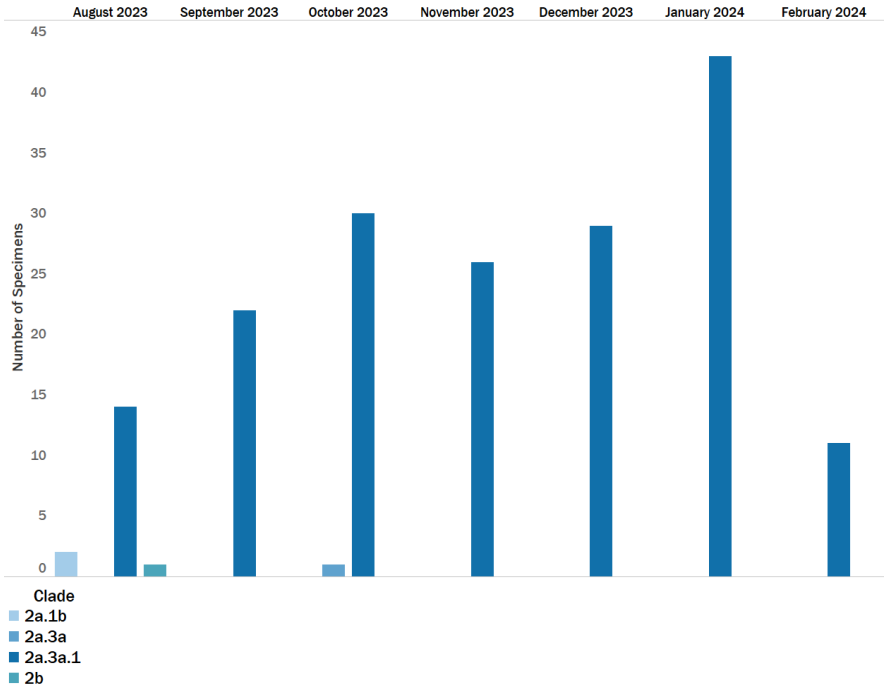
Clade/Subclade	No.	%
2a.3a.1	199	98.5%
J	41	20.3%
J.1	44	21.8%
J.2	90	44.6%
J.3	18	8.9%
J.4	6	3.0%
2a.1b	2	1.0%
G.1.1.2	2	1.0%
2b	1	0.5%
G.2.2	1	0.5%

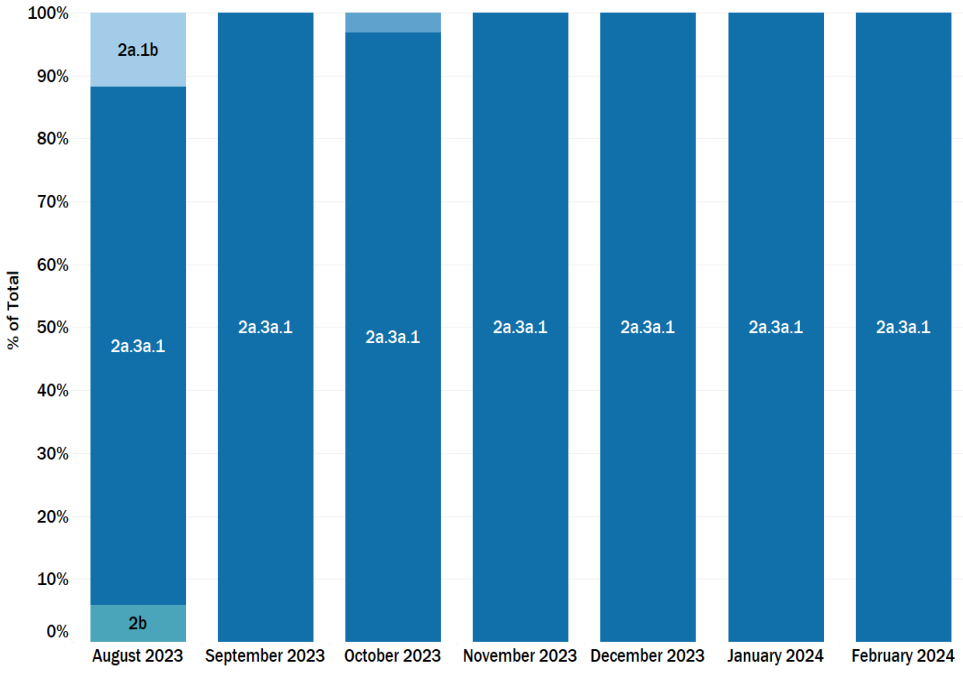
DoD Phylogenetic Analyses – A(H3N2) NA



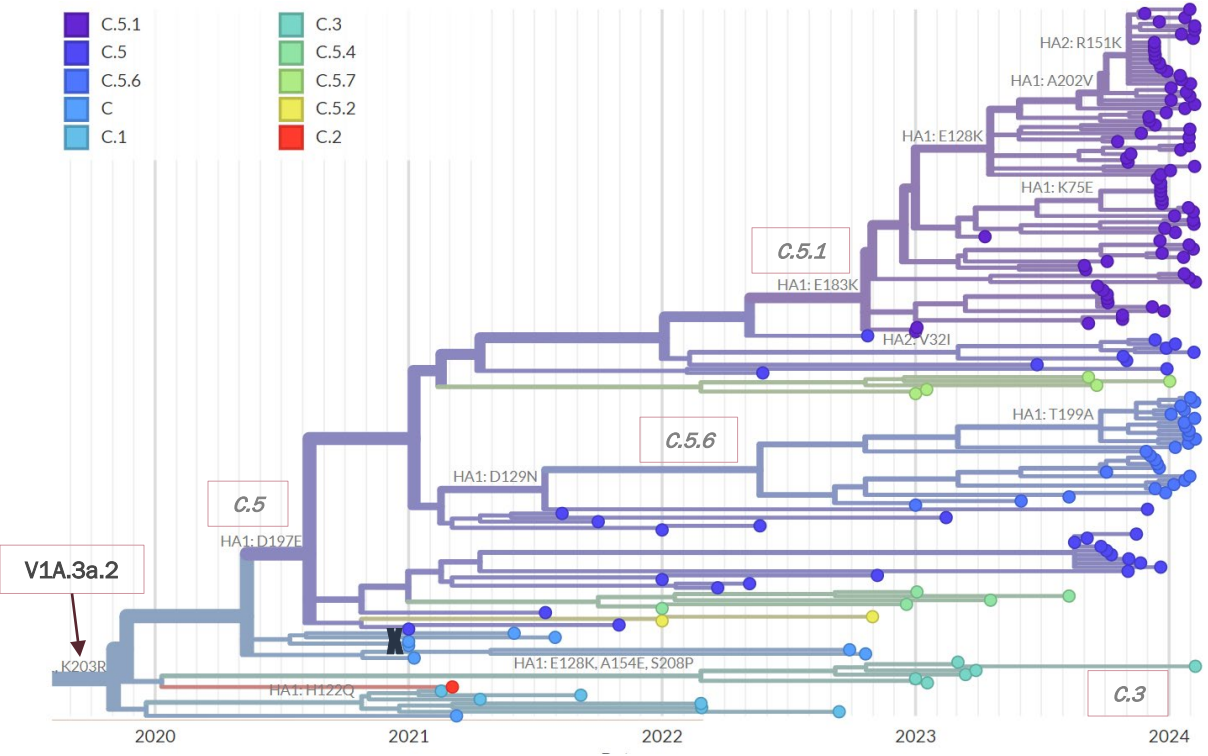
Clade	No.	%
B.2	1	0.6%
B.2.2	1	0.6%
B.4	167	98.8%

A(H3N2) Clade Dynamics



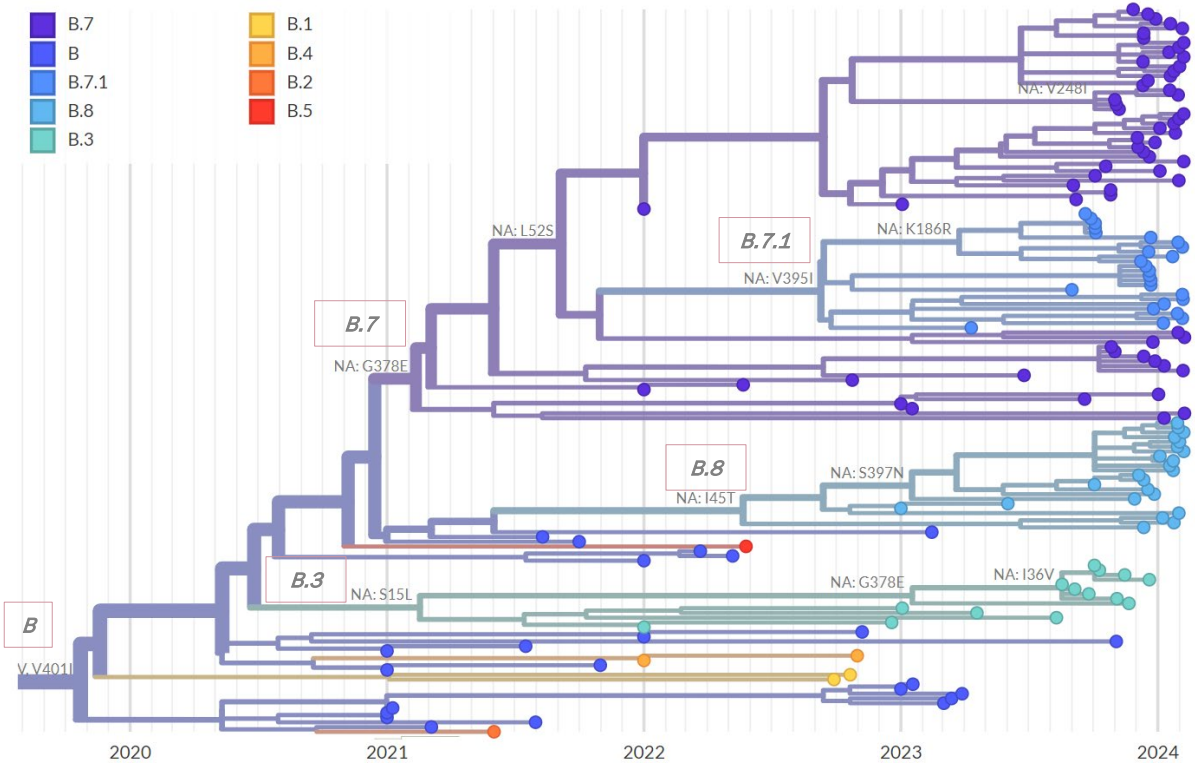


DoD Phylogenetic Analyses – B/Victoria HA



Clade/Subclade	No.	%
V1A.3a.2	123	100%
C.3	1	0.8%
C.5	18	14.6%
C.5.1	76	61.8%
C.5.4	1	0.8%
C.5.6	25	20.3%
C.5.7	2	1.6%

DoD Phylogenetic Analyses – B/Victoria NA

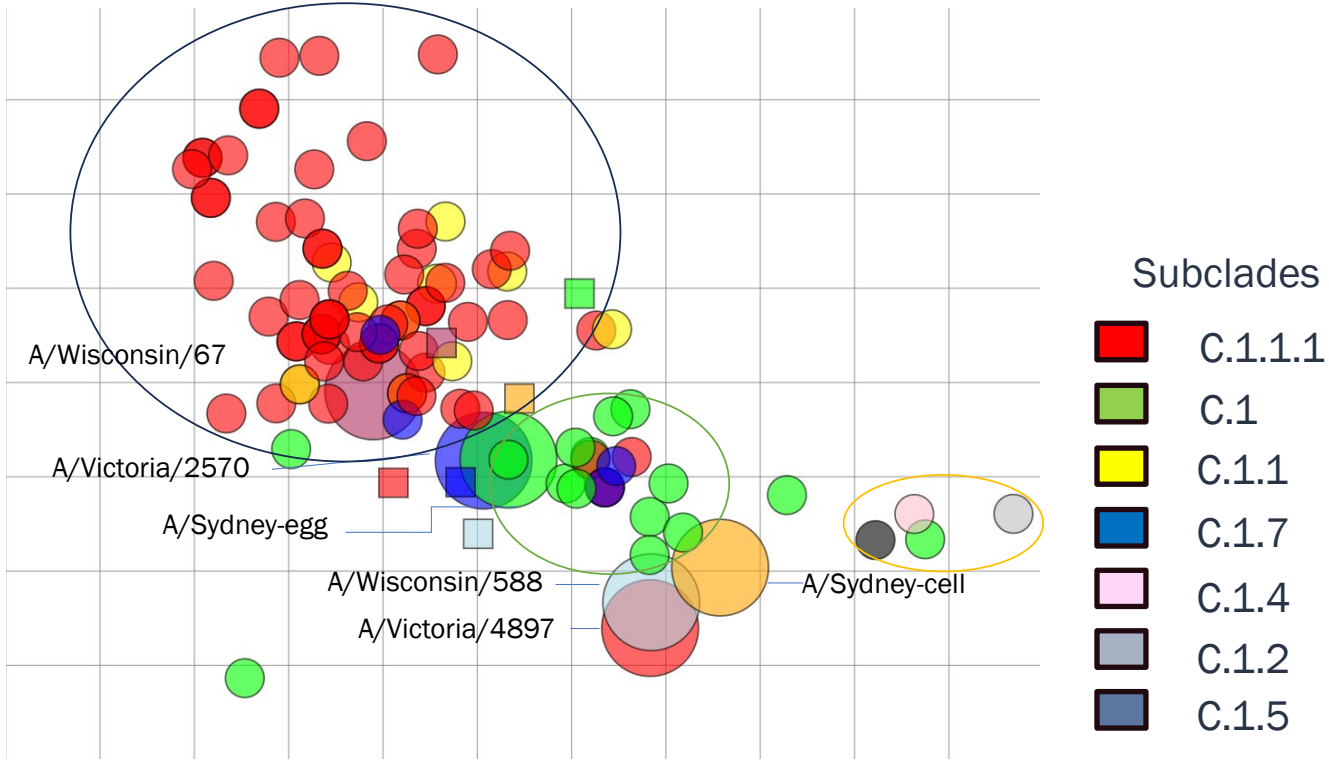


Clade	No.	%
B	1	0.9%
B.3	10	9.2%
B.7	53	48.6%
B.7.1	24	22.0%
B.8	21	19.3%

DoD Influenza Sequencing Summary

- 330 Influenza A(H1N1)pdm09 sequences were characterized, of which 68.5% were HA clade 5a.2a.1. The dominant HA subclade was C.1.1.1 and the dominant NA clade was C.5.3.
- 202 Influenza A(H3N2) sequences were characterized, of which 98.5% were HA clade 2a.3a.1. The dominant HA subclade was J.2 and the dominant NA clade was B.4.
- 123 Influenza B/Victoria sequences were characterized, all of which were HA clade V1A.3a.2. The dominant HA subclade was C.5.1 and the dominant NA clade was B.7.
- Sequence data were contributed by DCPH-D, AFRIMS, NAMRU-EAC (Ghana), NAMRU-IP, NAMRU-S, NHRC, TAMC, and WRAIR-AFRICA.
- Our data agree with the WHO Northern Hemisphere influenza vaccine strain selections.

DoD Antigenic Characterization: H1N1 strains



HAI titers for currently circulating representative H1N1 strains

	Victoria 4897	Wisconsin 67	Victoria 2570	Wisconsin 588	Sydney 5 egg	Sydney 5 cell
A/Victoria/4897/2022	10240	20480	20480	40960	10240	40960
A/Wisconsin/67/2022	81920	81920	40960	40960	40960	81920
A/Victoria/2570/2019	81920	81920	81920	163840	81920	163840
A/Wisconsin/588/2019	10240	40960	20480	40960	10240	40960
A/Sydney/5/2021 EGG	40960	81920	81920	163840	81920	163840
A/Sydney/5/2021 cell	10240	10240	5120	40960	10240	163840

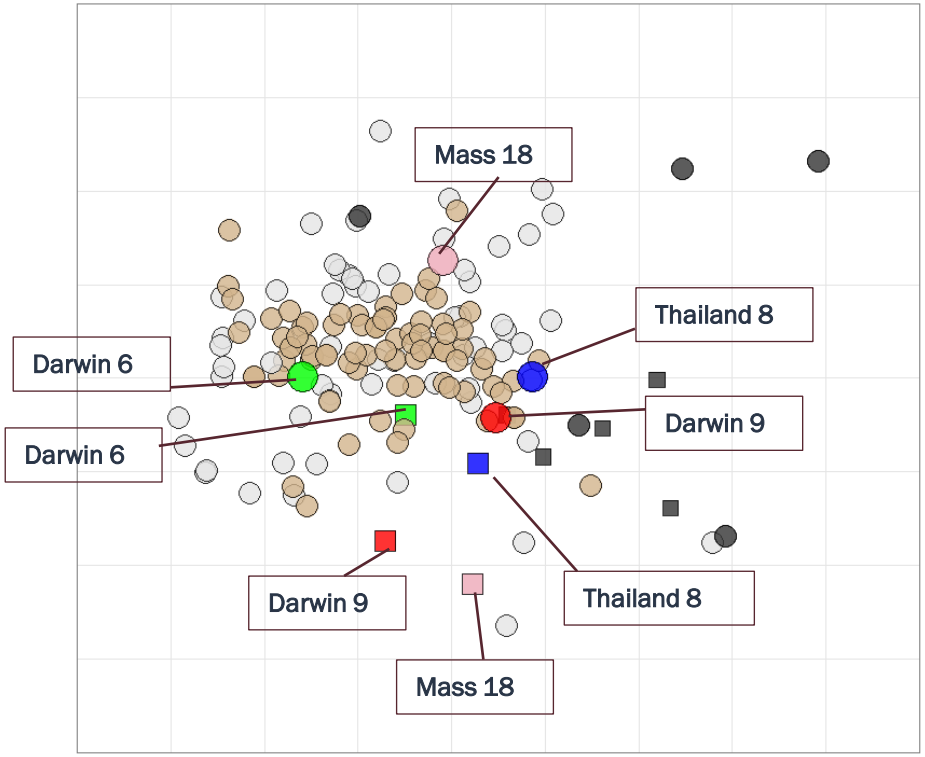
							Location	Collection Date	Old Clade	New Clade	Subclade	Additional Substitutions	
H1230701	5120	2560	2560	10240	10240	40960	Missouri	12/8/2022	6B.1A.5a2	5a.2a	C.1.5	K54Q A186T Q189E E224A R259K K308R	
H1230702	2560	1280	1280	2560	5120	10240	Nebraska	12/9/2022	6B.1A.5a2	5a.2a	C.1.2	A48P K54Q A186T Q189E E224A R259K K308R	
H1230720	2560	2560	2560	5120	5120	40960	Germany	12/18/2022	6B.1A.5a2	5a.2a	C.1	K54Q A186T Q189E E224A R259K K308R I418V	
H1230725	2560	2560	2560	5120	5120	81920	Germany	1/3/2023	6B.1A.5a.2a	5a.2a	C.1.4	V47I S85P D94N T216A E235D H273Q Y468F I513T	
H1230723	20480	40960	20480	81920	81920	163840	Germany	1/6/2023	6B.1A.5a2	5a.2a	C.1	K54Q A186T Q189E E224A R259K K308R I418V	
H1231203	40960	40960	40960	81920	40960	163840	Georgia	10/26/2023	6B.1A.5a.2a	5a.2a	C.1		
H1231212	20480	20480	20480	40960	20480	163840	Texas	9/17/2023	6B.1A.5a.2a	5a.2a	C.1	V26I	
H124010	40960	40960	20480	81920	40960	327680	Washington	12/14/2023	6B.1A.5a.2a	5a.2a	C.1	T120A K169Q	
H1231231	10240	10240	5120	20480	20480	40960	Missouri	12/1/2023	6B.1A.5a.2a	5a.2a	C.1	A197T	
H124001	40960	20480	10240	40960	20480	81920	North Dakota	12/20/2023	6B.1A.5a.2a	5a.2a	C.1	V47I I96T T120A	
H124003	81920	40960	20480	40960	20480	40960	North Dakota	12/20/2023	6B.1A.5a.2a	5a.2a	C.1	K142R G262E T270I	
H124006	40960	20480	10240	40960	40960	81920	Missouri	1/2/2024	6B.1A.5a.2a	5a.2a	C.1		
H124007	20480	10240	10240	40960	20480	163840	Florida	12/28/2023	6B.1A.5a.2a	5a.2a	C.1	T120A K169Q T216A E506D	
H124010	40960	40960	20480	81920	40960	327680	Washington	12/14/2023	6B.1A.5a.2a	5a.2a	C.1	T120A K169Q	
H124019	20480	10240	5120	20480	2080	81920	United Kingdom	1/3/2024	6B.1A.5a.2a	5a.2a	C.1	P137S N444K	
H124021	40960	40960	20480	81920	20480	327680	United Kingdom	1/3/2024	6B.1A.5a.2a	5a.2a	C.1	N38D T120A K169Q K480R	
H1230703	81920	40960	20480	40960	40960	163840	Missouri	12/19/2022	6B.1A.5a2	5a.2a	C.1	K54Q K142R A186T Q189E E224A R259K K308R I418V	
A10-09904-2-PCR	40960	20480	10240	81920	40960	327680	MD	1/8/2024		5a.2a	C.1		
H1230713	20480	40960	81920	10240	40960	163840	Nebraska	1/17/2023	6B.1A.5a2+T216	5a.2a.1	C.1.1.1	K54Q P137S K142R A186T Q189E E224A R259K T277A K308R E356D I418V N451H	
H1231213	40960	20480	40960	20480	40960	163840	Washington	9/26/2023	6B.1A.5a.2a.1	5a.2a.1	C.1.1.1	R45K T216A K302E	
H1230708	81920	81920	10240	20480	40960	81920	Florida	1/4/2023	6B.1A.5a2	5a.2a.1	C.1.1	K54Q P137S K142R A186T Q189E E224A R259K T277A K308R E356D I418V N451H	
H1230903	10240	40960	5120	20480	20480	20480	New Jersey	7/23/2023	6B1A.5a.2a.1	5a.2a.1	C.1.1.1	T120A I372V	
H1230911	10240	20480	5120	2560	10240	20480	New Jersey	7/23/2023	6B1A.5a.2a.1	5a.2a.1	C.1.1.1	T120A I372V	
H1230917	5120	20480	2560	5120	10240	10240	New Jersey	7/23/2023	6B1A.5a.2a.1	5a.2a.1	C.1.1.1	T120A I372V	
H1230918	20480	81920	10240	20480	81920	163840	New Jersey	7/24/2023	6B1A.5a.2a.1	5a.2a.1	C.1.1.1	T120A I372V	

Cluster 1

Cluster 2

Cluster 3

DoD Antigenic Characterization: H3N2 strains



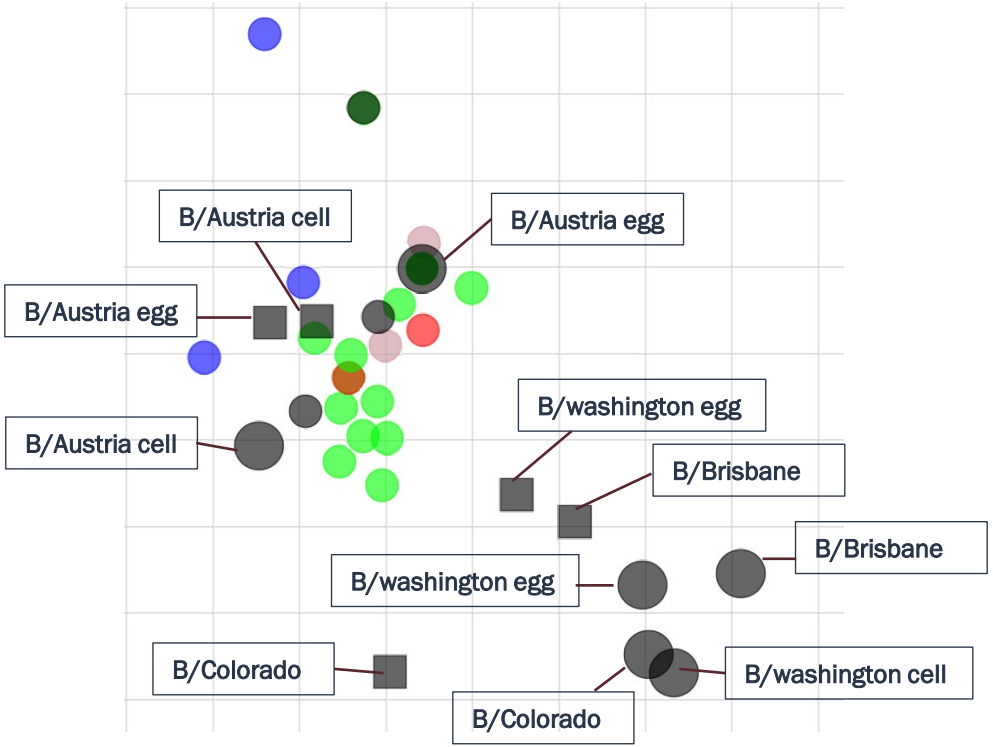
Subclades

- Darwin 6: G1
- Darwin 9: G.1
- Thailand 8: J
- Mass. 18: J
- Isolates from 2023
- Isolates from 2024

HAI titers for currently circulating representative H3N2 strains

	Darwin 6	Darwin 9	Thailand 8	Mass 18	Tasmania egg	Tasmania cell	HK 2671	HK 45	Kansas 14	South Australia 34						
Darwin 6	640	5120	5120	1280	1280	320	160	640	640	640					G.1	
Darwin 9	1280	20480	2560	2560	5120	2560	2560	1280	5120	5120					G.1	
Thailand 8	640	2560	5120	2560	2560	2560	1280	2560	1280	5120					J	
Mass 18	320	2560	5120	1280	1280	640	640	1280	320	320					J	
Tasmania egg	160	1280	2560	1280	1280	320	320	320	1280	320					F.1	
Tasmania cell	40	160	160	320	320	2560	160	320	2560	320					F.1	
HK 2671	160	640	2560	1280	1280	640	5120	1280	20480	1280					D	
HK 45	80	640	1280	320	320	2560	160	1280	5120	320					D	
Kansas 14	160	1280	2560	1280	2560	1280	1280	640	20480	1280						
South Australia 34	320	2560	5120	2560	5120	2560	2560	5120	5120	5120						
											Location	Collection Date	Old Clade	New Clade	Subclade	Additional Substitutions
H3230701	320	1280	1280	1280	320	160	160	320	640	320	Arizona	12/8/2022	3C.2a1b.2a2-D53N	2a.3b	G.1.3.2	N96S I140M I192F N378S N489T
H3230702	640	2560	1280	1280	640	640	160	640	640	1280	North Dakota	12/12/2022	3C.2a1b.2a2-D53G	2a.1b	G.1.1.2	D104G I140K K276R R299K
H3230703	1280	5120	1280	1280	640	320	160	640	640	5120	Texas	12/14/2022	3C.2a1b.2a2-D53G	2a.1	G.1.1	K276R K503R
H3230712	320	1280	5120	1280	2560	640	640	640	640	2560	New Jersey	1/4/2023	3C.2a1b.2a2-E50K	2b	G.2	F79V I140K S156H
H3230720	640	5120	5120	2560	2560	1280	1280	1280	640	1280	Alaska	12/14/2022	3C.2a1b.2a2-D53N	2a.3a.1	J	E50K N96S I140K I192F I223V N378S
H3230724	640	5120	5120	5120	640	320	320	640	2560	320	Japan	1/22/2023	3C.2a1b.2a2-D53N	2a.3a	G.1.3.1	E50K N96S N133A I192F I223V N378S
H3230735	320	2560	2560	1280	320	320	80	320	1280	320	Missouri	3/24/2023	3C.2a1b.2a.2a.3	2a.3	G.1.3	T135K I140K S145N N262S
H3231219	320	5120	2560	1280	320	80	160	320	640	640	Colorado	12/4/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.2	N122D K276E
H3231220	320	1280	2560	1280	640	160	320	640	320	1280	Japan	12/5/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.1	I25V R33Q V347M I418V
H3231221	640	2560	5120	2560	1280	1280	640	1280	320	1280	Japan	11/20/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.1	I25V N145S V347M I418V
H324001	1280	10240	5120	5120	1280	320	640	1280	5120	5120	Maryland	12/20/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.2	N122D R141K K276E L409I
H324002	1280	10240	2560	1280	5120	640	640	1280	640	2560	Missouri	12/26/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.2	N122D S145G V223I K276E
H324012	1280	10240	5120	5120	2560	2560	1280	2560	640	5120	Japan	12/26/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.1	I25V V347M I418V
H324013	640	5120	1280	1280	640	640	640	2560	1280	2560	Germany	12/27/2023	3C.2a1b.2a.2a.3a.1	2a.3a.1	J.2	N122D S124N K276E
A10-09689-8-PCR	640	5120	1280	1280	640	320	160	320	640	1280	MD	8/30/2023		2a.3a.1	J.2	
A10-09903-5-PCR	640	10240	5120	5120	1280	1280	1280	320	320	2560	MD	1/8/2024		2a.3a.1	J.1	
A10-09908-0-PCR	1280	10240	2560	1280	1280	640	640	640	640	2560	MD	1/9/2024		2a.3a.1	J.2	
A10-09910-3-PCR	640	1280	2560	1280	2560	320	160	640	640	640	MD	1/10/2024		2a.3a.1	J.2	

DoD Antigenic Characterization: B strains



HAI titers for currently circulating Influenza B strains

	B/Austria/ cell	B/Austria/ Egg	B/Washington/ egg	B/Colorado/6/2017	B/Bris/60/2008
Austria Cell	5120	2560	640	1280	1280
Austria Egg	5120	2560	640	320	2560
B/Washington cell	80	80	2560	1280	5120
Washington Egg	160	160	2560	1280	20480
B/Colorado	80	40	2560	2560	20480
B/Brisbane	80	80	1280	320	20480

						Location	Collection Date	Old Clade	New Clade	Subclade	Additional Substitutions
B24001	5120	5120	1280	320	2560	Oklahoma	12/15/2023	V1A.3a.2	V1A.3a.2	C.5.1	K75E E183K
B24002	10240	5120	1280	2560	2560	Florida	12/20/2023	V1A.3a.2	V1A.3a.2	C.5.1	E128K E183K
B24003	10240	5120	1280	1280	2560	Maryland	12/26/2023	V1A.3a.2	V1A.3a.2	C.5.1	E183K T189S
B24004	10240	2560	5120	10240	2560	Florida	12/8/2023	V1A.3a.2	V1A.3a.2	C.5.1	E183K
B24005	10240	5120	1280	1280	2560	Oklahoma	1/8/2024	V1A.3a.2	V1A.3a.2	C.5.6	D129N V252M
B24006	10240	10240	1280	640	5120	New York	12/28/2023	V1A.3a.2	V1A.3a.2	C.5.1	E128K E183K
B24007	10240	10240	1280	640	1280	Oklahoma	12/22/2023	V1A.3a.2	V1A.3a.2	C.5.1	K75E E183K
A10-07566-4-PCR	10240	10240	320	160	2560	MD	4/10/2023		V1A.3a.2	C.3	
A10-07605-0-PCR	5120	5120	80	640	2560	MD	4/11/2023		V1A.3a.2	C.3	
A10-08393-5-PCR	5120	5120	1280	1280	5120	MD	5/1/2023		V1A.3a.2	C.5.1	
BV230701	2560	1280	320	80	320	United Kingdom	3/20/2023	V1A.3a.2	V1A.3a2	C.5.1	E183K
BV230702	2560	1280	320	80	320	Wyoming	3/7/2023	V1A.3a.2	V1A.3a2	C.5	N129D
BV230704	2560	640	80	40	160	Germany	1/30/2023	V1A.3a.2	V1A.3a2	C.3	I76T E128K A154E S208P
BV231201	5120	5120	2560	2560	5120	Florida	10/19/2023	V1A.3a.2	V1A.3a.2	C.5.1	
BV231202	5120	5120	640	1280	2560	Missouri	10/3/2023	V1A.3a.2	V1A.3a.2	C.5	D129N
BV231203	5120	2560	1280	2560	2560	Oklahoma	10/4/2023	V1A.3a.2	V1A.3a.2	C.5.1	E183K
BV231204	5120	5120	2560	2560	2560	South Carolina	9/28/2023	V1A.3a.2	V1A.3a.2	C.5.1	E183K
BV231205	5120	2560	640	160	2560	South Carolina	11/7/2023	Unk	Unk	Unk	
BV231206	5120	5120	1280	640	2560	Oklahoma	11/14/2023	Unk	Unk	Unk	
BV231207	5120	5120	640	640	2560	South Carolina	10/27/2023	V1A.3a.2	V1A.3a.2	C.5	V117I V379I
BV231208	5120	2560	640	320	2560	South Carolina	11/1/2023	V1A.3a.2	V1A.3a.2	C.5	V117I V379I
BV231211	5120	2560	1280	640	2560	Missouri	12/5/2023	V1A.3a.2	V1A.3a.2	C.5.6	
BV231214	5120	1280	1280	320	2560	Maryland	12/12/2023	V1A.3a.2	V1A.3a.2	C.5.1	E128K N129D E183K
BV231212	5120	2560	640	320	2560	Florida	12/4/2023	V1A.3a.2	V1A.3a.2	C.5.1	E128K N129D V177I E183K

Acknowledgements (1)

AFHSD
Col Patrick Kennedy
CDR Matthew Kasper
MAJ Christan Stager
LCDR Shayne Gallaway
Ms. Dara Russell
Capt Manuel Moncada
Dr. Angelia Cost
Dr. Kathleen Creppage
Ms. June Early
Ms. Zheng Hu
Ms. Marissa Hetrich

DCPH-D
Dr. Anthony Fries
Lt Col Anthony Robbins
Dr. Fabrice Evengue
Col Kathryn Shaw
Dr. Elizabeth Macias
Maj Peter Wasik (Ret.)
Ms. Tamara Hartless
Ms. Amy Bogue
Ms. Laurie DeMarcus
Ms. Caroline Smith
Mr. Jeffrey Thervil
Mr. Bismark Kwaah
Ms. Whitney Jenkins
Dr. Victor Heh
Mr. Christian Polleys
Dr. Deanna Muehleman
Mr. William Gruner
Dr. Jimmaline Hardy
Mr. James Hanson
Ms. Denise Kramer
Mr. Matthew Sanders
Ms. Aleta Yount
Ms. Debby Koontz
Mr. Renell Capati
SrA Michelle Dondiego-Valdez
Mr. Andrew Martin
Ms. Dannielle Parlett
Mr. Thomas Longeway
Ms. Sarah Purves

NHRC
LCDR Michelle Lane
LCDR Daniel Crouch
Dr. Francisco Mimica Porras
Dr. Matthew Esona
Ms. Misbah Rashad
Mr. Roger Pan
Ms. Erica Duarte

NMRC
Ms. Zhaodong Liang
Mr. Daniel Ewing
Dr. Appavu Sundaram

LRMC
Mr. Fritz Castillo
Ms. Jennifer Black
Ms. Pilar Mandujano
CPT Cole Anderson

AFRIMS
MAJ Thomas Cotrone
LTC Stefan Fernandez
LTC Aaron Farmer
Dr. Chonticha Klungthong
Dr. Piyawan Chinnawirotpisan
Dr. Wudtichai Manasatienkij
Ms. Thipwipha Phonpakobsin
Mr. Khajohn Joonlasak

NAMRU-EURAFCENT
CDR Samuel Levin
Dr. Mayar Said
Bassem Hamdy
Omar Nowar
Dr. Jae Dugan
LCDR Rebecca Pavlicek
LT Emily K. Stefanov

Central Public Health Lab, Jordan
Dr. Mohmaud Gazo

380th Expeditionary Medical Squadron (EMDS), UAE
Lt Col Matthew Stratmeyer

Acknowledgements (2)

NAMRU-SOUTH
LCDR W. Graham
Dr. Sonia Ampuero
Dr. Maria Silva
Mr. Cristopher Cruz
Ms. Gilda Troncos
Ms. Victoria Espejo
Mr. Roger Castillo
Ms. Angélica Espinoza
Ms. Gladys Carrión
Mr. Julio Evangelista
Ms. Patricia Galván
Dr. Yeny Tinoco

NAMRU-INDO PACIFIC
LCDR Nathaniel Christy
Dr. Elizabeth Ashley
Siribun Panapruksachat
Audrey Dubot-Pérès
Dr. KimKee Tan
Mr. Jefree Johari
CAPT Andrew Letizia

WRAIR-Africa
Maj Gen (Dr.) Charles Emilio Mwanziva
Dr. Gerald Misinzo
Dr. Chesnodi Kulanga
Dr. Denis Byarugaba
Dr. Bernard Erima
Dr. Fred Wabwire-Mangen
Dr. Edison Mworozi
Dr. Hannah Kibuuka
Jude Ssensamba
Dr. John Waitumbi
Dr. Beth Mutai
Gathii Kimita
Stephen Ochola
Eric Murimi Muthanje

Recruit Surveillance Sites
Marine Corps Recruit Depot San Diego
Marine Corps Recruit Depot Parris Island
Recruit Training Command Great Lakes
Fort Leonard Wood
Fort Jackson
Lackland Air Force Base

TAMC
Maj Gen (Dr.) Charles Emilio Mwanziva
Dr. Gerald Misinzo
Dr. Chesnodi Kulanga
Dr. Denis Byarugaba
Dr. Bernard Erima
Dr. Fred Wabwire-Mangen
Dr. Edison Mworozi
Dr. Hannah Kibuuka
Jude Ssensamba
Dr. John Waitumbi
Dr. Beth Mutai
Gathii Kimita
Stephen Ochola
Eric Murimi Muthanje

WRAIR-Middle East
MAJ Thomas Musich
Dr. Nino Mitaischvili

Questions?

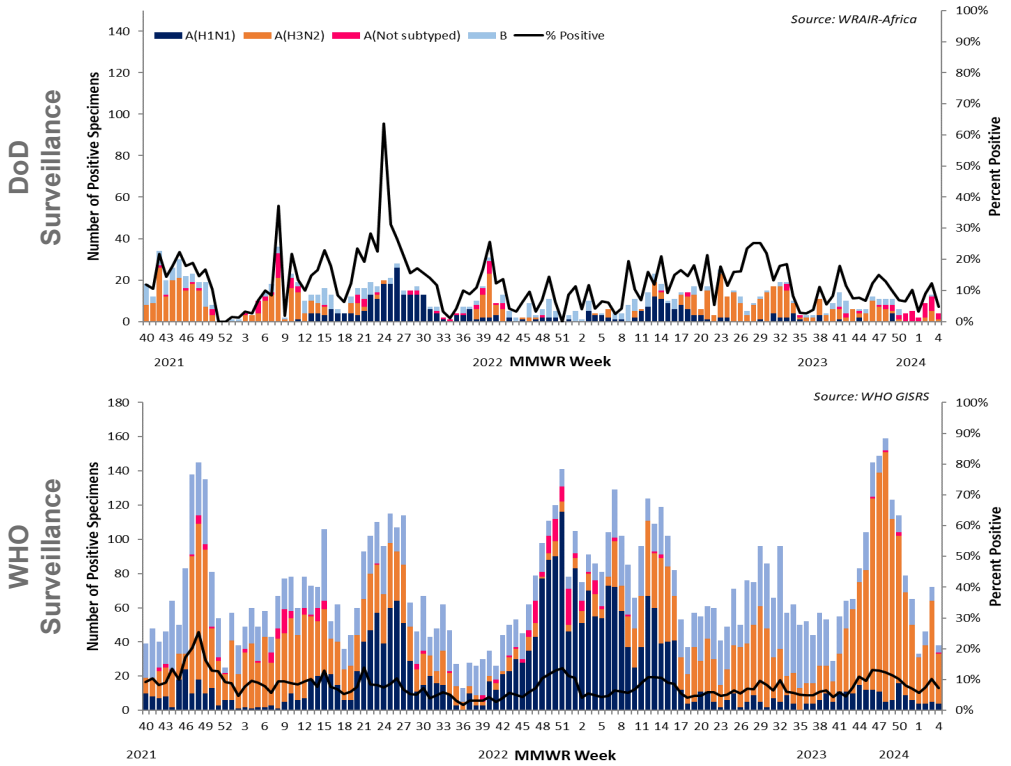
Anthony C. Fries, PhD
Applied Technology & Genomics Division
U.S. Air Force School of Aerospace Medicine Public Health Department
Email: anthony.fries.1@us.af.mil

LCDR Shayne Gallaway, PhD
Respiratory Focus Area Lead, AFHSD-Global Emerging Infections Surveillance Branch
Email: michael.s.gallaway.mil@health.mil

CDR Matthew Kasper, PhD
Chief, AFHSD-Global Emerging Infections Surveillance Branch
Email: matthew.r.kasper2.mil@health.mil

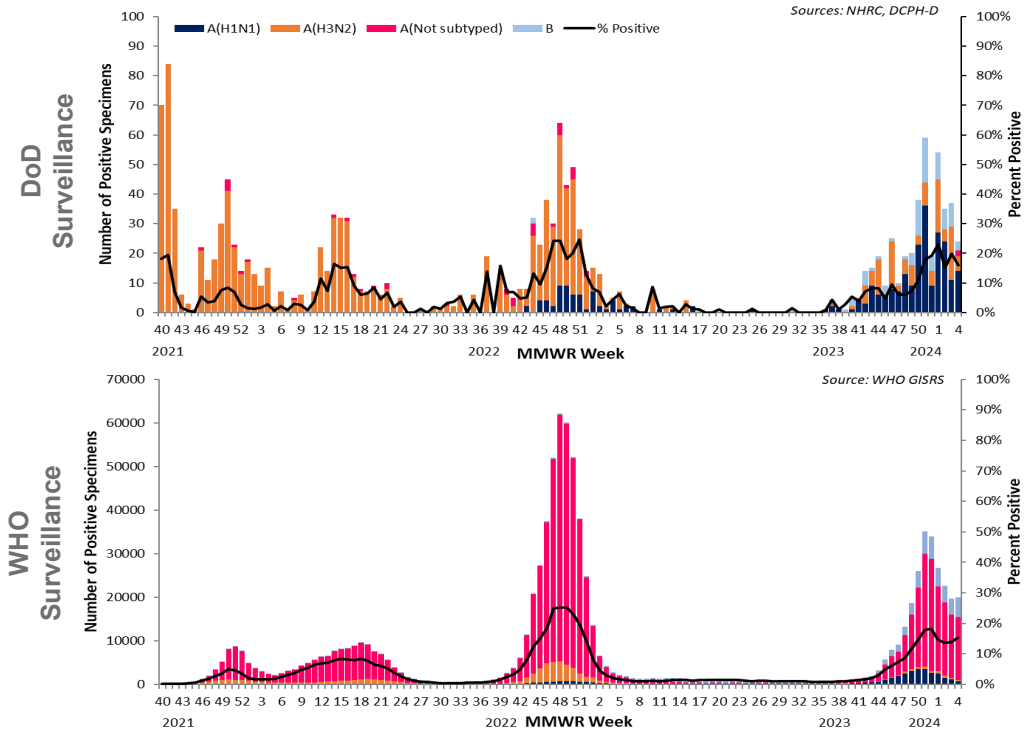
Influenza Surveillance: Subtype Circulation – E. Africa

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization



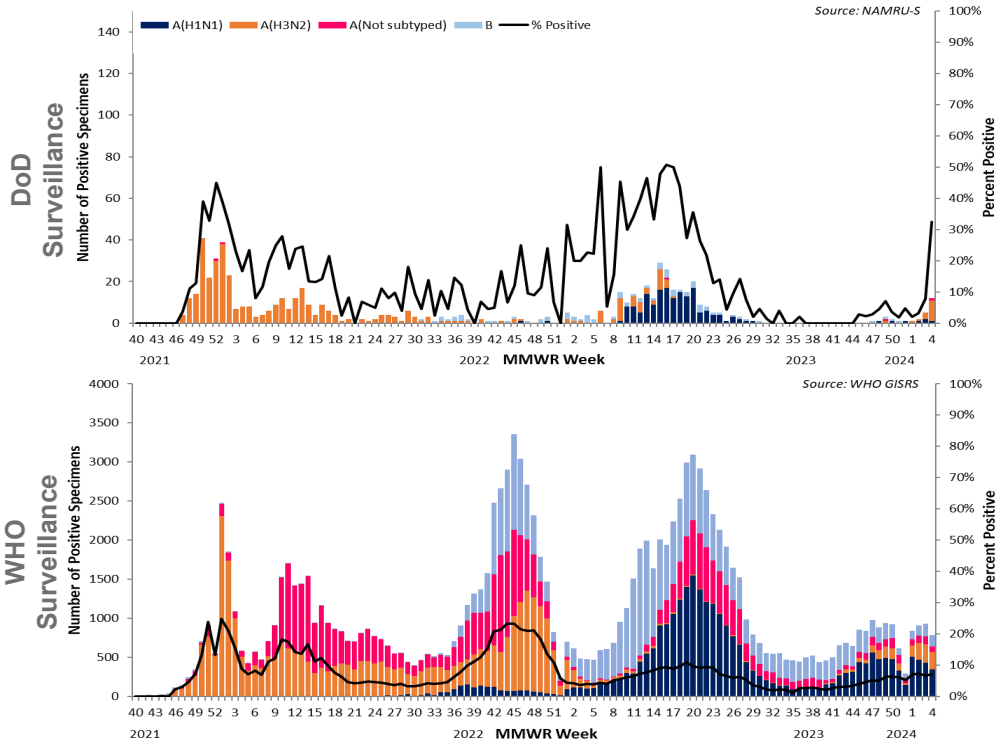
Influenza Surveillance: Subtype Circulation - N. America

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization



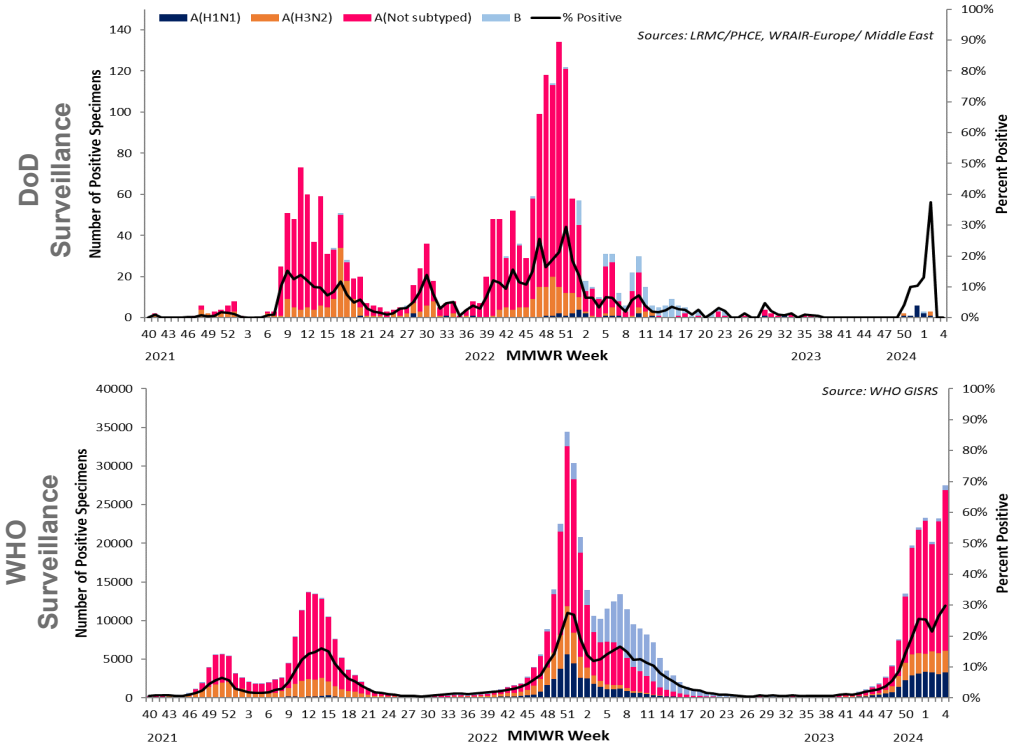
Influenza Surveillance: Subtype Circulation - S. America

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization



Influenza Surveillance: Subtype Circulation - Europe

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization



Influenza Surveillance: Subtype Circulation – Middle East

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization