

USDA Surveillance and Research Updates

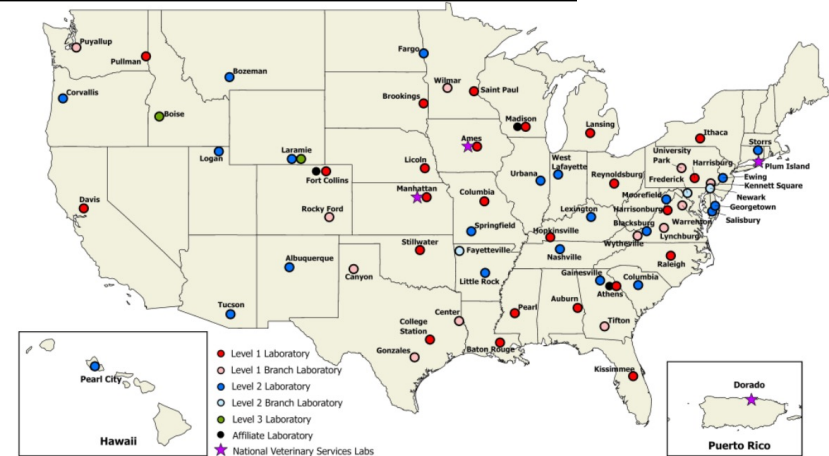
Amy Baker, Tavis Anderson &
Mia Torchetti
USDA-ARS & USDA-APHIS-VS

OFFLU SWINE INFLUENZA EXPERTS TECHNICAL MEETING
28 – 29 April 2026
WOAH Headquarters, Paris

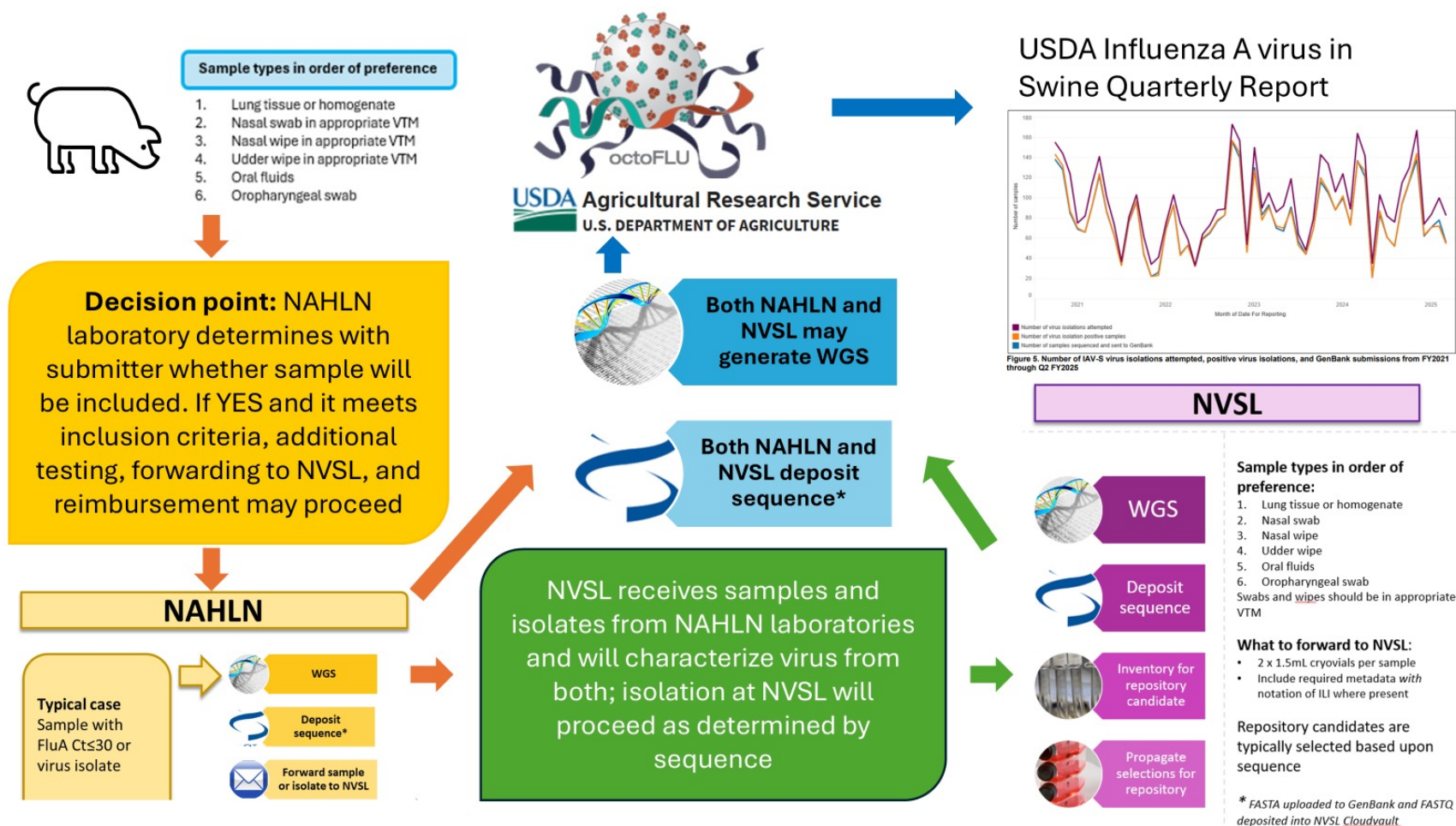


USDA IAV in Swine Surveillance System

- Implemented in November 2009
 - ~1000 submissions a year
- Sequencing
 - 2010-2023 subset are WGS
 - 2023-> *all submissions*
 - *Curation and release by NVSL*
- Sequences in GenBank and summary in octoFLUshow at flu-crew.org:
 - A/swine/lowa/**A02524480**/2020
 - ~12,000 strains <https://flu-crew.org/>
- Isolates requested at: nvsl.dvl.comm@usda.gov
- Reports at: <https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information/influenza-a-virus>
- Revisions to program announced (easier to qualify and participate!!)



Updated USDA testing algorithm



octoFLUshow: visualizing and searching the repository

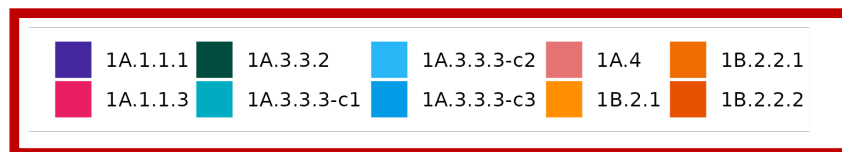
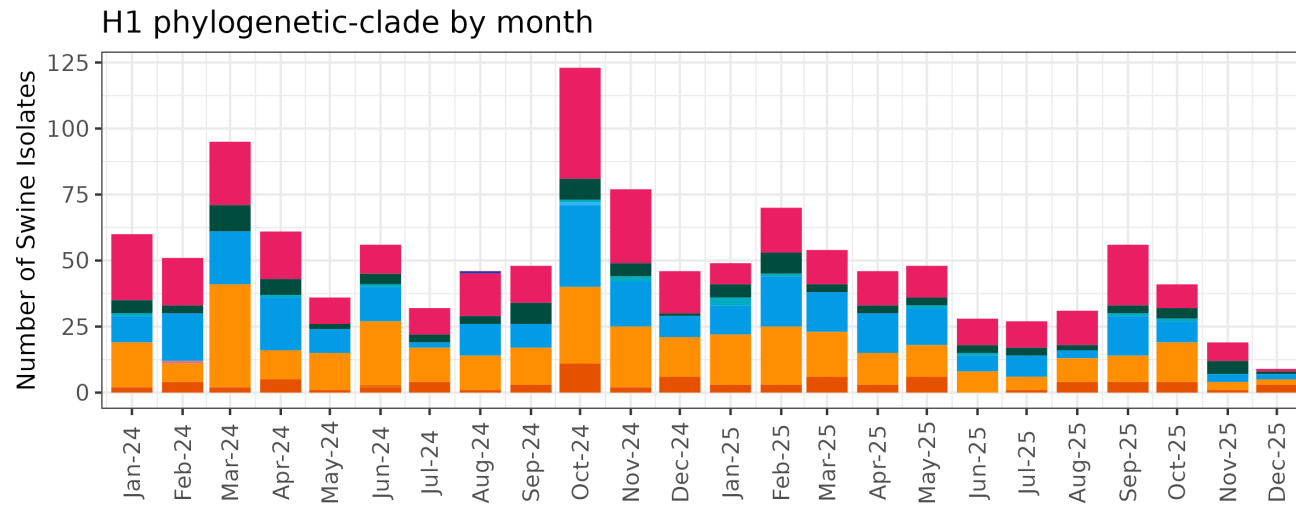
The screenshot displays the octoFLUshow web interface. At the top, there are navigation tabs: octoFLUshow, Landing page, Data, Clades by time, HA/NA by time, HA/NA/Const by time, Clades by state, Clade heatmap, and Constellation heatmap. The 'Data' tab is active. Below the tabs, there is a 'Select Columns' button and a 'Download Excel' button. A 'Segment nomenclature' section has radio buttons for 'US' and 'global', with 'global' selected. A text input field for 'Select strains (comma-delimited list of barcodes, strains, or regular expressions)' contains the text 'A01104056, Illinois/A01565507, Utah.*201[89]'. A 'Show 25 entries' dropdown is visible. Below this, a search bar is present. The main data table has columns: Barcode, Date, Collection_Q, State, Subtype, H_Genbank, Strain, US_Clade, H1, H3, N1, N2, Constellation, and WGS. Several columns (Date, State, H1, H3) have filter dropdowns. The table lists six entries with their respective barcodes, dates, collection quarters, states, subtypes, H_Genbank IDs, strain names, US_Clade names, H1 and H3 segment names, N1 and N2 segment names, constellation names, and WGS status.

Barcode	Date	Collection_Q	State	Subtype	H_Genbank	Strain	US_Clade	H1	H3	N1	N2	Constellation	WGS
A02862183	2023-12-28	24Q1	IA	H3N2	PP175292	A/swine/Iowa/A02862183/2023	2010 human-like	/	A	/	/	All	false
A02862186	2023-12-28	24Q1	IA	H3N2	PP175294	A/swine/Iowa/A02862186/2023	2010 human-like	/	/	/	/	All	false
A02862188	2023-12-28	24Q1	IA	H1N1	PP175298	A/swine/Iowa/A02862188/2023	alpha-del	1A.1.1.3	/	N1.C.3.2	/	/	false
A02862189	2023-12-28	24Q1	IA	H1N1	PP175300	A/swine/Iowa/A02862189/2023	gamma-c3	1A.3.3.3-c3	/	N1.C.3.2	/	/	false
A02862180	2023-12-27	24Q1	IA	H1N2	PP175286	A/swine/Iowa/A02862180/2023	alpha-del	1A.1.1.3	/	/	2002B	/	false
A02862182	2023-12-27	24Q1	MN	H1N2	PP175290	A/swine/Minnesota/A02862182/2023	delta2	1B.2.1	/	/	1998B	/	false

- <https://flu-crew.org> = a big interactive excel spreadsheet – what you select is what is visualized
- Updated every 3 months, with static reports shared on USDA-APHIS-VS websites

Blake Inderski, Lauren Abrahamsen, Scott Kramer

Constant circulation of different H1 HA

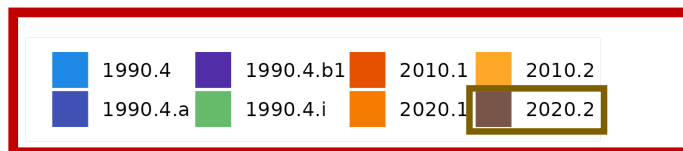
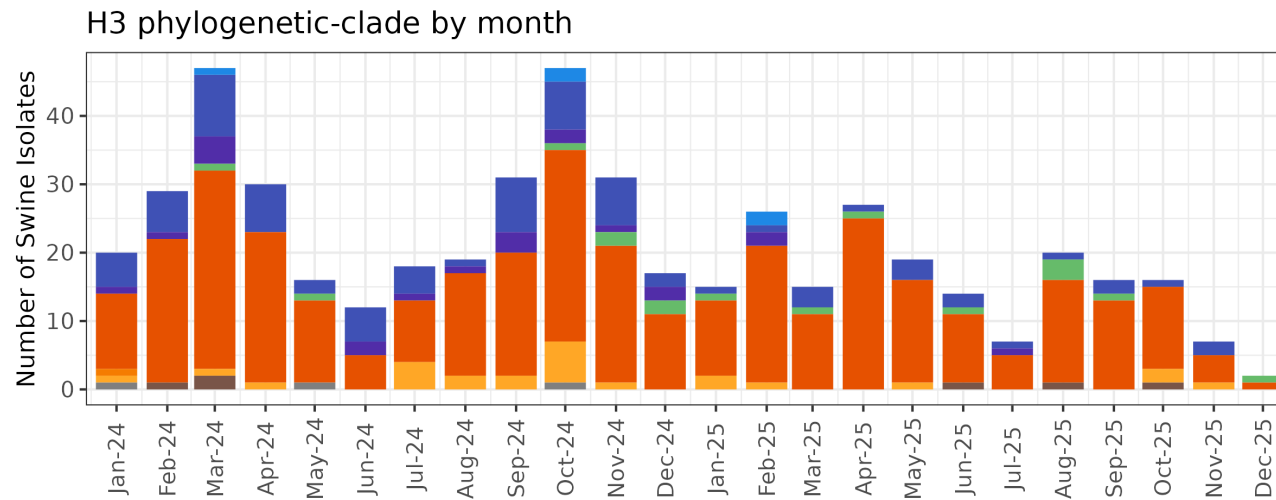


n=10

<https://github.com/flu-crew/octoFLU> and <https://github.com/flu-crew/octoflushow>

Blake Inderski
Arendsee et al (2021) *MRA*

Constant circulation of different H3 HA



n=7

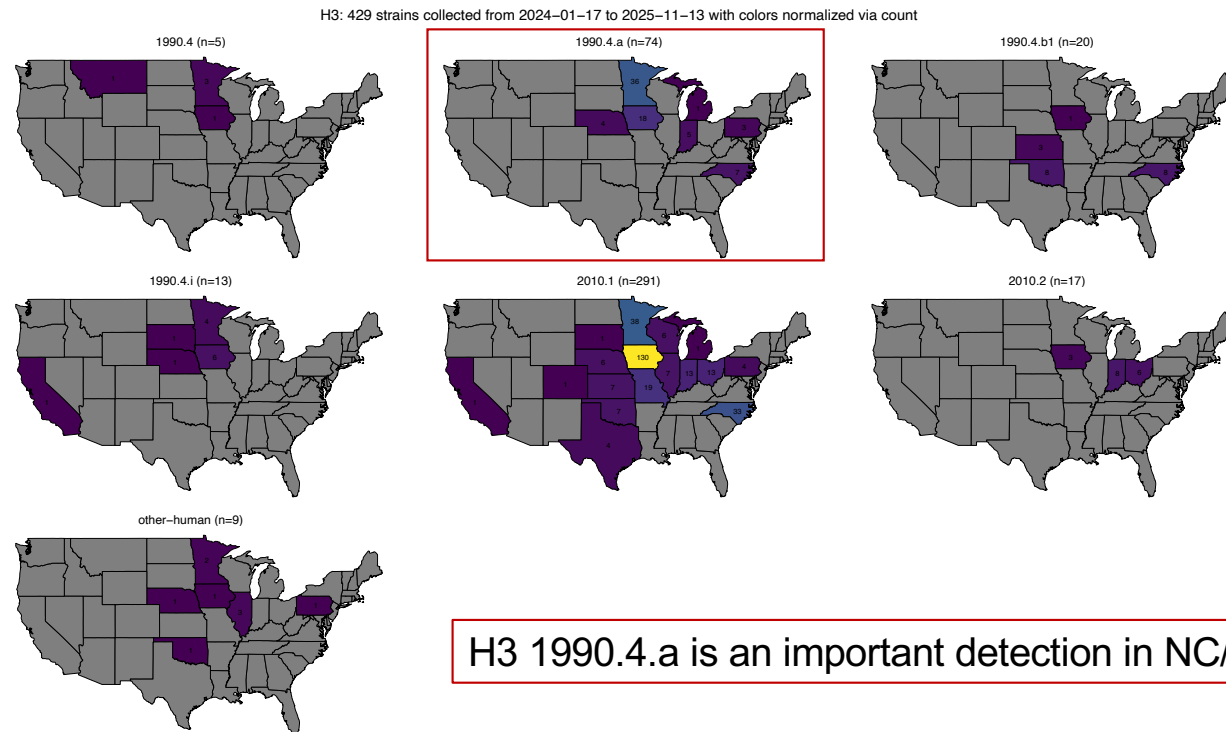
Blake Inderski
Arendsee et al (2021) *MRA*

7 major HA/NA pairings over the last 2 years

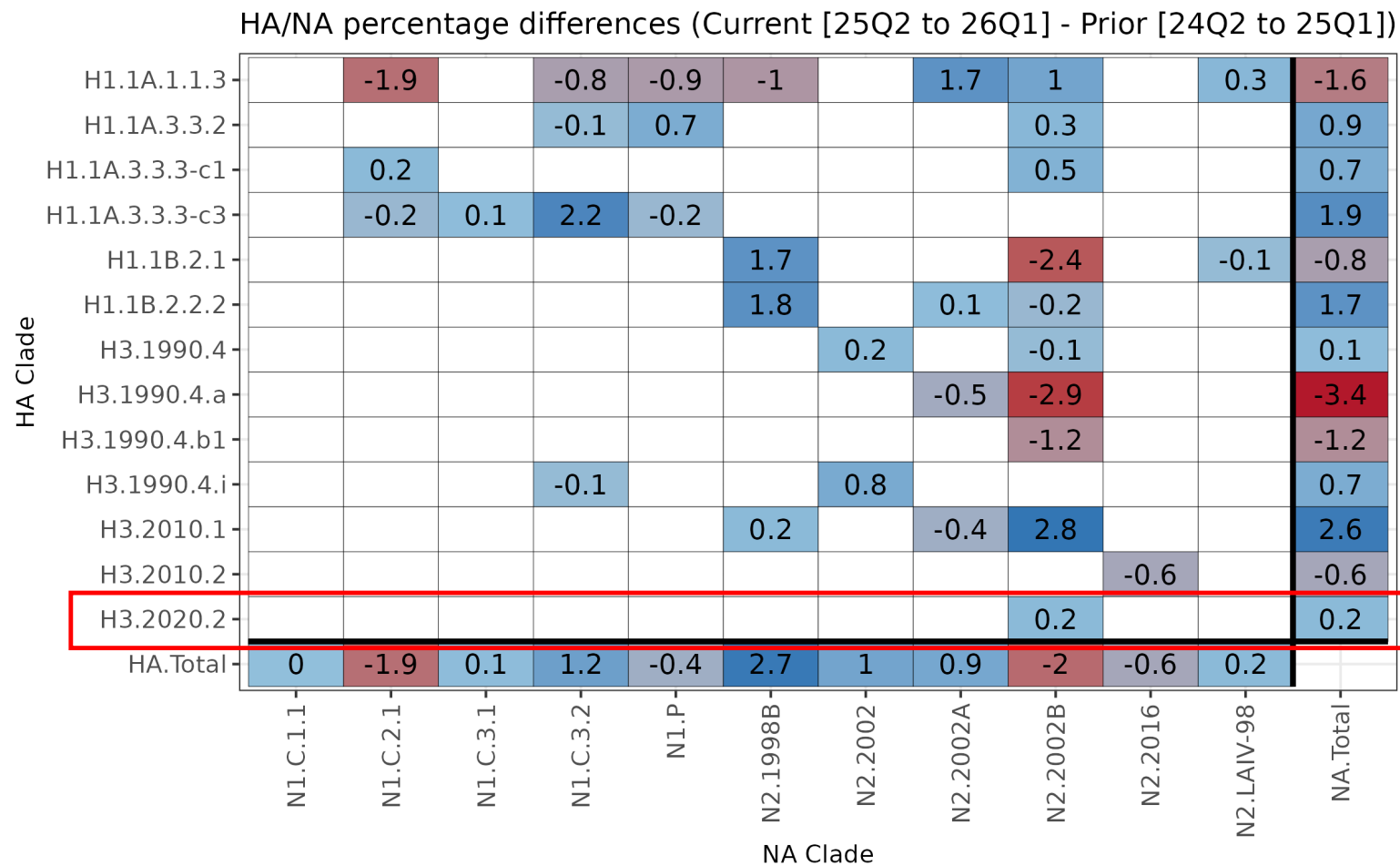
Percentage of HA and NA combinations - Jan 2025 to Dec 2025

H1.1A.1.1.3		2.7		2.9	3.3	6.2		1.8	3.2		0.5	20.6
H1.1A.3.3.2					6				0.5			6.5
H1.1A.3.3.3-c1		0.8							0.5			1.3
H1.1A.3.3.3-c3			0.5	17.5								18
H1.1B.2.1						17.5			2.7			20.2
H1.1B.2.2.2						1.8		1.2	2.6		0.2	5.8
H3.1990.4							0.2		0.2			0.4
H3.1990.4.a									2.7			2.7
H3.1990.4.b1									0.5			0.5
H3.1990.4.i							1.4					1.4
H3.2010.1	0.2			0.2		0.2		0.9	20.1			21.6
H3.2010.2										1.1		1.1
H3.2020.2									0.5			0.5
NA.Total	0.2	3.5	0.5	20.6	9.3	25.7	1.6	3.9	33.5	1.1	0.7	
	N1.C.1.1	N1.C.2.1	N1.C.3.1	N1.C.3.2	N1.P	N2.1998B	N2.2002	N2.2002A	N2.2002B	N2.2016	N2.LAIV-98	HA.Total

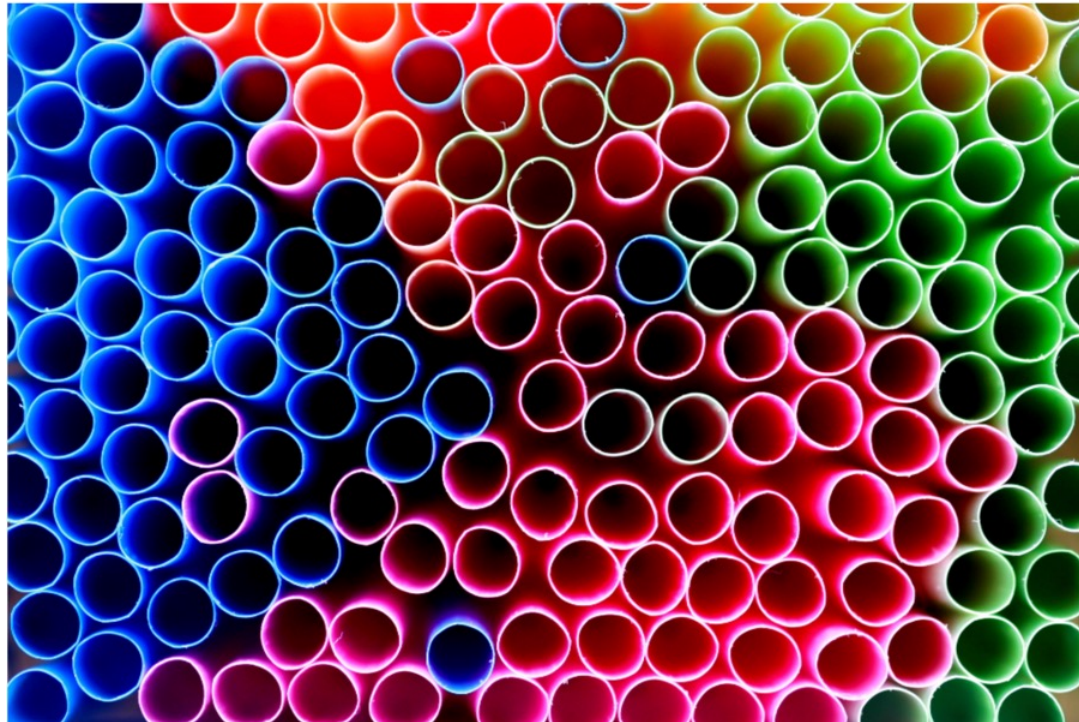
AND IAV in each region and state are different



Some HA/NA pairing increasing, with more pairings decreasing (but relative)



PARNAS: an objective selection of representative strains



Markin et al. (2023) Systematic Biology: <https://github.com/flu-crew/PARNAS>

IAV-S Surveillance - NADC Representative HA genes

Strain	GenBank	Global Clade
A/swine/Illinois/A02858720/2025	PX068528	H1-1A.1.1.3
A/swine/Minnesota/A02980710/2025	PX596405	H1-1A.3.3.2
A/swine/Iowa/A02858735/2025	PX114466	H1-1A.3.3.3-c3
A/swine/Minnesota/A02978936/2025	PX443067	H1-1B.2.1
A/swine/Iowa/A02858843/2025	PX459590	H1-1B.2.2.2
A/swine/Minnesota/A02980758/2025	PX934434	H3-1990.4.a
A/swine/North_Carolina/A02858783/2025	PX368848	H3-2010.1
A/swine/Iowa/A02858897/2025	PX504850	H3-2010.1

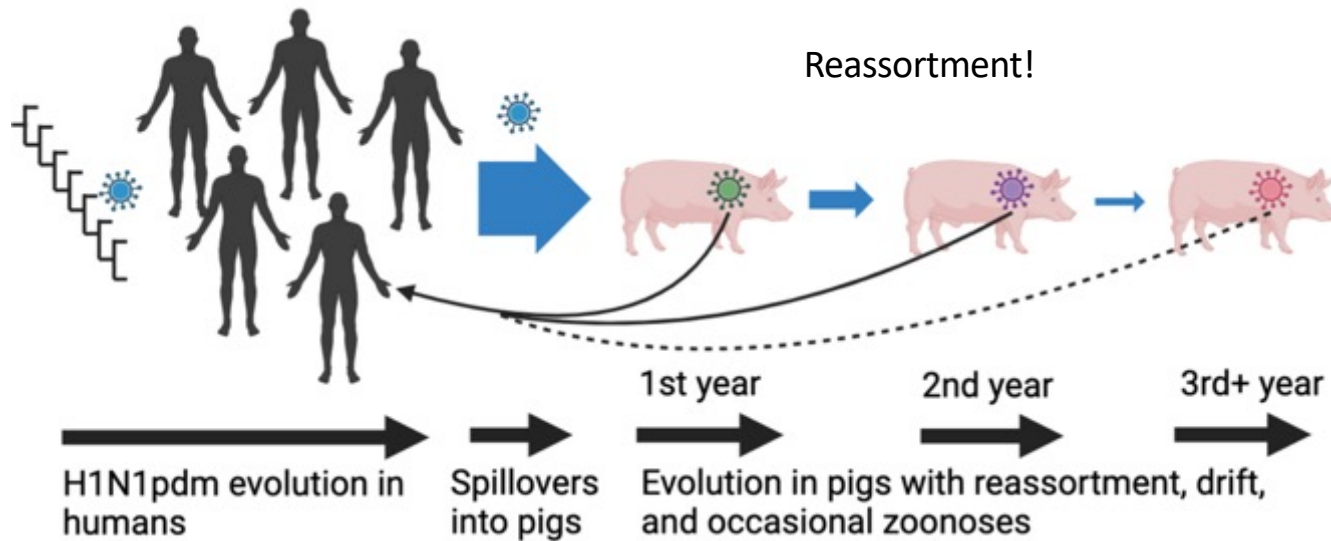
- July 2025 to December 2025 USDA HA data downloaded ($n = 183$ H1, $n = 68$ H3) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (<https://github.com/flu-crew/parnas>).
- Clades were required to have a detection rate of at least 2% to be considered for selection ($n \geq 6$).
 - Omitted H1-1A.3.3.3-c1 ($n=2$), H3-1990.4.b1 ($n=1$), H3-1990.4.i ($n=5$), H3-2010.2 ($n=3$), and H3-2020.2 ($n=2$)
- The 5 H1 selections cover **85%** of observed diversity; 3 H3 selections cover **54%** of observed diversity.
- Note that 2 selections were made within H3-2010.1, which represents 86% of all H3 detections.

IAV-S Surveillance - NADC Representative NA genes

Strain	GenBank	Global Clade
A/swine/Minnesota/A02980500/2025	PX060475	N1-C.3.2
A/swine/Minnesota/A02980703/2025	PX596391	N1-P
A/swine/Iowa/A02858726/2025	PX114451	N2-1998B
A/swine/Missouri/A02858773/2025	PX340079	N2-2002A
A/swine/Iowa/A02858770/2025	PX310588	N2-2002B

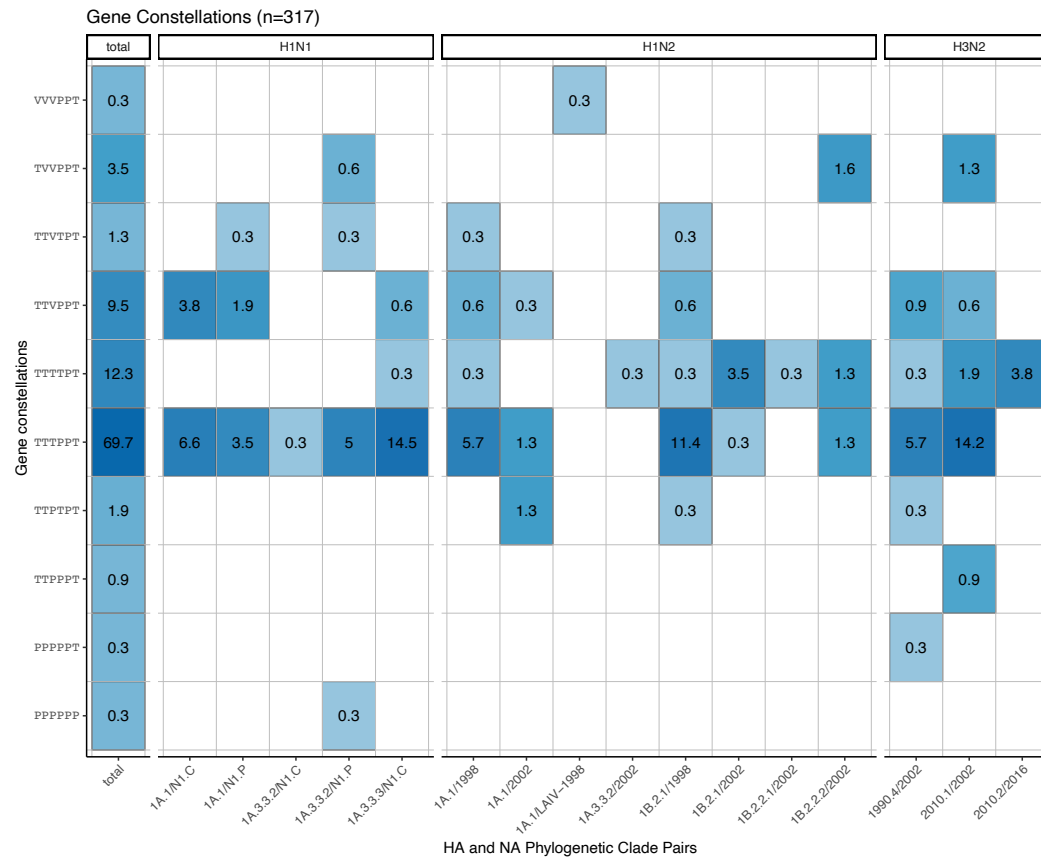
- July 2025 to December 2025 USDA NA data downloaded ($n = 82$ N1, $n = 169$ N2) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (<https://github.com/flu-crew/parnas>).
- Clades were required to have a detection rate of at least 2% to be considered for selection ($n \geq 7$).
 - Omitted N1-C.2.1 ($n=4$), N2-2002 ($n=5$), N2-2016 ($n=3$), N2-LAIV-98 ($n=1$)
- The 2 N1 selections cover **82%** of observed diversity; 3 N2 selections cover **61%** of observed diversity.

Human-to-swine, swine-to-swine, **reassortment** and movement

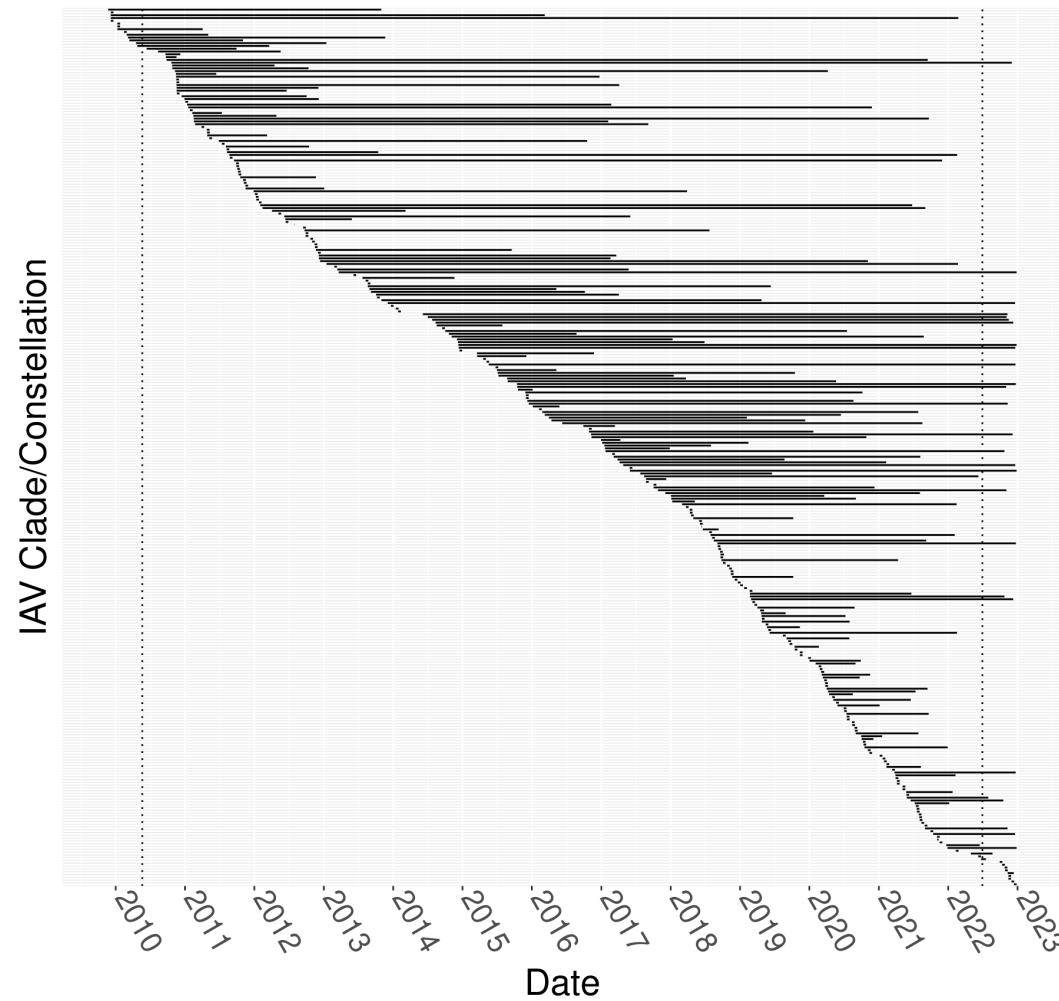


Markin et al (2023)
Ciacci Zanella et (2025)

Major internal gene combinations, but continual exchange with human seasonal H1N1pdm09

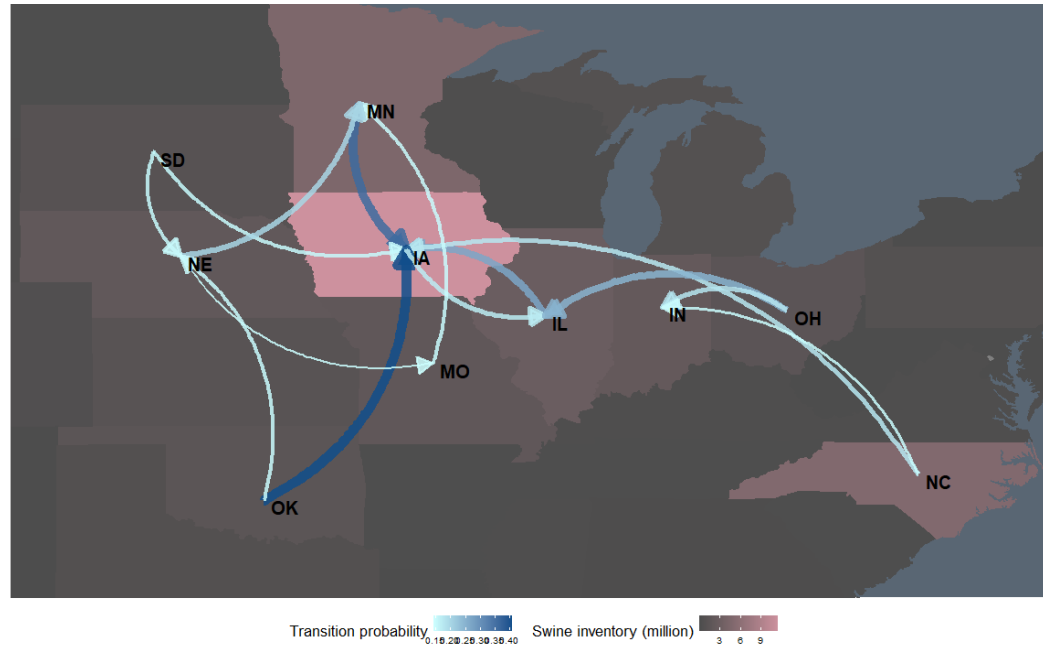


297 genotypes, with 118 longer than a year!



Garrett Janzen et al. (2025) JVI

Diversity emerges locally, but jumps on the pig network



- Discrete-time Markov chain model (hoping to make it more useful soon!)
- On first detection of novel virus,
 - predict dispersal to “XX” ~45%
 - predict persistence/extinction ~55%

Garrett Janzen et al. (2025) Journal of Virology

Anderson Lab Sequence Tool Development

- Assess whether a virus detected in collections “matters” for the pigs...
 -  Classify HA and NA clades (BV-BRC, octoflu, splicer)
 -  Visualize changes in the diversity (octoFLUshow)
 -  Generate selections based on observed diversity (PARNAS)
 -  Detect reassortment (TreeSort)
- All software is available at <https://github.com/flu-crew>

TreeSort: identifying reassortment and novelty

Services

Influenza Reassortment Analysis

The TreeSort tool infers both recent and ancestral reassortment events along the branches of a phylogenetic tree of a fixed genomic segment. It uses a statistical hypothesis testing framework to identify branches where reassortment with other segments has occurred and reports these events. TreeSort was created by the Flu-crew at the National Animal Disease Center.

For further explanation, please see the TreeSort Service [Quick Reference Guide](#) and [Tutorial](#).

IMPORTANT notes about the FASTA input file:

- This service can **only** be used with Influenza nucleotide sequences!
- Segment names in the FASTA file headers are limited to PB2, PB1, PA, HA, NP, NA, MP, and NS.
- The segment name **must** be surrounded by `|` characters and can be followed by a date in the format YYYY-MM-DD.

For example:

```
>A/swine/Michigan/A02635726/2021|1B.2.1|1998B|TTTTPT|HA|2021-04-23
```

where the segment is `HA` and the date is `2021-04-23` (April 23, 2021).

- TreeSort can accept 3 different strain name formats within a FASTA header:
 - The strain name is everything that remains after the segment name is removed.
 - The strain name starts with "EPI_ISL_" followed by a numeric (integer) value.
 - A strain name starts with A, B, C, or D followed by 3 to 5 spans of text inside `|` characters. For example: `A/swine/Iowa/A02635718/2021`. Note that `|` characters are not allowed in the strain name.
- After you select a FASTA input file, your file will be automatically validated to make sure TreeSort will be able to find the strain and segment names. An error message will be displayed if any errors are found.
- If your FASTA file is successfully validated, a summary of the number of strains and segments will be displayed. Please confirm that the summary is consistent with the contents of your file.

Input sequence

☒ SELECT FASTA FILE ☐ GENOME GROUP

Parameters

OUTPUT FOLDER

OUTPUT NAME

REFERENCE SEGMENT

SEGMENTS

☒ PB2 ☒ PB1 ☒ PA ☒ HA ☒ NP ☒ NA ☒ MP ☒ NS

▶ ADVANCED OPTIONS

Reset

Submit

Annex 1. Geographic Distribution of swine HA phylogenetic clades by country

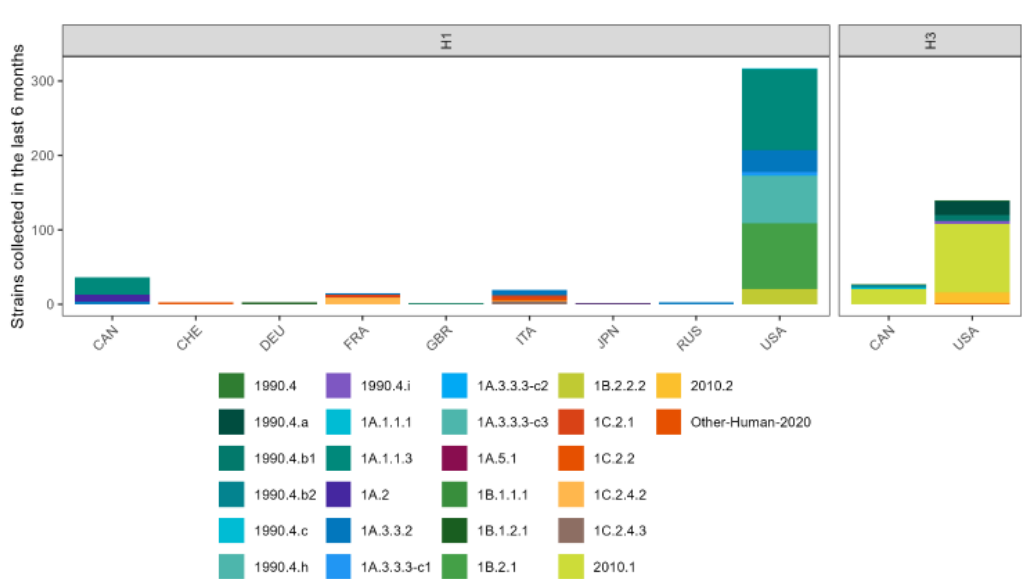


Figure A1. Summary of swine HA genes colored by phylogenetic clade for sequences deposited between July 1 2024 and January 1 2025 (n = 567).

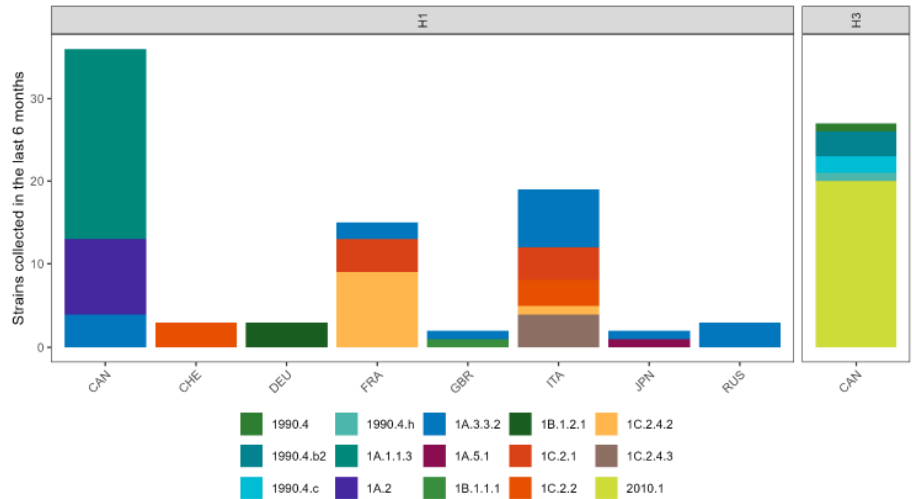


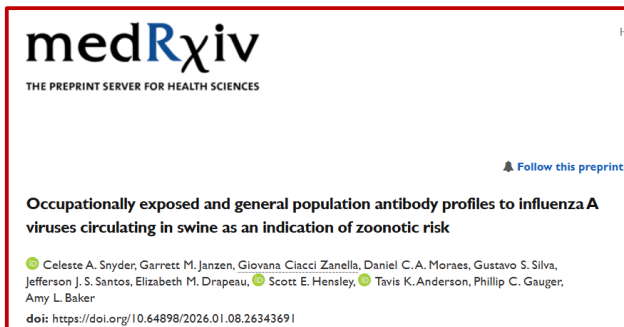
Figure A3. Summary of swine HA genes colored by phylogenetic clade for sequences deposited between July 1 2024 and January 1 2025, in any country other than the United States of America (n = 110).

OFFLU SWINE INFLUENZA REPORT

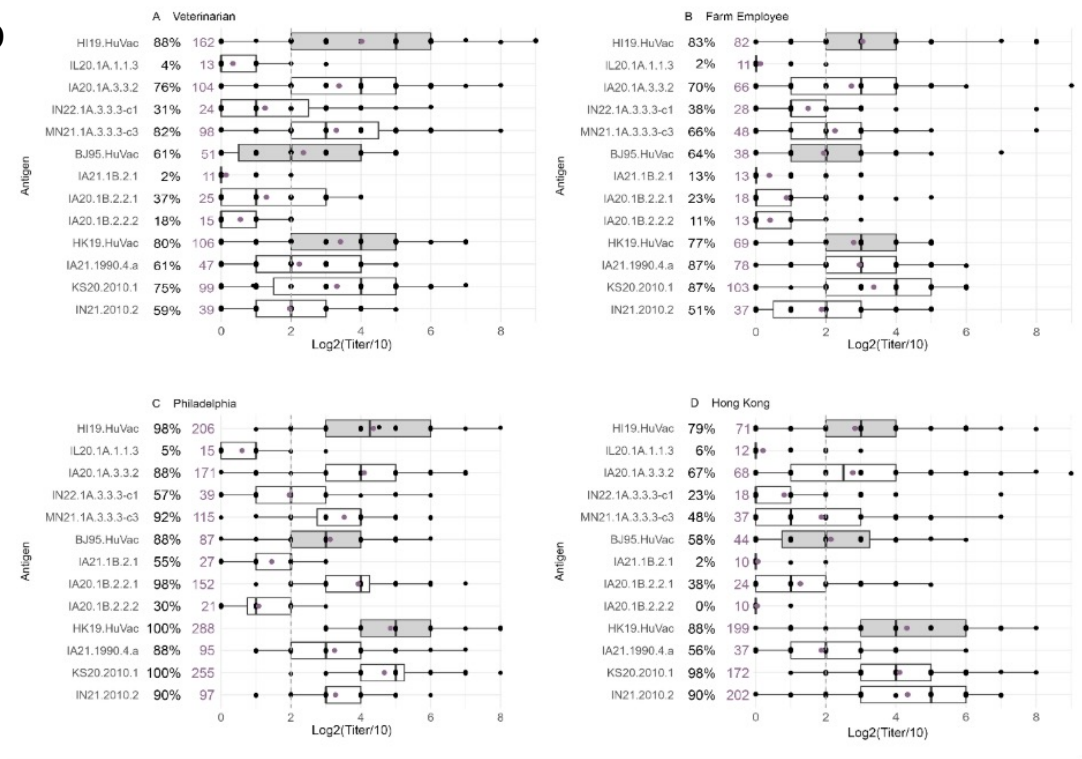
JULY 2024 TO DECEMBER 2024

Occupationally exposed and general population antibody profiles to influenza A viruses circulating in swine as an indication of zoonotic risk

Preprint available (MedRxiv); In Peer Review at EID



- Occupationally exposed did not have elevated antibody positivity against swine strains.
- Vaccination history and birth year correlated with cross-reactivity to swine strains.
- 1A.1.1.3 and 1B clades identified as greatest risk to human population immunity.



Swine publications

- **Impact of maternal antibodies and weaning stress on the replication and transmission of human H3N2 influenza A in piglets.** Ciacci Zanella G, et. al. J Virol. 2026 Mar 27:e0197525. doi: 10.1128/jvi.01975-25.
- **Elevated Exposure to Influenza A Viruses in Wild Pigs (*Sus scrofa*), Texas, USA.** Chalkowski K, et. al. J Wildl Dis. 2026 Feb 9;62(1):185-191. doi: 10.7589/JWD-D-25-00031.
- **Pathogenesis and Transmission of a Reassorted H1 Influenza A Virus Detected in North American Swine.** Goulart DB, et. al. Influenza Other Respir Viruses. 2026 Feb;20(2):e70228. doi: 10.1111/irv.70228.
- **Active surveillance for influenza A virus in swine reveals within-farm reassortment and cocirculation of distinct subtypes and genetic clades.** Thomas MN, et. al. Vet Microbiol. 2025 Oct;309:110681. doi:10.1016/j.vetmic.2025.110681.
- **Sources and sinks of influenza A virus genomic diversity in swine from 2009 to 2022 in the United States.** Janzen GM, et. al. J Virol. 2025 Sep 23;99(9):e0054125. doi: 10.1128/jvi.00541-25.
- **Revealing Reassortment in Influenza A Viruses with TreeSort.** Markin A, et.al. Mol Biol Evol. 2025 Jul 30;42(8):msaf133. doi: 10.1093/molbev/msaf133.
- **Porcine Sample Type Characteristics Associated with Sequencing and Isolation of Influenza A Virus.** Moraes DCA, et.al. Vet Sci. 2025 Jul 19;12(7):683. doi: 10.3390/vetsci12070683.
- **Transmission and Pathologic Findings of Divergent Human Seasonal H1N1pdm09 Influenza A Viruses Following Spillover Into Pigs in the United States.** Ciacci Zanella G, et. al. Influenza Other Respir Viruses. 2025 Jul;19(7):e70128. doi:10.1111/irv.70128.
- **A neuraminidase-based inactivated influenza virus vaccine significantly reduced virus replication and pathology following homologous challenge in swine.** Kaplan BS, et. al. Vaccine. 2025 Feb 6;46:126574. doi:10.1016/j.vaccine.2024.126574.





NADC flucrow

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 - Sriram Vijendran
 - Sid Grover
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- **Michael Zeller (Iowa State)**
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- **IRD/BV-BRC team**
- **Mia Torchetti (USDA)**
- **Scott Kramer (USDA)**
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- **Lauren Abrahamsen (USDA)**
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- **Daniel Perez (UGA)**
- **Scott Hensley (Penn)**
- **Seema Lakdawala (Emory)**
- **Val Le Sage (Pitt)**
- **Todd Davis (CDC)**
- **Han Di (CDC)**
- **Richard Webby (St. Jude)**
- **OFFLU**



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Thank you

