2024 - OFFLU Swine Influenza virus Technical Meeting

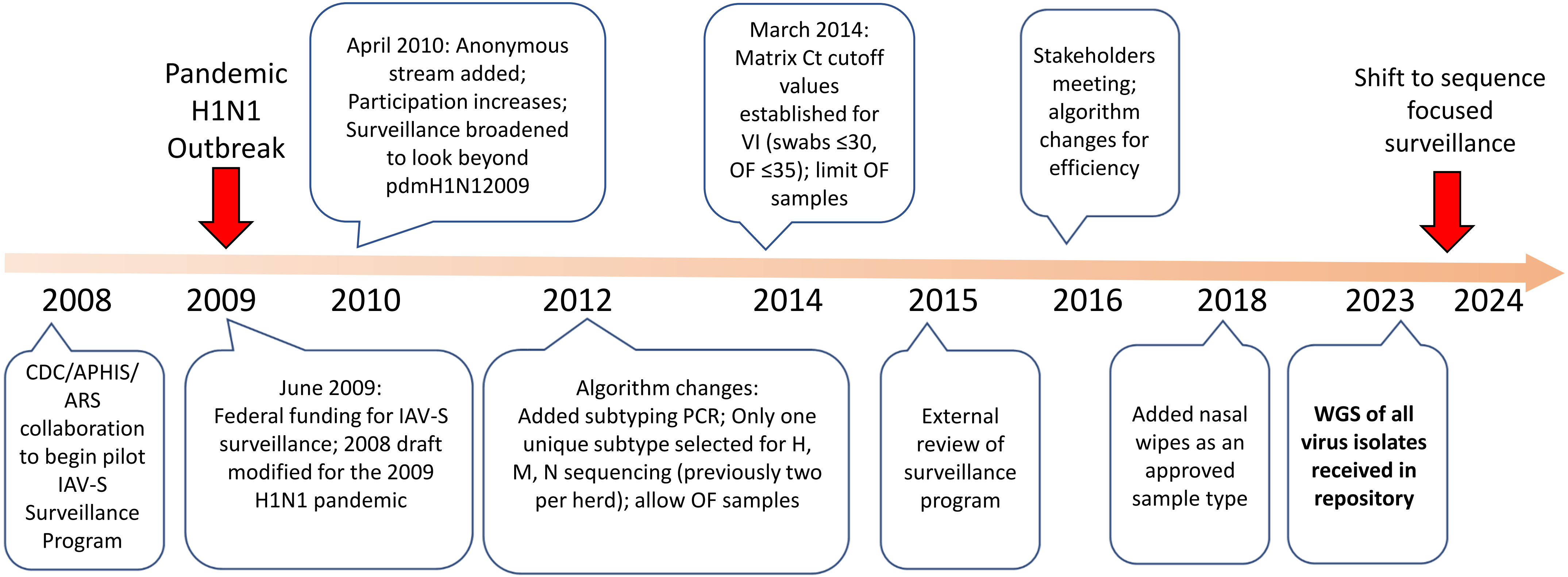
USDA Updates

- Amy Baker, DVM PhD
- Research Veterinary Medical Officer, USDA-ARS National Animal Disease Center, USA
- Dr. Mia Torchetti, DVM MS PhD
- Director, Diagnostic Virology Laboratory, USDA National Veterinary Services Laboratories, USA

offlu
WOAH FAO
network of expertise on animal influenza

3 - 4 April 2024

Surveillance Program Timeline



2008

CDC/APHIS/ ARS collaboration to begin pilot IAV-S Surveillance Program

2009

Pandemic H1N1 Outbreak

June 2009: Federal funding for IAV-S surveillance; 2008 draft modified for the 2009 H1N1 pandemic

2010

April 2010: Anonymous stream added; Participation increases; Surveillance broadened to look beyond pdmH1N12009

2012

Algorithm changes: Added subtyping PCR; Only one unique subtype selected for H, M, N sequencing (previously two per herd); allow OF samples

2014

March 2014: Matrix Ct cutoff values established for VI (swabs ≤30, OF ≤35); limit OF samples

2015

External review of surveillance program

2016

Stakeholders meeting; algorithm changes for efficiency

2018

Added nasal wipes as an approved sample type

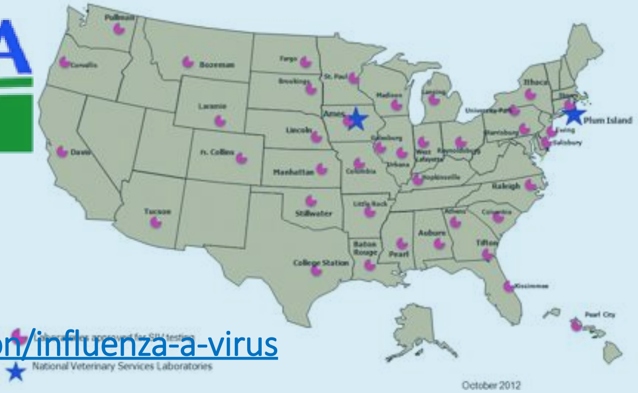
2023

WGS of all virus isolates received in repository

2024

Shift to sequence focused surveillance

- USDA IAV Surveillance System in swine active since 2009
- Virus isolates have HA and NA sequenced for all, WGS for all qualifying at NVSL
- Sequences in GenBank and summary in octoFLUshow at flu-crew.org:
  - A/swine/Iowa/A02524480/2020
- Isolates available through USDA NVSL repository (~11,000 strains available):
  - https://www.aphis.usda.gov/animal_health/lab_info_services/downloads/OrderingIAV-SRepositoryIsolates.pdf
  - Email your request to: nvsl.dvl.comm@usda.gov
- Reports at: https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information/influenza-a-virus



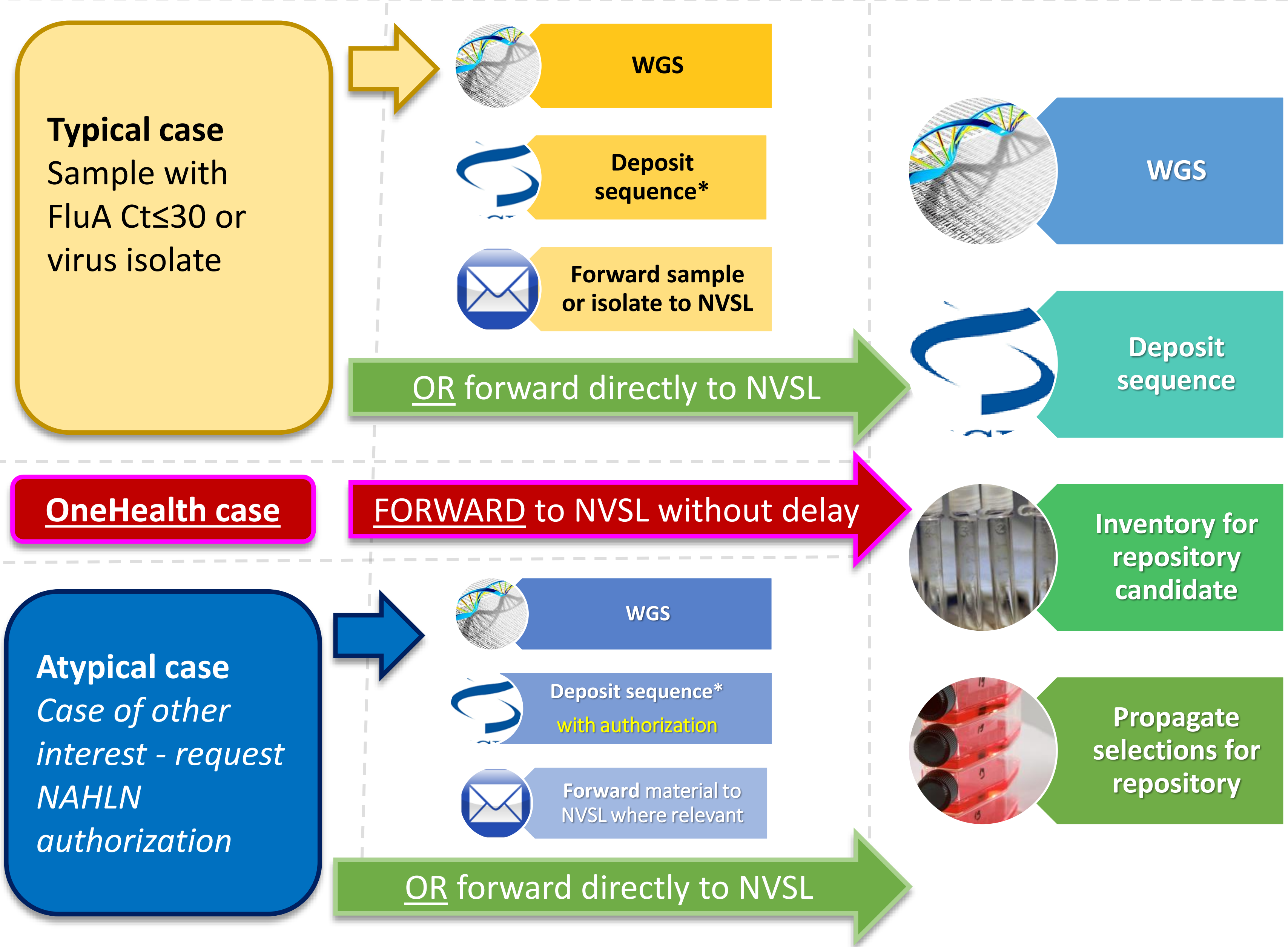
Testing Streams & Repository

1. Case-compatible swine accessions submitted to the NAHLN system
    - Pigs on farm exhibiting influenza-like illness
    - >99% of samples in the surveillance program
2. Swine populations epidemiologically linked to a human case of IAV
3. Swine exhibiting influenza-like illness (ILI) at commingling event (auctions, markets, fairs, or other swine exhibition events).

Transitioning to Ct based threshold for all positive samples- regardless of ILI status

NAHLN

NVSL



Typical case
Sample with FluA Ct≤30 or virus isolate

- **WGS**
- **Deposit sequence***
- **Forward sample or isolate to NVSL**

<u>OR</u> forward directly to NVSL

<u>OneHealth case</u>

<u>FORWARD</u> to NVSL without delay

Atypical case
Case of other interest - request NAHLN authorization

- **WGS**
- **Deposit sequence*** **with authorization**
- **Forward material to NVSL where relevant**

<u>OR</u> forward directly to NVSL

NVSL:

- **WGS**
- **Deposit sequence**
- **Inventory for repository candidate**
- **Propagate selections for repository**

Sample types in order of preference

1. Lung tissue or homogenate
2. Nasal Swab or Nasal wipe (avoid dry swabs or wipes)
3. Udder Wipes (avoid dry wipes)
4. Oral Fluids
5. Other tissues

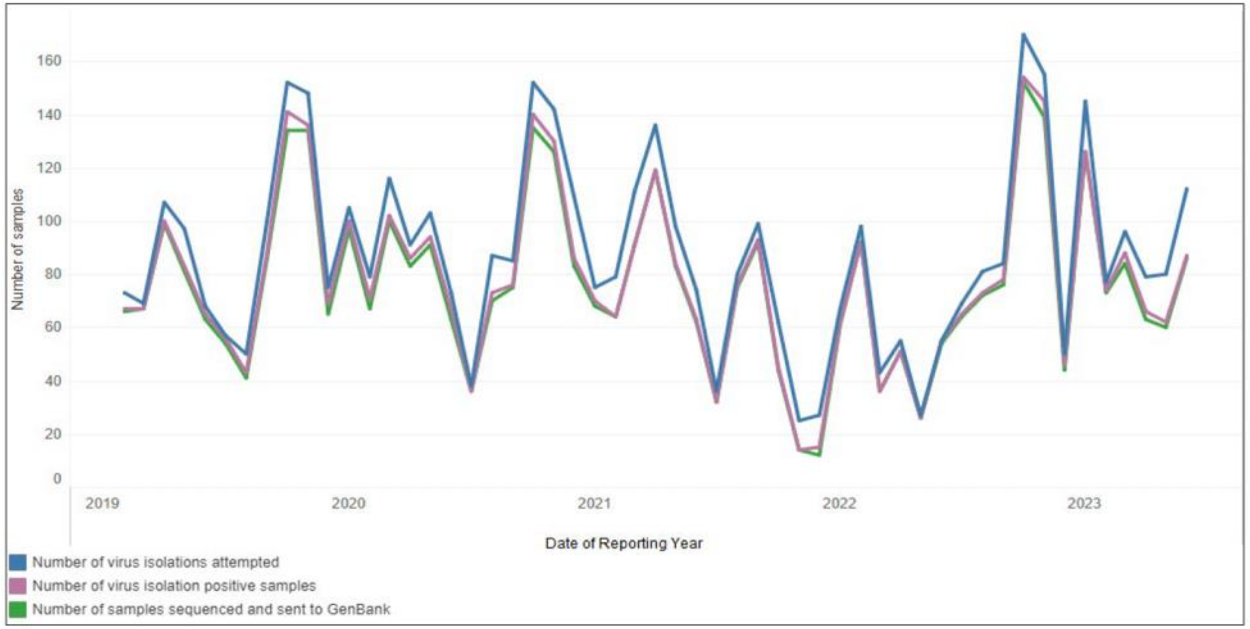
What to forward to NVSL:

- 2 x 1.5mL cryovials per sample
- Include required metadata *with* notation of ILI where present

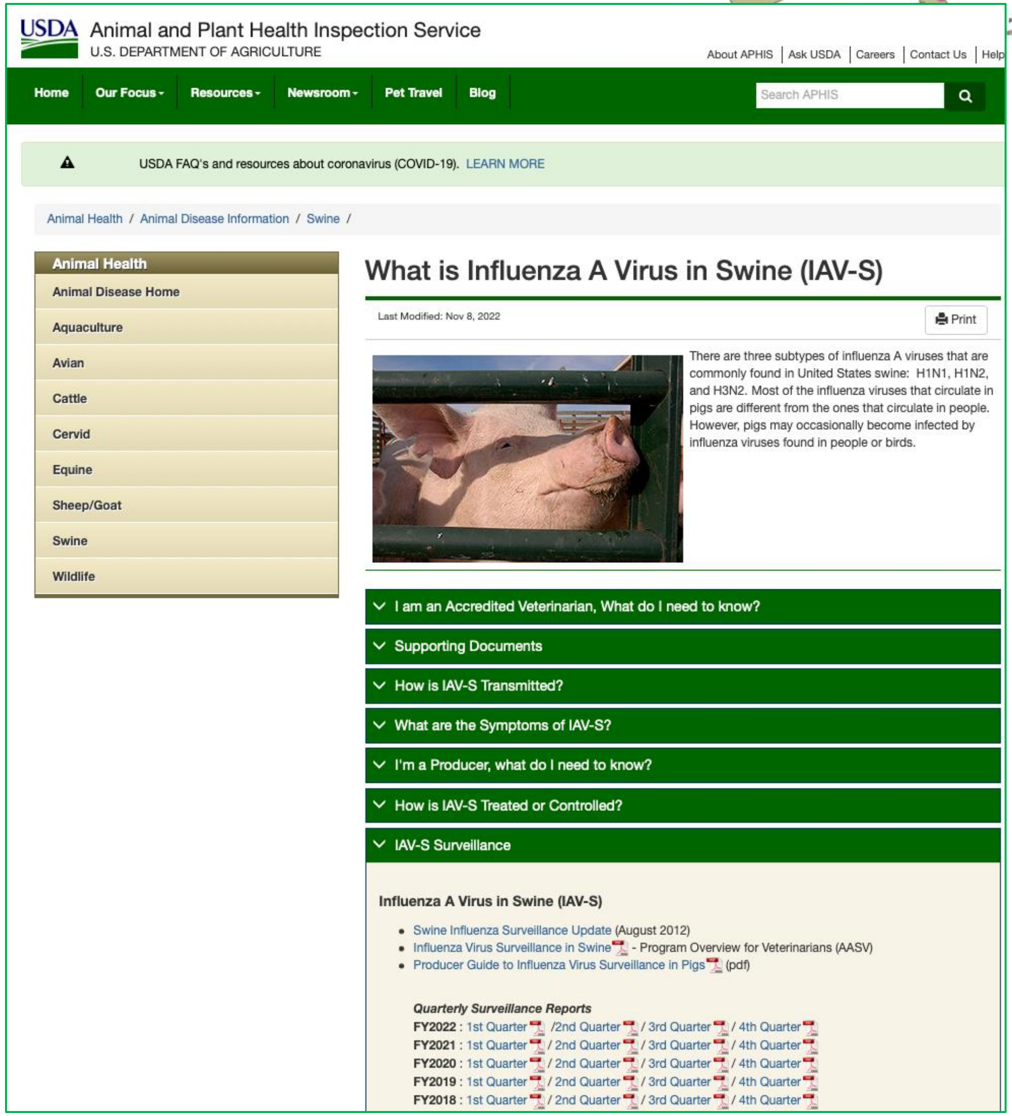
Repository candidates are typically selected based upon sequence

**FASTA upload and FASTQ deposit to specified BioProject*

What IAV are predominant in the U.S. swine population?



- USDA IAV Surveillance System in swine active since 2009
- Virus isolates have HA and NA sequenced for all, WGS for all qualifying at NVSL
- Sequences in GenBank and summary in octoFLUshow at flu-crew.org:
  - A/swine/Iowa/A02524480/2020
- Isolates available through USDA NVSL repository (11,000 strains):
  - https://www.aphis.usda.gov/animal_health/lab_info_services/downloads/OrderingIAV-SRepositoryIsolates.pdf
  - Email your request to: nvsl.dvl.comm@usda.gov
- Reports at: https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information/influenza-a-virus



USDA FAQ's and resources about coronavirus (COVID-19). LEARN MORE

Animal Health / Animal Disease Information / Swine /

What is Influenza A Virus in Swine (IAV-S)

Last Modified: Nov 8, 2022

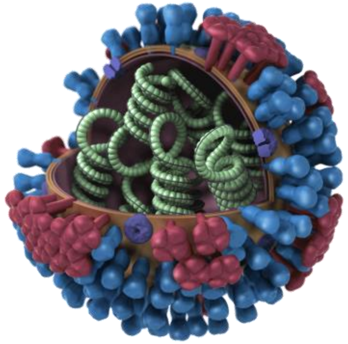
There are three subtypes of influenza A viruses that are commonly found in United States swine: H1N1, H1N2, and H3N2. Most of the influenza viruses that circulate in pigs are different from the ones that circulate in people. However, pigs may occasionally become infected by influenza viruses found in people or birds.

Influenza A Virus in Swine (IAV-S)

- Swine Influenza Surveillance Update (August 2012)
- Influenza Virus Surveillance in Swine - Program Overview for Veterinarians (AASV)
- Producer Guide to Influenza Virus Surveillance in Pigs (pdf)

Quarterly Surveillance Reports

FY2022 : 1st Quarter /2nd Quarter / 3rd Quarter / 4th Quarter
FY2021 : 1st Quarter / 2nd Quarter / 3rd Quarter / 4th Quarter
FY2020 : 1st Quarter / 2nd Quarter / 3rd Quarter / 4th Quarter
FY2019 : 1st Quarter / 2nd Quarter / 3rd Quarter / 4th Quarter
FY2018 : 1st Quarter / 2nd Quarter / 3rd Quarter / 4th Quarter

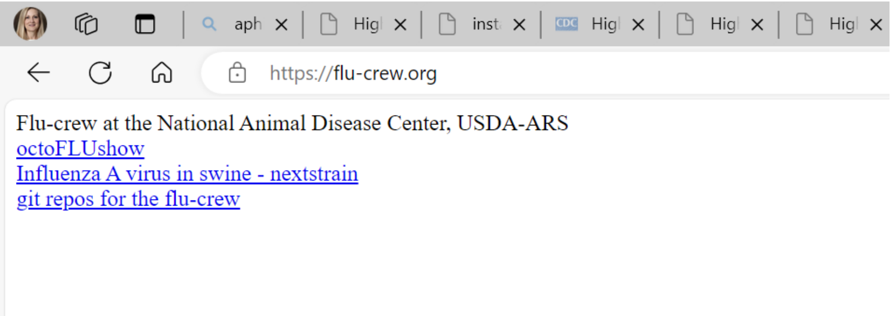


Q1 FY2024 (October-December)

Prepared: March 1, 2024

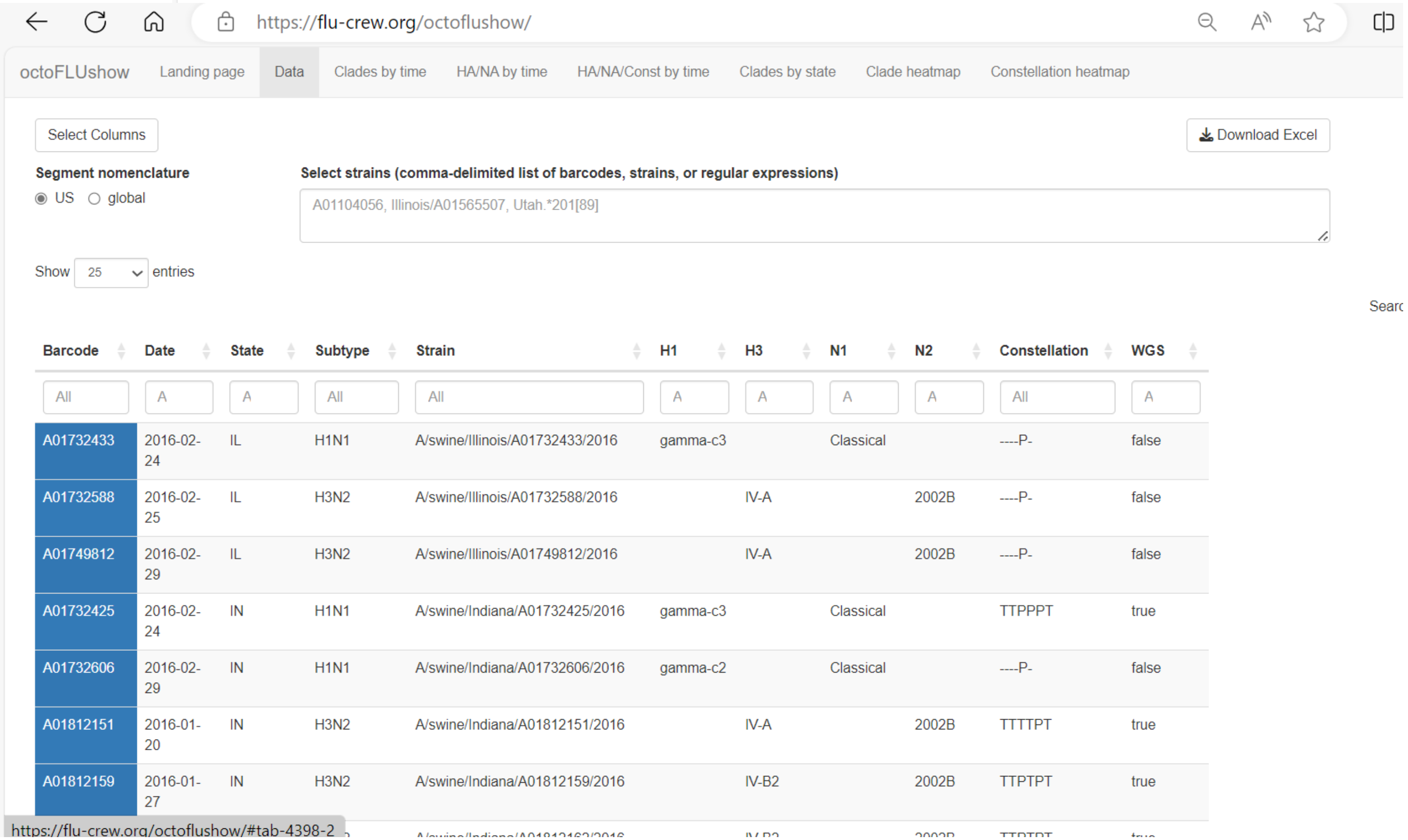
USDA-NADC Team: Blake Inderski & Tavis Anderson

USDA-NVSL
USDA-NAHLN Laboratories
USDA-SPRS
US Swine Producers and Veterinarians



https://flu-crew.org

Flu-crew at the National Animal Disease Center, USDA-ARS
octoFLUshow
Influenza A virus in swine - nextstrain
git repos for the flu-crew



https://flu-crew.org/octoflushow/

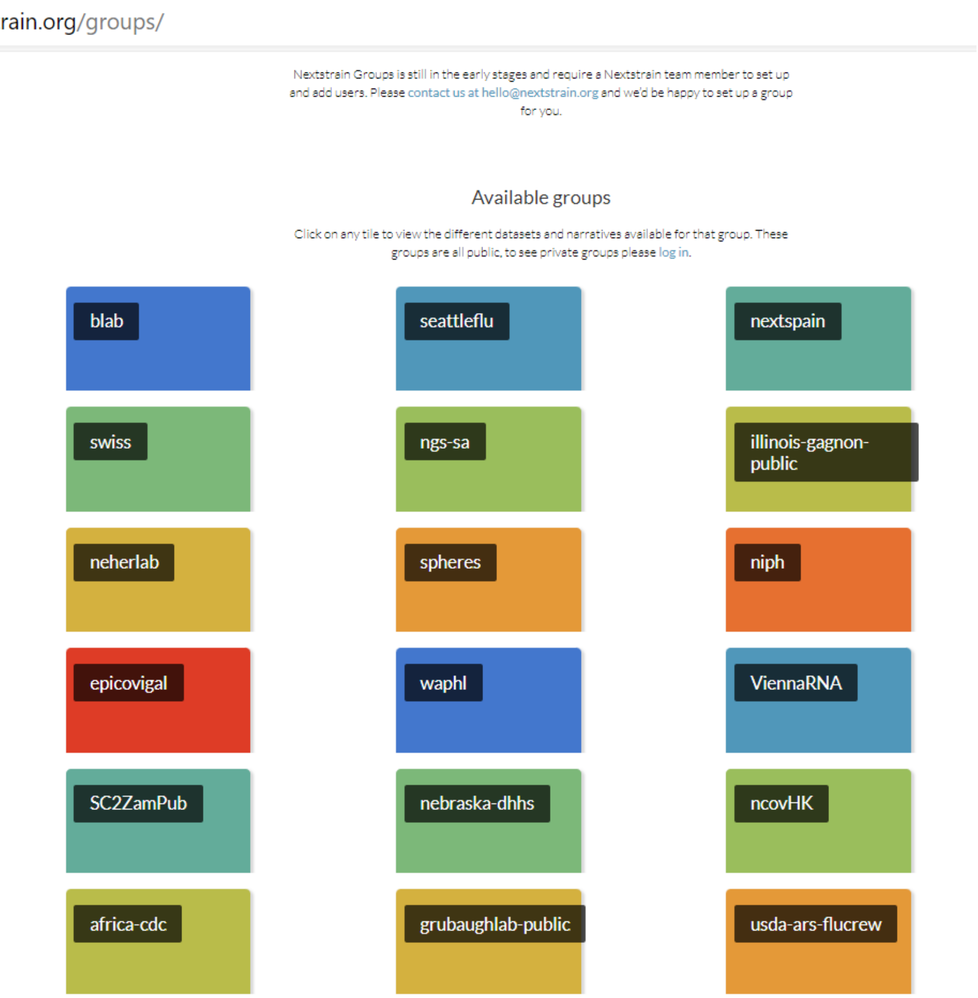
Segment nomenclature
● US ○ global

Select strains (comma-delimited list of barcodes, strains, or regular expressions)
A01104056, Illinois/A01565507, Utah.*201[89]

Show 25 entries

Barcode	Date	State	Subtype	Strain	H1	H3	N1	N2	Constellation	WGS
All	A	A	All	All	A	A	A	A	All	A
A01732433	2016-02-24	IL	H1N1	A/swine/Illinois/A01732433/2016	gamma-c3		Classical		----P-	false
A01732588	2016-02-25	IL	H3N2	A/swine/Illinois/A01732588/2016		IV-A		2002B	----P-	false
A01749812	2016-02-29	IL	H3N2	A/swine/Illinois/A01749812/2016		IV-A		2002B	----P-	false
A01732425	2016-02-24	IN	H1N1	A/swine/Indiana/A01732425/2016	gamma-c3		Classical		TTPPPT	true
A01732606	2016-02-29	IN	H1N1	A/swine/Indiana/A01732606/2016	gamma-c2		Classical		----P-	false
A01812151	2016-01-20	IN	H3N2	A/swine/Indiana/A01812151/2016		IV-A		2002B	TTTTPT	true
A01812159	2016-01-27	IN	H3N2	A/swine/Indiana/A01812159/2016		IV-B2		2002B	TTPTPT	true

https://flu-crew.org/octoflushow/#tab-4398-2



https://nextstrain.org/groups/

Nextstrain Groups is still in the early stages and require a Nextstrain team member to set up and add users. Please contact us at hello@nextstrain.org and we'd be happy to set up a group for you.

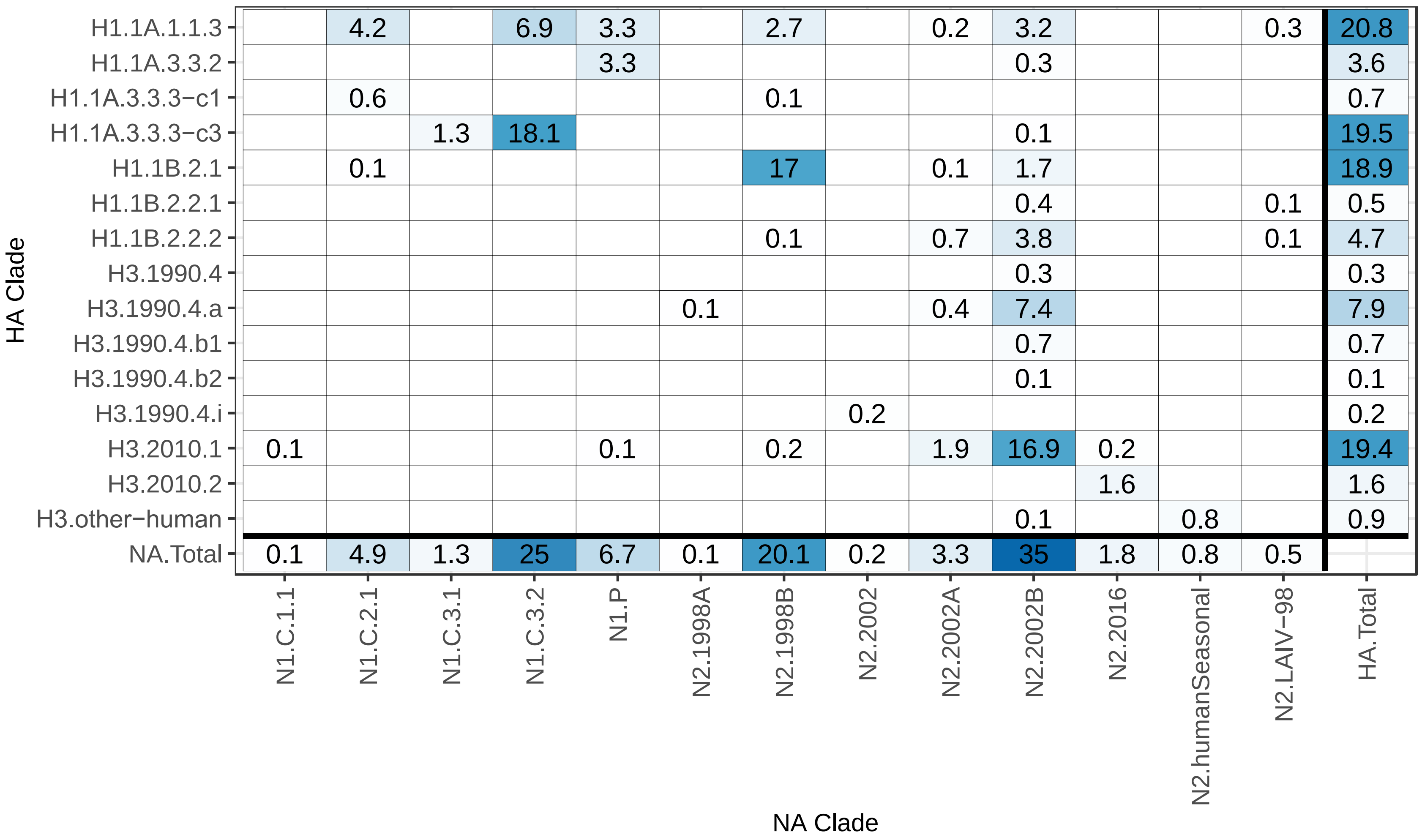
Available groups

Click on any tile to view the different datasets and narratives available for that group. These groups are all public, to see private groups please log in.

IAV-S Surveillance, Summary – Q1FY24

- H1 (n=221), H3 (n=96)
  - 7 H1 clades and 5 H3 clades were detected
  - H1-1A.1.1.3, H1-1A.3.3.3-c3, and H1-1B.2.1 represented 60.9% of all HA detections
  - H3-2010.1 and the H3-1990.4.a represented 28.4% of all HA
- HA clade changes over the last year
  - H1-1A.1.1.3 (+6.7%), H1-1B.2.1 (+2.9%), H3-2010.1 (+2.2%)
  - H3-1990.4.a (-4.8%), H1-1A.3.3.3.-c3 (-3.8%)
- N1 (n=124)
  - N1-C.3.2 represented 70.2% of N1 collections
- N2 (n=193)
  - N2-2002B represented 57.0% of N2 collections
- The most common constellations were TTTPPT (74.4%), TTTTPT (11.2%), and TVVPPT (4.6%)

HA/NA pair frequency over the last year



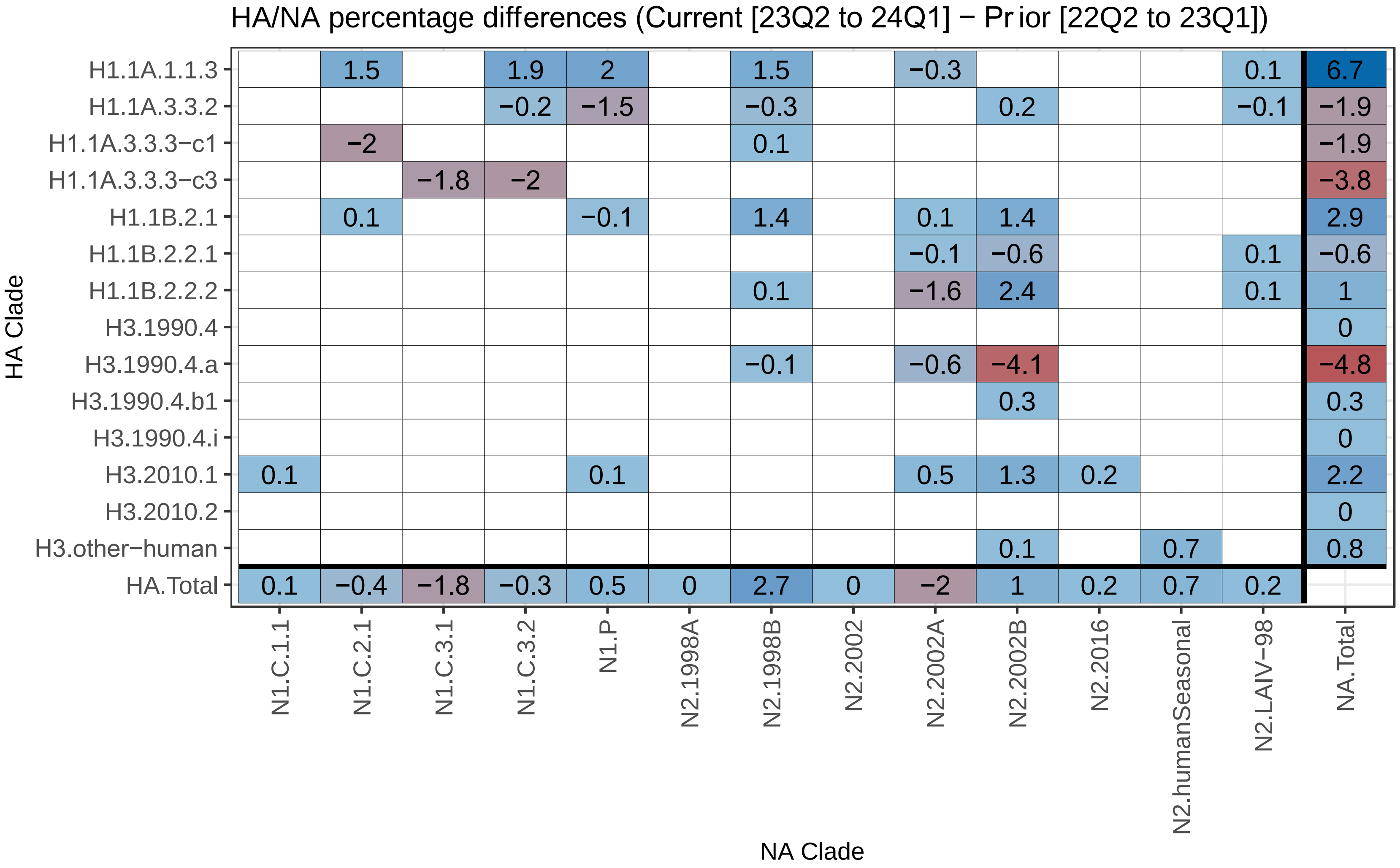
Percentage of HA and NA combinations − Jan 2023 to Dec 2023

HA Clade \ NA Clade	N1.C.1.1	N1.C.2.1	N1.C.3.1	N1.C.3.2	N1.P	N2.1998A	N2.1998B	N2.2002	N2.2002A	N2.2002B	N2.2016	N2.humanSeasonal	N2.LAIV−98	HA.Total
H1.1A.1.1.3		4.2		6.9	3.3		2.7		0.2	3.2			0.3	20.8
H1.1A.3.3.2					3.3					0.3				3.6
H1.1A.3.3.3−c1		0.6					0.1							0.7
H1.1A.3.3.3−c3			1.3	18.1						0.1				19.5
H1.1B.2.1		0.1					17		0.1	1.7				18.9
H1.1B.2.2.1										0.4			0.1	0.5
H1.1B.2.2.2							0.1		0.7	3.8			0.1	4.7
H3.1990.4										0.3				0.3
H3.1990.4.a						0.1			0.4	7.4				7.9
H3.1990.4.b1										0.7				0.7
H3.1990.4.b2										0.1				0.1
H3.1990.4.i								0.2						0.2
H3.2010.1	0.1				0.1		0.2		1.9	16.9	0.2			19.4
H3.2010.2											1.6			1.6
H3.other−human										0.1		0.8		0.9
NA.Total	0.1	4.9	1.3	25	6.7	0.1	20.1	0.2	3.3	35	1.8	0.8	0.5	

Total HA & NA combinations – 975

Number excludes missing data and mixed strains for NA and HA genes

Change in HA/NA pairing from this year and last year

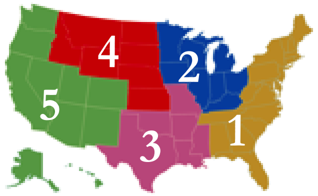


HA/NA percentage differences (Current [23Q2 to 24Q1] − Prior [22Q2 to 23Q1])

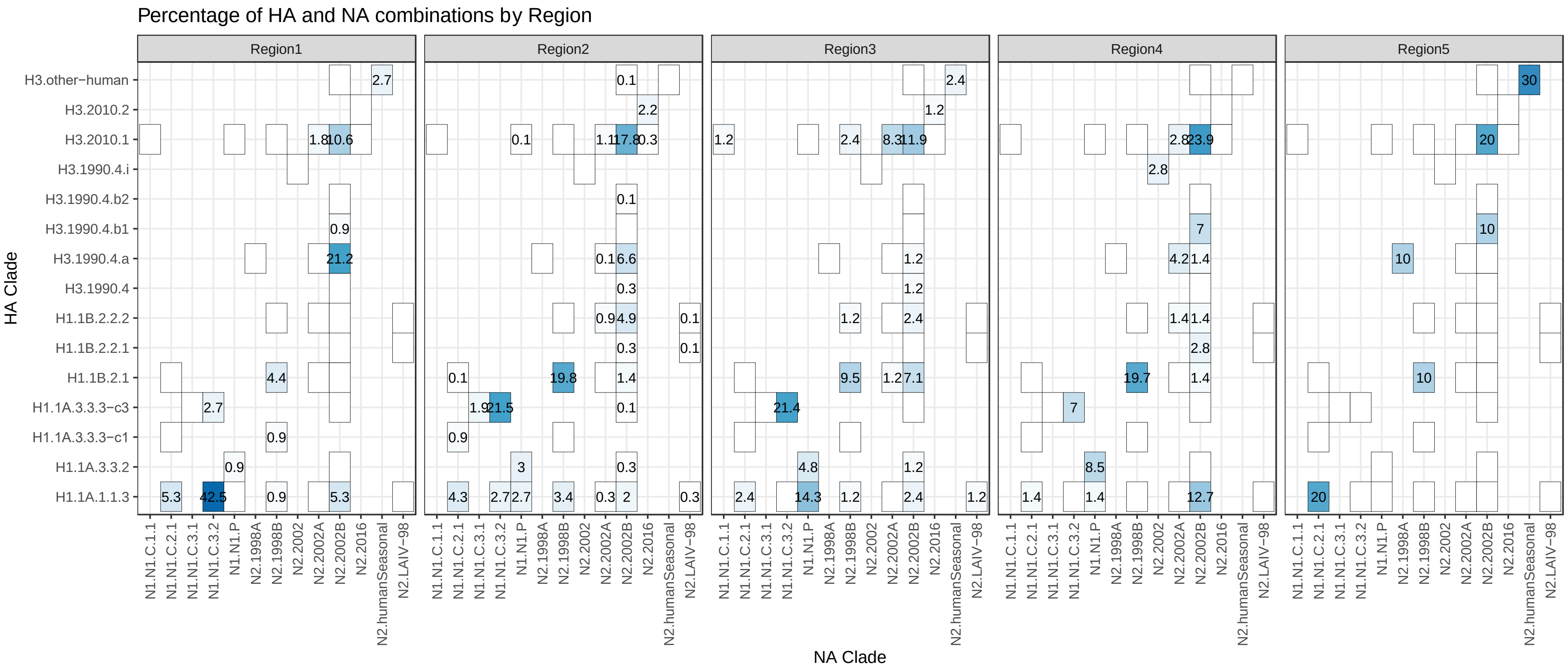
HA Clade	N1.C.1.1	N1.C.2.1	N1.C.3.1	N1.C.3.2	N1.P	N2.1998A	N2.1998B	N2.2002	N2.2002A	N2.2002B	N2.2016	N2.humanSeasonal	N2.LAIV−98	NA.Total
H1.1A.1.1.3		1.5		1.9	2		1.5		−0.3				0.1	6.7
H1.1A.3.3.2				−0.2	−1.5		−0.3			0.2			−0.1	−1.9
H1.1A.3.3.3−c1		−2					0.1							−1.9
H1.1A.3.3.3−c3			−1.8	−2										−3.8
H1.1B.2.1		0.1			−0.1		1.4		0.1	1.4				2.9
H1.1B.2.2.1									−0.1	−0.6			0.1	−0.6
H1.1B.2.2.2							0.1		−1.6	2.4			0.1	1
H3.1990.4														0
H3.1990.4.a							−0.1		−0.6	−4.1				−4.8
H3.1990.4.b1										0.3				0.3
H3.1990.4.i														0
H3.2010.1	0.1				0.1				0.5	1.3	0.2			2.2
H3.2010.2														0
H3.other−human										0.1		0.7		0.8
HA.Total	0.1	−0.4	−1.8	−0.3	0.5	0	2.7	0	−2	1	0.2	0.7	0.2	

Total HA & NA combinations – 975

Number excludes missing data and mixed strains for NA and HA genes



Regional Data: Jan 2023 – Dec 2023



n=113 n=697 n=84 n=71 n=10

IAV-S Surveillance - NADC Representative HA genes

Strain	GenBank	Global Clade
A/swine/Ohio/A02861689/2023	OR491759	H1-1B.2.2.2
A/swine/Iowa/A02861642/2023	OR480701	H1-1B.2.1
A/swine/Iowa/A02861755/2023	OR597068	H1-1A.3.3.2
A/swine/Minnesota/A02978562/2023	OR862105	H1-1A.3.3.3-c3
A/swine/Iowa/A02861940/2023	OR957784	H1-1A.1.1.3
A/swine/Ohio/A02978544/2023	OR636694	H3-1990.4.a
A/swine/Iowa/A02861814/2023	OR677861	H3-2010.1

- *July 2023 to December 2023 USDA HA data downloaded (n = 352 H1, n = 150 H3) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (https://github.com/flu-crew/parnas).*
- *Clades were required to have a detection rate of at least 2% to be considered for selection (n >= 11).*
    - *Omitted H1-1B.2.2.1 (n=1), H1-1A.3.3.3-c1 (n=3), H3-1990.4.i (n=1), H3-1990.4.b1 (n=1), H3-1990.4.b2 (n=1), H3-1990.4 (n=3), H3-2010.2 (n=5)*
- *The 5 H1 selections cover **88%** of observed diversity; the 2 H3 selections cover **55%** of observed diversity.*

IAV-S Surveillance - NADC Representative NA genes

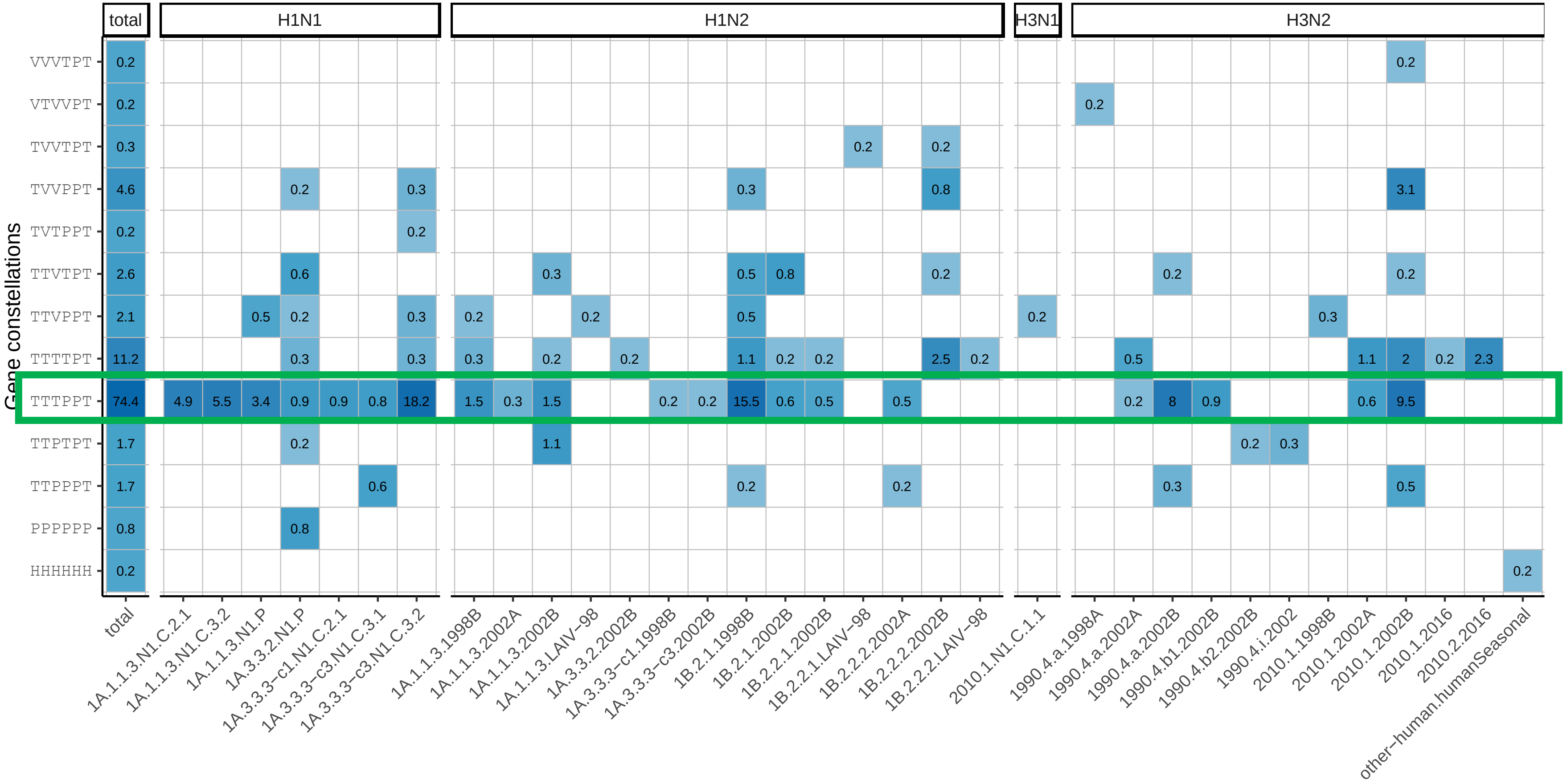
Strain	GenBank	Global Clade
A/swine/Indiana/A02861883/2023	OR792155	N1-P
A/swine/Illinois/A02861792/2023	OR622891	N1-C.2.1
A/swine/Minnesota/A02861972/2023	OR957825	N1-C.3.2
A/swine/Iowa/A02861925/2023	OR840638	N2-2002B
A/swine/Iowa/A02862126/2023	PP103633	N2-1998B
A/swine/Missouri/A02978597/2023	OR862333	N2-2002A

- *July 2023 to December 2023 USDA NA data downloaded (n = 189 N1, n = 313 N2) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (https://github.com/flu-crew/parnas).*
- *Clades were required to have a detection rate of at least 2% to be considered for selection (n >= 9).*
    - *Omitted N1-C.3.1 (n=7), N2-2002 (n=1), N2-2016 (n=6), N2-LAIV (n=3)*
- *The 3 N1 selections cover **75%** of observed diversity; the 3 N2 selections cover **~64%** of observed diversity.*

Whole genome patterns over the 12 months

HA
NA
PB2
PB1
PA
NP
M
NS

Gene Constellations for Jan 2023 to Oct 2023 (n=653)



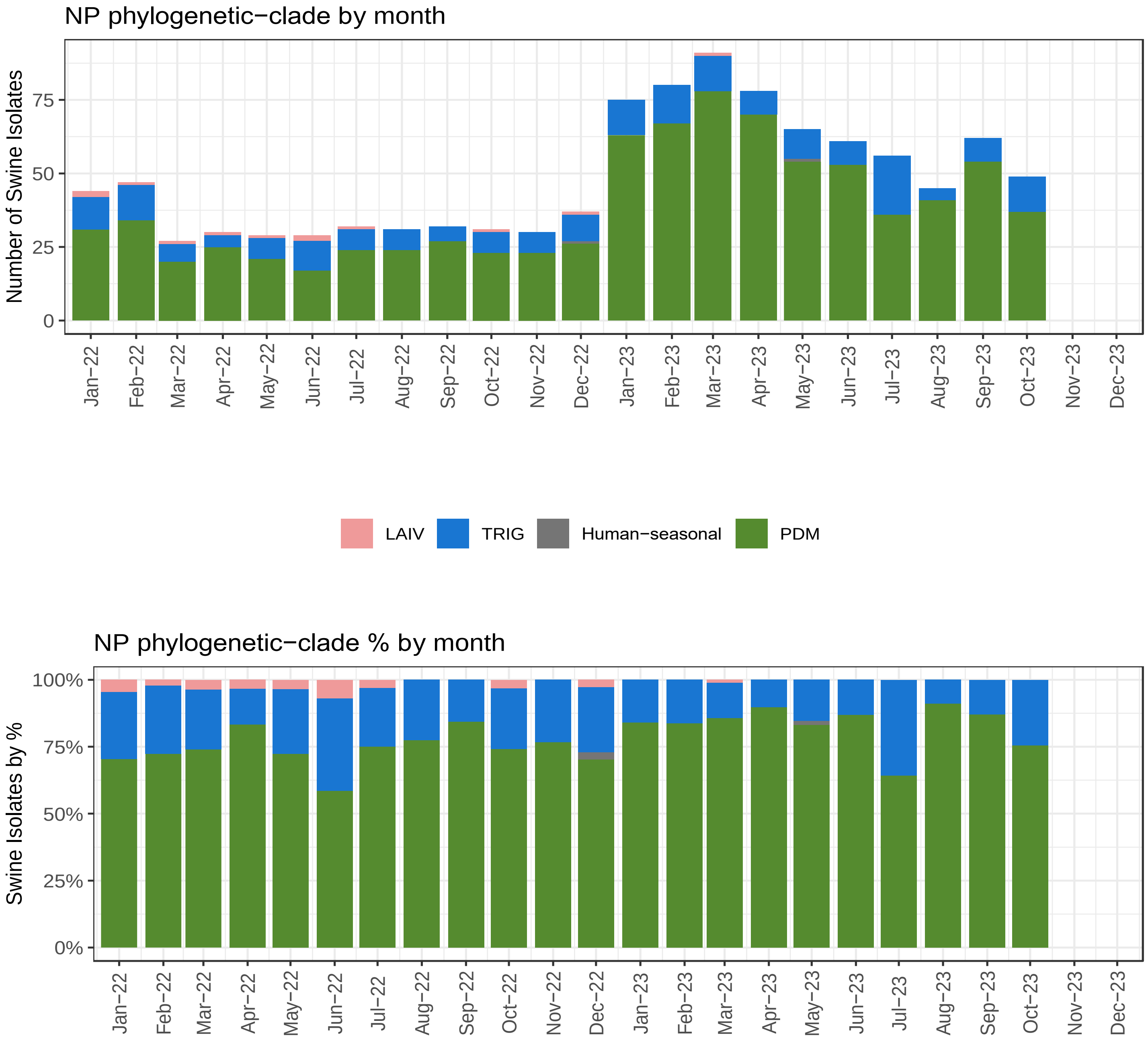
Gene constellations	total	H1N1							H1N2														H3N1	H3N2											
	total	1A.1.1.3.N1.C.2.1	1A.1.1.3.N1.C.3.2	1A.1.1.3.N1.P	1A.3.3.2.N1.P	1A.3.3.3−c1.N1.C.2.1	1A.3.3.3−c3.N1.C.3.1	1A.3.3.3−c3.N1.C.3.2	1A.1.1.3.1998B	1A.1.1.3.2002A	1A.1.1.3.2002B	1A.1.1.3.LAIV−98	1A.3.3.2.2002B	1A.3.3.3−c1.1998B	1A.3.3.3−c3.2002B	1B.2.1.1998B	1B.2.1.2002B	1B.2.2.1.2002B	1B.2.2.1.LAIV−98	1B.2.2.2.2002A	1B.2.2.2.2002B	1B.2.2.2.LAIV−98	2010.1.N1.C.1.1	1990.4.a.1998A	1990.4.a.2002A	1990.4.a.2002B	1990.4.b1.2002B	1990.4.b2.2002B	1990.4.i.2002	2010.1.1998B	2010.1.2002A	2010.1.2002B	2010.1.2016	2010.2.2016	other−human.humanSeasonal
VVVTPT	0.2																															0.2			
VTVVPT	0.2																							0.2											
TVVTPT	0.3																		0.2		0.2														
TVVPPT	4.6				0.2			0.3								0.3					0.8											3.1			
TVTPPT	0.2							0.2																											
TTVTPT	2.6				0.6						0.3					0.5	0.8				0.2					0.2						0.2			
TTVPPT	2.1			0.5	0.2			0.3	0.2			0.2				0.5							0.2							0.3					
TTTTPT	11.2				0.3			0.3	0.3		0.2		0.2			1.1	0.2	0.2			2.5	0.2			0.5						1.1	2	0.2	2.3	
TTTPPT	74.4	4.9	5.5	3.4	0.9	0.9	0.8	18.2	1.5	0.3	1.5			0.2	0.2	15.5	0.6	0.5		0.5					0.2	8	0.9				0.6	9.5			
TTPTPT	1.7				0.2						1.1																	0.2	0.3						
TTPPPT	1.7						0.6									0.2				0.2						0.3						0.5			
PPPPPP	0.8				0.8																														
HHHHHH	0.2																																		0.2

H1N1pdm09 M and now NP genes

- **653 strains with WGS** in total (38.9% are H1N1, 30.5% are H1N2, 30.5% are H3N2 and 0.1% are H3N1)
- 13 unique gene constellations
- 35 unique HA/NA pairs
- Most frequently detected constellations were TTTPPT (74.4%), TTTTPT (11.2%), and TVVPPT (4.6%)

Internal gene constellation in the order of PB2-PB1-PA-NP-M-NS on y-axis: T=TRIG; P=Pandemic; V=Vaccine; H=Human-seasonal

HA
NA
PB2
PB1
PA
NP
M
NS



* incomplete data from November 2023 to December 2023

Novel spillovers detected in surveillance program

Barcode	Date	Strain	H3	N2	Constellation
A02216473	2016-11-14	A/swine/North_Carolina/A02216473/2016(H3N2)	other-human		
A02155577	2018-01-09	A/swine/Illinois/A02155577/2018(H3N2)	other-human		
A02478581	2019-04-22	A/swine/Virginia/A02478581/2019(H3N2)	other-human	human seasonal	HHHHHH
A02478737	2019-06-28	A/swine/Michigan/A02478737/2019(H3N2)	other-human	human seasonal	HHHHHH
A02478738*	**2019-08-29**	**A/swine/Virginia/A02478738/2019(H3N2)**	**other-human**	**human seasonal**	**HHHHHH**
A02751184	2022-11-07	A/swine/North_Carolina/A02751184/2022(H3N2)	other-human		
A02751292	2022-12-01	A/swine/Ohio/A02751292/2022(H3N2)	other-human		
A02751330	2022-12-07	A/swine/North_Carolina/A02751330/2022(H3N2)	other-human		
A02751333*	**2022-12-13**	**A/swine/North_Carolina/A02751333/2022(H3N2)**	**other-human**	**human seasonal**	**HHHHHH**
A02751500	2023-01-09	A/swine/North_Carolina/A02751500/2023(H3N2)	other-human		
A02524408	2023-01-13	A/swine/Missouri/A02524408/2023(H3N2)	other-human	human seasonal	
A02758600	2023-01-19	A/swine/Pennsylvania/A02758600/2023(H3N2)	other-human	human seasonal	
A02758601	2023-01-26	A/swine/Illinois/A02758601/2023(H3N2)	other-human	2002B	
A02758605	2023-02-07	A/swine/Missouri/A02758605/2023(H3N2)	other-human	human seasonal	
A02758604	2023-02-17	A/swine/Indiana/A02758604/2023(H3N2)	other-human		
A02758606	2023-04-26	A/swine/Colorado/A02758606/2023(H3N2)	other-human	human seasonal	
A02758607	2023-05-01	A/swine/North_Carolina/A02758607/2023(H3N2)	other-human	human seasonal	
A02758608	2023-05-10	A/swine/Colorado/A02758608/2023(H3N2)	other-human	human seasonal	
A02758609	2023-05-11	A/swine/Colorado/A02758609/2023(H3N2)	other-human	human seasonal	
A02758610*	**2023-05-22**	**A/swine/North_Carolina/A02758610/2023(H3N2)**	**other-human**	**human seasonal**	**HHHHHH**

***Available in Repository**

*** other-human represents novel human-to-swine spillovers from the 2022-23 human seasonal H3 flu season**

World Health Organization

offlu
WOAH FAO
network of expertise on animal influenza

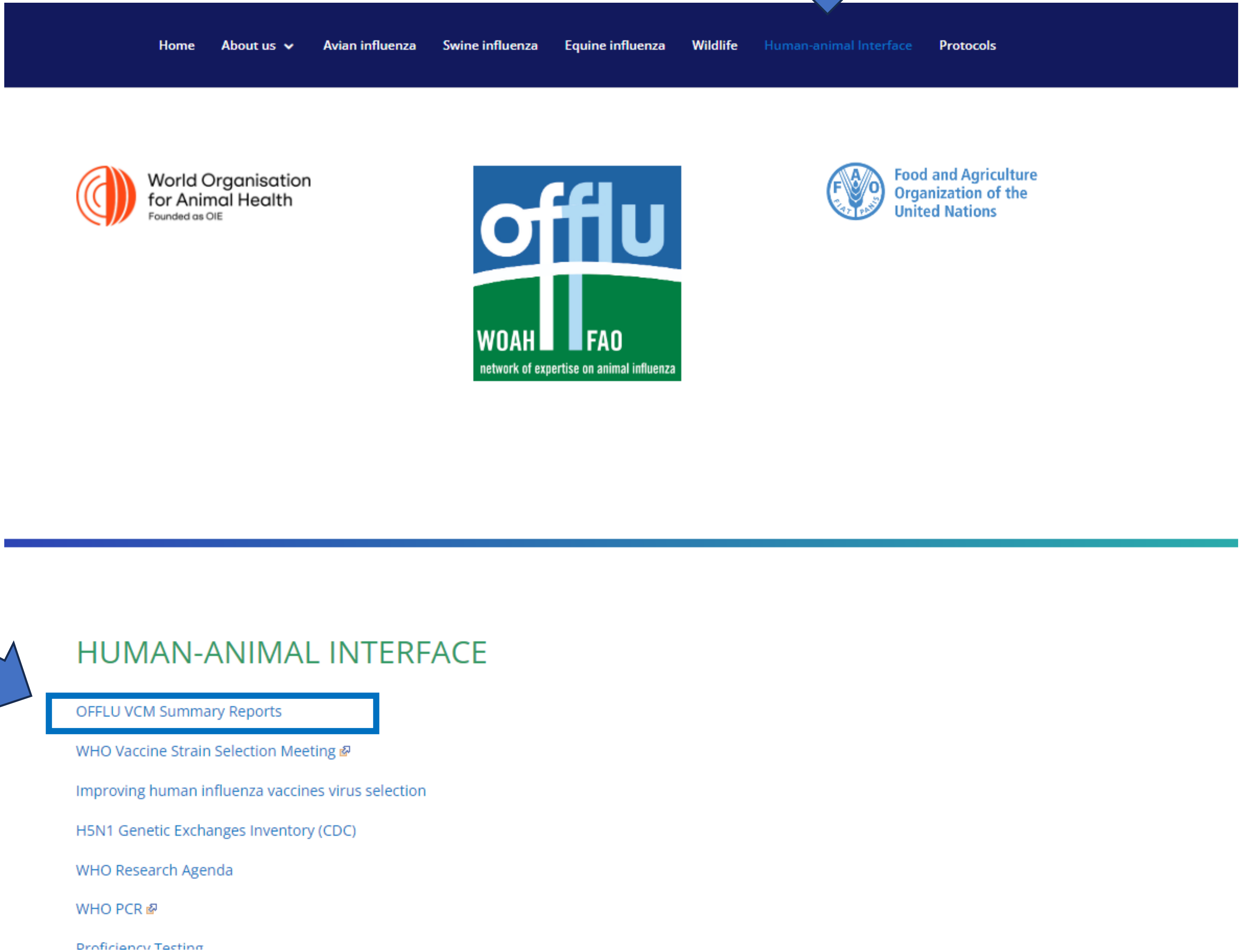
Genetic and antigenic characteristics of zoonotic influenza A viruses and development of candidate vaccine viruses for pandemic preparedness

February 2024

OFFLU SWINE INFLUENZA REPORT

JULY 2023 TO DECEMBER 2023

OFFLU.org



HUMAN-ANIMAL INTERFACE

OFFLU VCM Summary Reports

WHO Vaccine Strain Selection Meeting

Improving human influenza vaccines virus selection

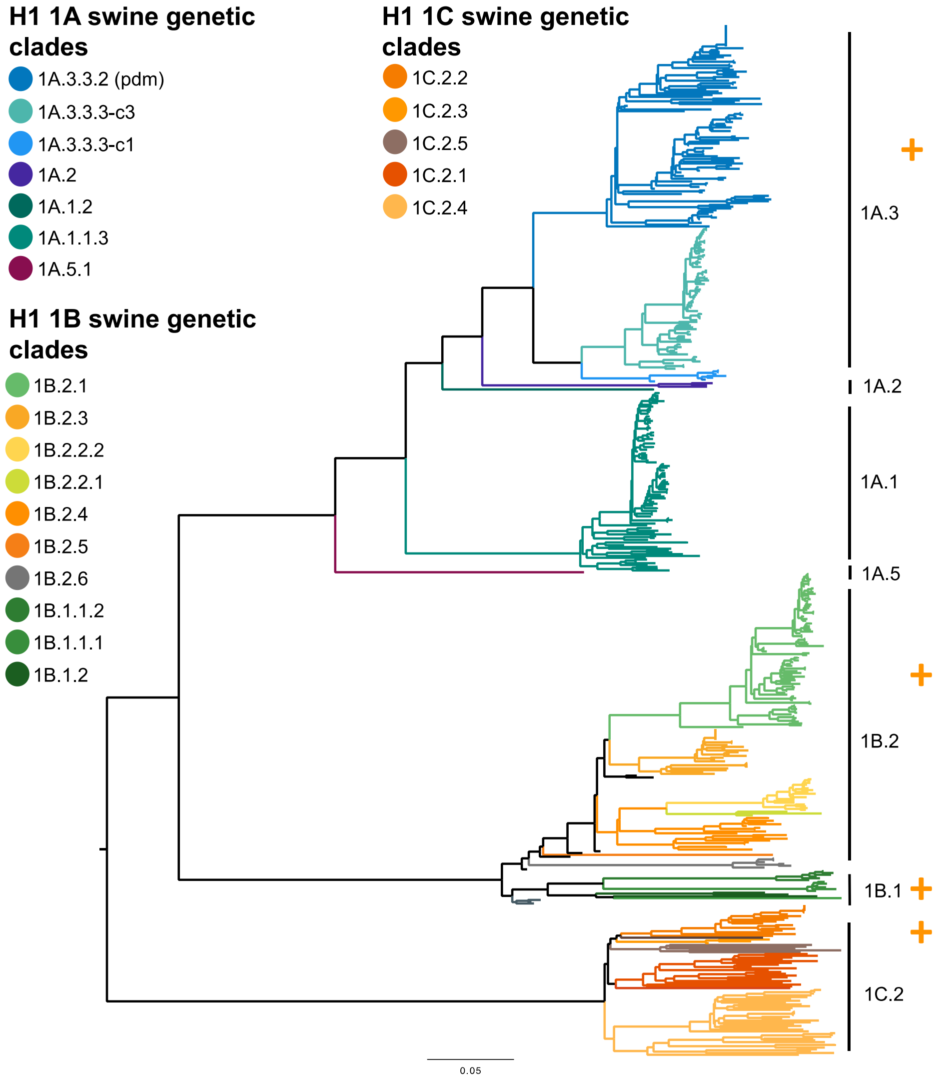
H5N1 Genetic Exchanges Inventory (CDC)

WHO Research Agenda

WHO PCR

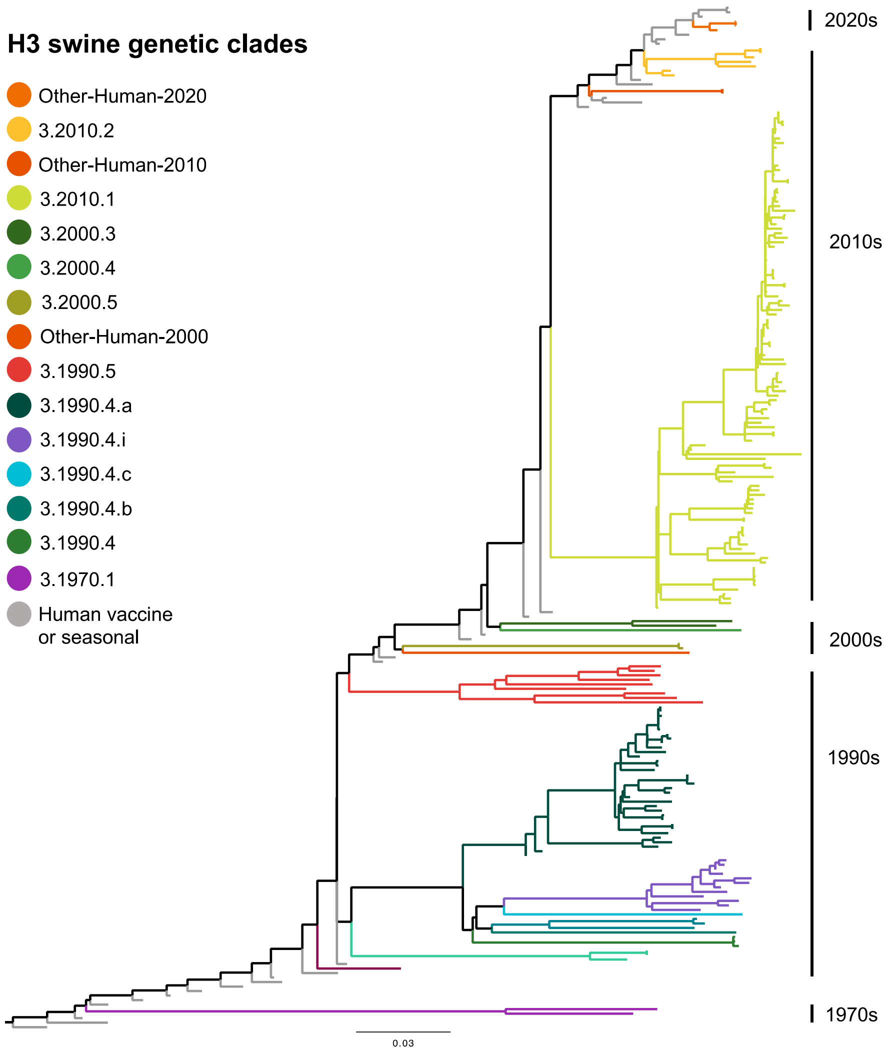
Proficiency Testing

Contemporary Global H1 swine IAV: genetic diversity



n=512, data deposited within last 6 months.

Contemporary Global H3 swine IAV: genetic diversity

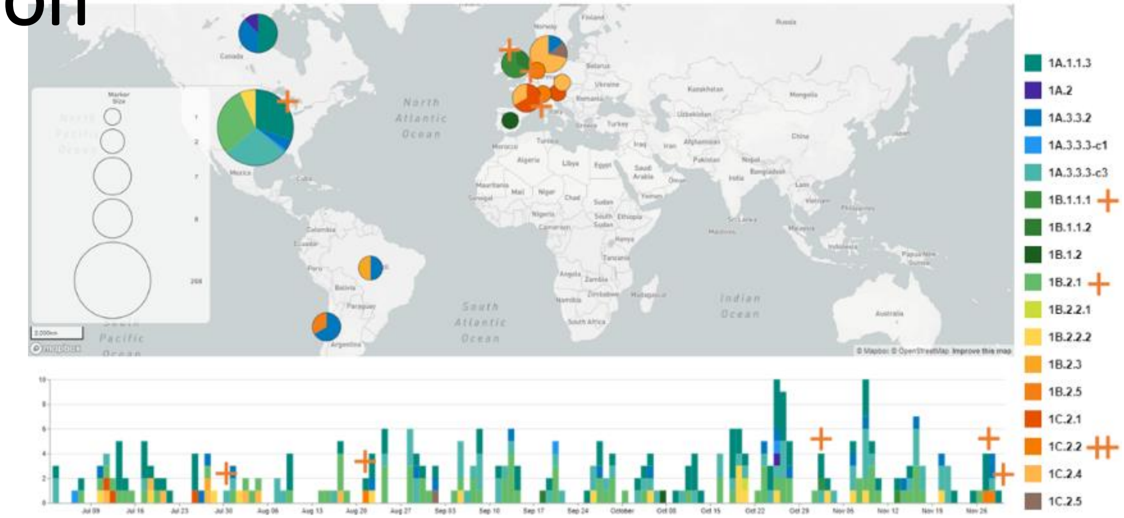


n=173, data deposited within last 6 months, and n=55 reference genes.

Over 680 swine influenza detections from 39 lineages in 24 countries.

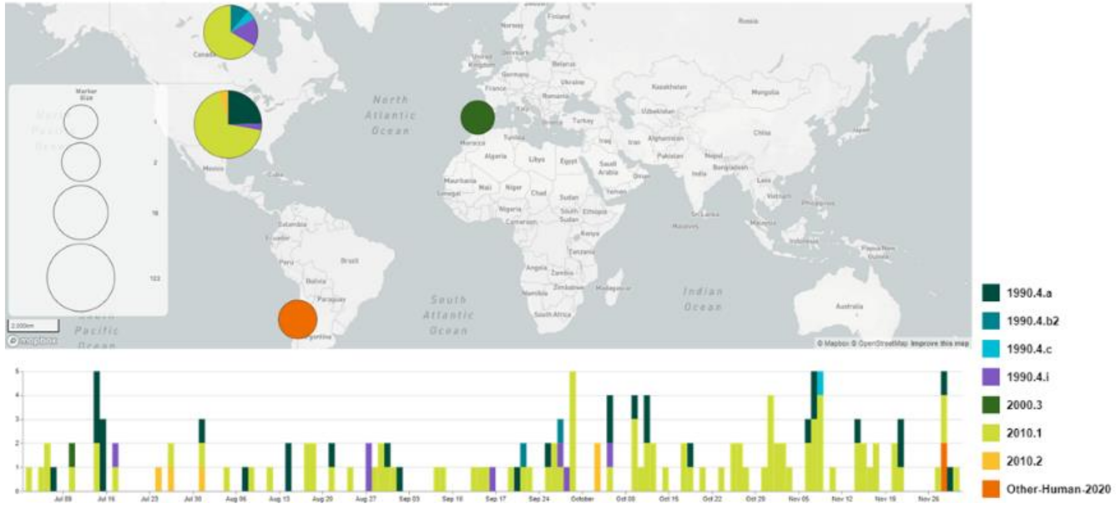
Swine H1 geographic distribution

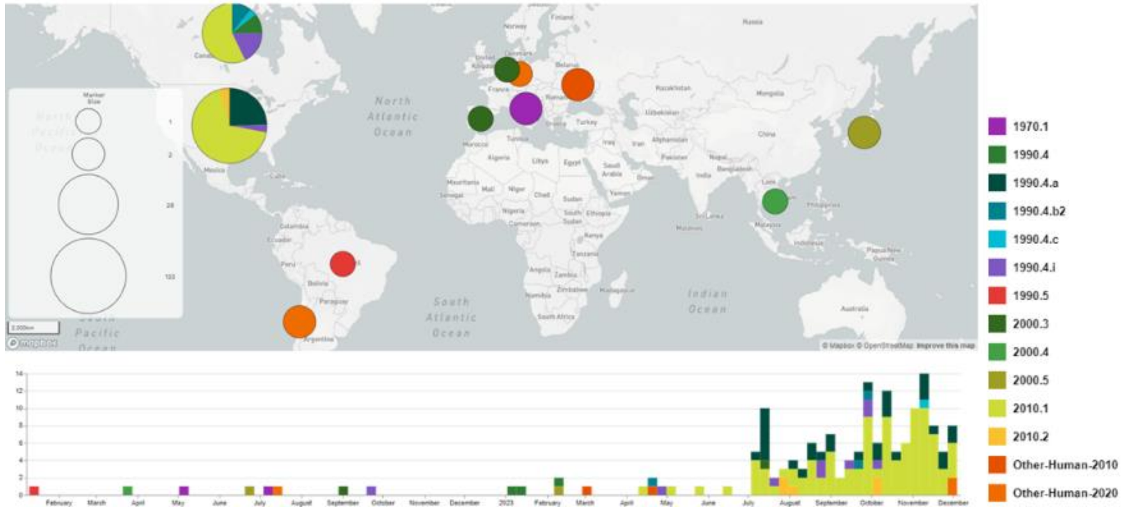
- 22 clades were H1 subtype, with detections from: 1A classical swine lineage (7 clades); 1B human-seasonal lineage (10 clades); and 1C Eurasian avian lineage (5 clades).
  - The 1A classical swine lineage viruses have global detection: 1A.1.1.3 in USA and Canada; 1A.2 in Canada; 1A.3.3.3-c1 in USA; 1A.3.3.3-c3 in USA and Canada; 1A.5.1 in Japan. The 1A.3.3.2 (pdm09) circulated in all countries that deposited sequence (5 countries).
  - 1B.1 human seasonal lineage was only in Europe, and the 1B.2 human seasonal lineage was only in the Americas.
  - The 1C.2 Eurasian avian lineage was detected in Europe. Additional detections of 1C.2 were reported in Asia outside the reporting period of Jan 1 – June 30, 2023.
  - **Diversity, detection frequency in swine, and H1N2v in the United Kingdom warranted new nomenclature: 1B.1.1.1, 1B.1.1.2, and 1B.1.1.3**.
  - **Undersurveilled regions reported novel clades including: 1A.1.2 (Cambodia), 1B.2.3 (Brazil), 1B.2.4 (Brazil), 1B.2.5 (Chile), and 1B.2.6 (Brazil).**



Swine H3
geographic distribution

- 12 H3 clades were detected in swine in 8 distinct lineages grouped by the decade of introduction (1970.1; 1990.4; 1990.5; 2000.3; 2000.4; 2000.5; 2010.1; 2010.2) **and 3 novel human seasonal spillovers (Other-Human-2000, Other-Human-2010, Other-Human-2020).**
  - Most lineages exhibited regional circulation: the 1970.1 lineage in Italy; the 1990.5 lineage in Brazil; the 2000.4 in Cambodia; the 2000.5 lineage was detected in Japan; and the 2010.2 lineage was detected in the USA.
  - The remaining lineages demonstrated broader distributions: the 1990.4 lineage was detected in the USA and Canada; and the 2010.1 lineage was detected in the USA and Canada.
  - Regionally restricted lineages had new detections outside of prior geography: 2010.1 (Canada); 2000.3 (Netherlands).
  - **Undersurveilled regions reported an uncharacterized lineage, 2000.4 (Cambodia). Novel human-to-swine spillovers were detected in Brazil (Other-Human-2000), the Ukraine (Other-Human-2010), and Germany and Chile (Other-Human-2020).**





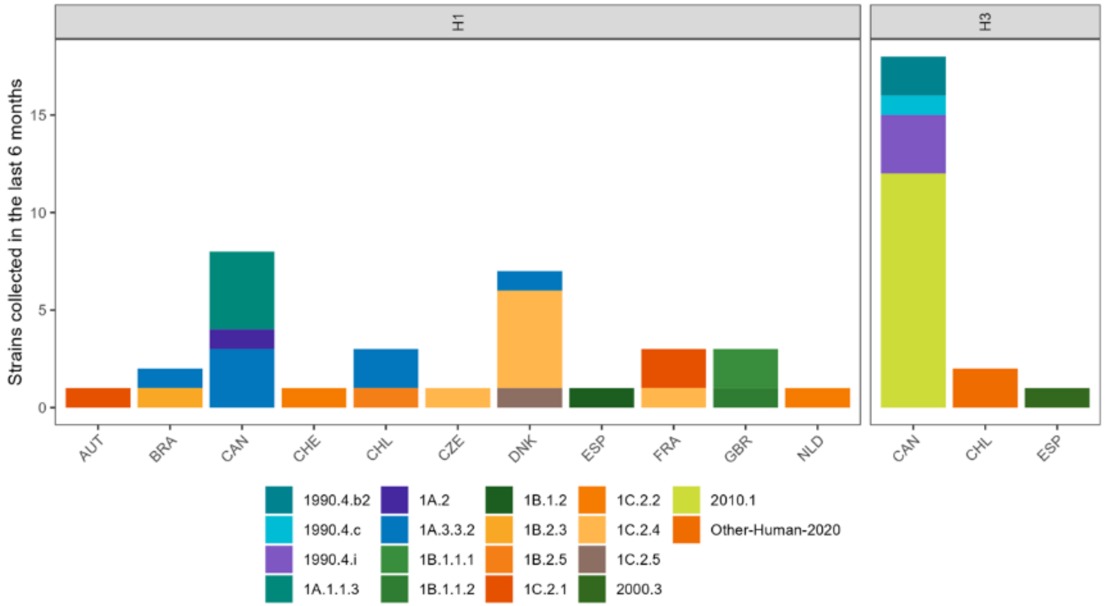
Participation outside of USA

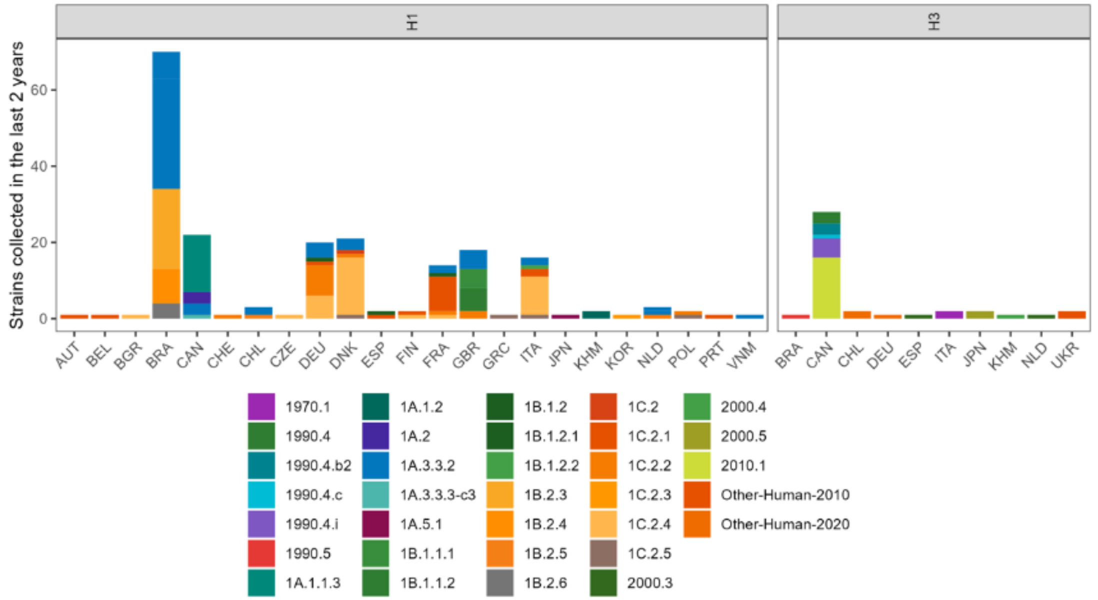
NIH National Library of Medicine
National Center for Biotechnology Information

GISAID

offlu
WOAH FAO
network of expertise on animal influenza

ESFLU
European Swine Influenza Network





EMERGING INFECTIOUS DISEASES®
ISSN: 1080-6059

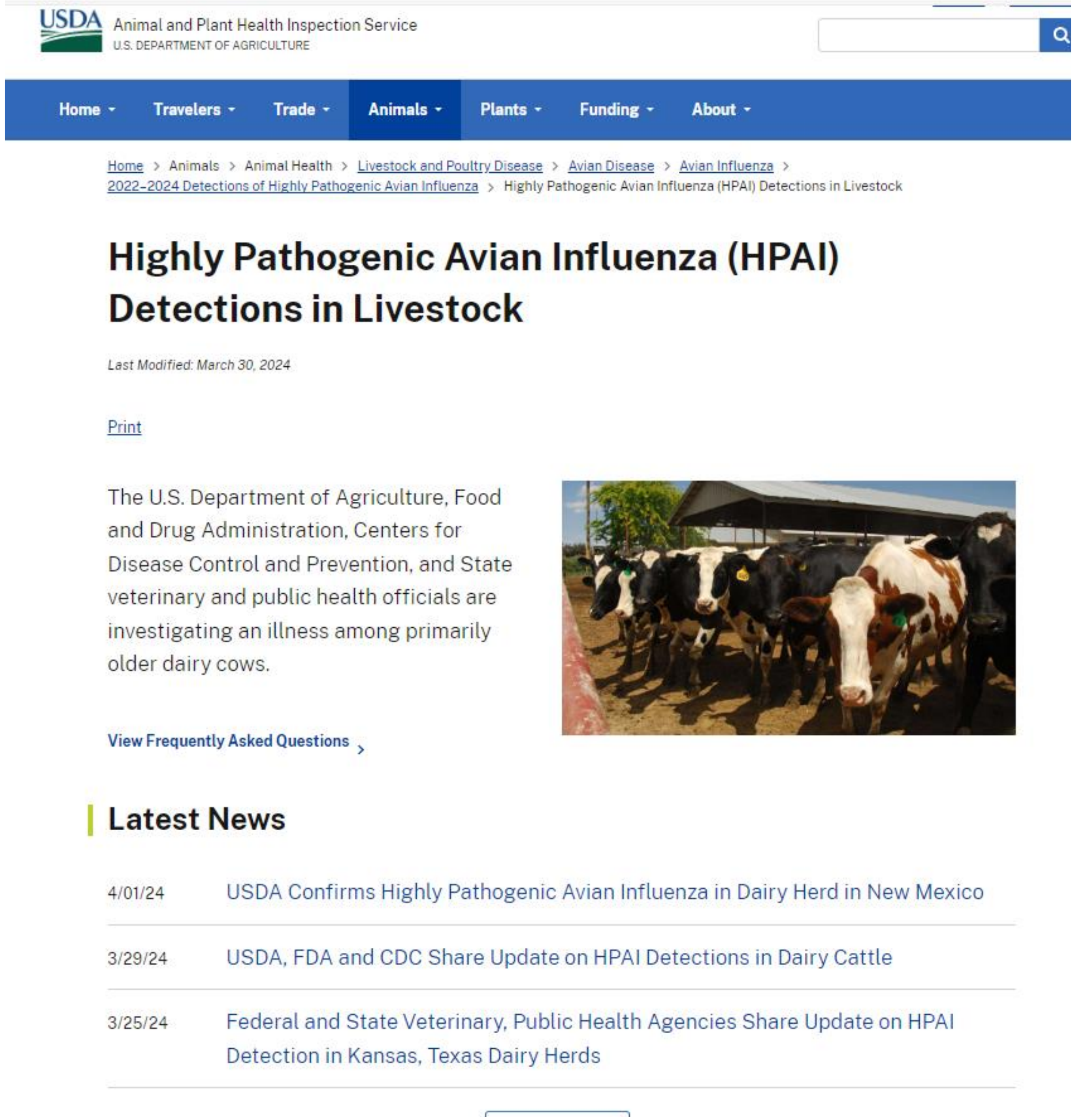
Volume 30, Number 4—April 2024

Research

Divergent Pathogenesis and Transmission of Highly Pathogenic Avian Influenza A(H5N1) in Swine

Bailey Arruda✉ , Amy L. Vincent Baker, Alexandra Buckley, Tavis K. Anderson, Mia Torchetti, Nichole Hines Bergeson, Mary Lea Killian, and Kristina Lantz
Author affiliations: Agriculture Research Service, Ames, Iowa, USA (B. Arruda, A.L. Vincent Baker, A. Buckley, T.K. Andersen); Animal and Plant Health Inspection Service, Ames (M. Torchetti, N. Hines Bergeson, M.L. Killian, K. Lantz)

US Cattle Updates: Mia, Marie, Amy



Highly Pathogenic Avian Influenza (HPAI) Detections in Livestock

Last Modified: March 30, 2024

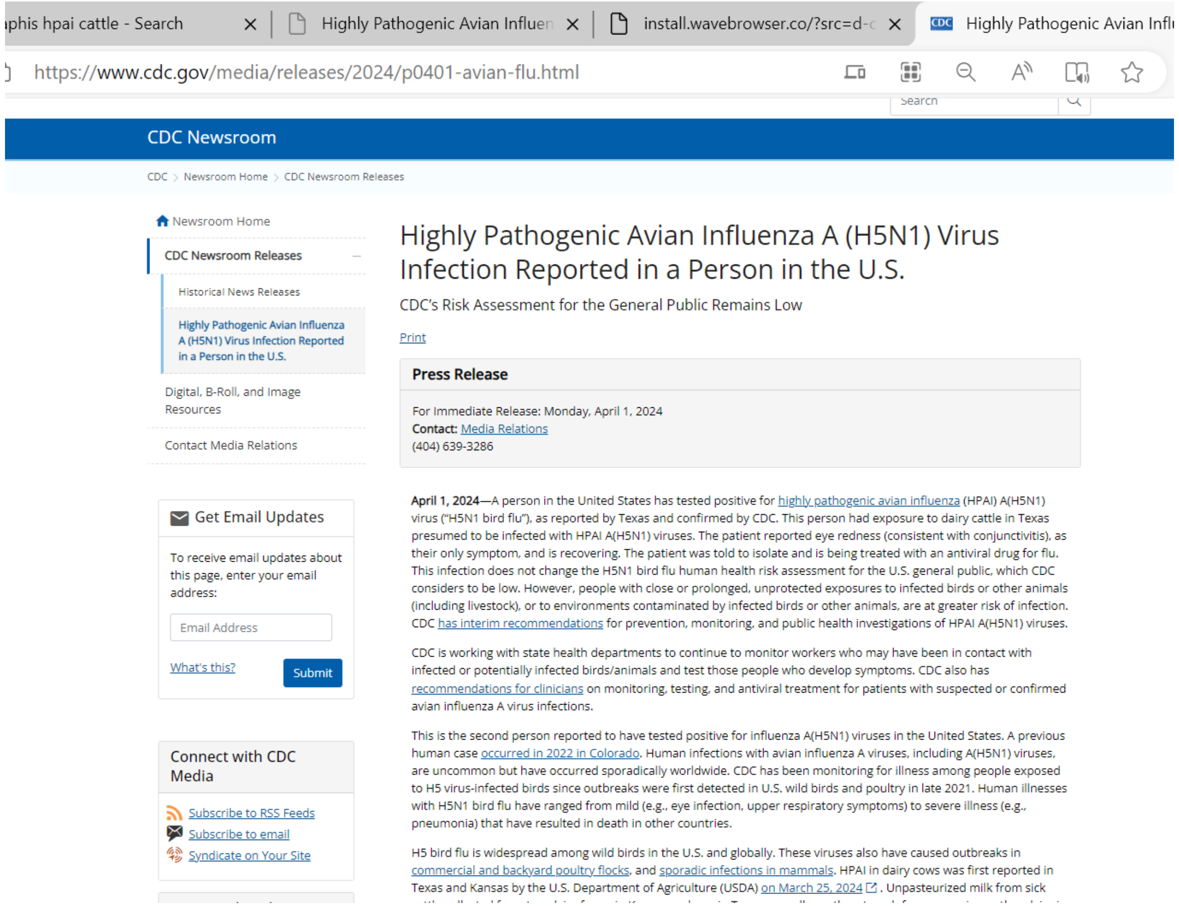
Print

The U.S. Department of Agriculture, Food and Drug Administration, Centers for Disease Control and Prevention, and State veterinary and public health officials are investigating an illness among primarily older dairy cows.

View Frequently Asked Questions ›

Latest News

4/01/24	USDA Confirms Highly Pathogenic Avian Influenza in Dairy Herd in New Mexico
3/29/24	USDA, FDA and CDC Share Update on HPAI Detections in Dairy Cattle
3/25/24	Federal and State Veterinary, Public Health Agencies Share Update on HPAI Detection in Kansas, Texas Dairy Herds



Highly Pathogenic Avian Influenza A (H5N1) Virus Infection Reported in a Person in the U.S.

CDC's Risk Assessment for the General Public Remains Low

Print

Press Release

For Immediate Release: Monday, April 1, 2024
Contact: Media Relations
(404) 639-3286

April 1, 2024—A person in the United States has tested positive for highly pathogenic avian influenza (HPAI) A(H5N1) virus ("H5N1 bird flu"), as reported by Texas and confirmed by CDC. This person had exposure to dairy cattle in Texas presumed to be infected with HPAI A(H5N1) viruses. The patient reported eye redness (consistent with conjunctivitis), as their only symptom, and is recovering. The patient was told to isolate and is being treated with an antiviral drug for flu. This infection does not change the H5N1 bird flu human health risk assessment for the U.S. general public, which CDC considers to be low. However, people with close or prolonged, unprotected exposures to infected birds or other animals (including livestock), or to environments contaminated by infected birds or other animals, are at greater risk of infection. CDC has interim recommendations for prevention, monitoring, and public health investigations of HPAI A(H5N1) viruses.

CDC is working with state health departments to continue to monitor workers who may have been in contact with infected or potentially infected birds/animals and test those people who develop symptoms. CDC also has recommendations for clinicians on monitoring, testing, and antiviral treatment for patients with suspected or confirmed avian influenza A virus infections.

This is the second person reported to have tested positive for influenza A(H5N1) viruses in the United States. A previous human case occurred in 2022 in Colorado. Human infections with avian influenza A viruses, including A(H5N1) viruses, are uncommon but have occurred sporadically worldwide. CDC has been monitoring for illness among people exposed to H5 virus-infected birds since outbreaks were first detected in U.S. wild birds and poultry in late 2021. Human illnesses with H5N1 bird flu have ranged from mild (e.g., eye infection, upper respiratory symptoms) to severe illness (e.g., pneumonia) that have resulted in death in other countries.

H5 bird flu is widespread among wild birds in the U.S. and globally. These viruses also have caused outbreaks in commercial and backyard poultry flocks, and sporadic infections in mammals. HPAI in dairy cows was first reported in Texas and Kansas by the U.S. Department of Agriculture (USDA) on March 25, 2024. Unpasteurized milk from sick

Acknowledgements

NADC Flu Crew

- Tavis Anderson
- Katharine Young
- Alexey Markin
- Garrett Janzen
- Blake Inderski
- Carine Souza
- Celeste Snyder
- Bailey Arruda
- Nick Otis
- Alexa Buckley
- Giovana Zanella
- Megan Neveau Thomas
- Meghan Wymore Brand
- Janice Ciacci Zanella
- Debora Goulart
- Alessandra Campos

Collaborators

- Phil Gauger
- Seema Lakdawala & Val Le Sage
- Scott Hensley
- Ben Cowling
- Todd Davis
- OFFLU Swine Network
- US Pork Producers & Swine Vets
- Nicola Lewis & APHA
- Mia Torchetti & NVSL
- Alicia Janas-Martindale
- Daniela Rajao
- Daniel Perez
- Bryan Kaplan
- Brian Kimble
- Joshua Powell

offlu
WOAH FAO
network of expertise on animal influenza

Funding:

USDA

CEIRR
CENTERS OF EXCELLENCE FOR INFLUENZA RESEARCH AND RESPONSE

CDC

offlu

WOAH FAO

network of expertise on animal influenza

Thank you