



# OFFLU SWINE INFLUENZA REPORT

JANUARY 2024 TO JUNE 2024

## SCOPE

In this document we present a summary of H1 and H3 swine influenza A virus evolution.

<b><u>ACKNOWLEDGEMENTS AND METHODS</u></b>	<b>3</b>
<b><u>GLOBAL INFLUENZA A EVENTS IN SWINE</u></b>	<b>4</b>
<b>MICROREACT MAPS</b>	<b>4</b>
<b>GLOBAL H1 PHYLOGENETIC ANALYSIS</b>	<b>6</b>
<b>GLOBAL H3 PHYLOGENETIC ANALYSIS</b>	<b>7</b>
<b>REGIONAL GEOGRAPHIC SUMMARY</b>	<b>8</b>
<b>H1 LINEAGE 1A</b>	<b>9</b>
PHYLOGENETIC ANALYSIS	9
ANTIGENIC ANALYSES	10
VACCINE/CVV COMPARISONS	12
<b>H1 LINEAGE 1B</b>	<b>16</b>
PHYLOGENETIC ANALYSIS	16
ANTIGENIC ANALYSES	17
VACCINE/CVV COMPARISONS	19
<b>H1 LINEAGE 1C</b>	<b>24</b>
PHYLOGENETIC ANALYSIS	24
ANTIGENIC ANALYSES	25
VACCINE/CVV COMPARISONS	26
<b>H3 LINEAGES</b>	<b>29</b>
PHYLOGENETIC ANALYSIS	29
ANTIGENIC ANALYSES	30
VACCINE/CVV COMPARISONS	31
<b>SUMMARY: ANTIGENIC, GENETIC AND RISK ASSESSMENT</b>	<b>36</b>
<b><u>ANNEX 1</u></b>	<b>37</b>
<b>SWINE HA PHYLOGENETIC CLADES GRAPHED BY COUNTRY</b>	<b>37</b>
<b>TABLES OF SWINE H1 CLADES BY COUNTRY OF COLLECTION</b>	<b>39</b>
<b>TABLES OF SWINE H3 CLADES BY COUNTRY OF COLLECTION</b>	<b>41</b>
<b>TABLES OF RECENT SWINE AND VARIANT ACTIVITY</b>	<b>42</b>
<b><u>ANNEX 2</u></b>	<b>43</b>
<b>PHYLOGENIES ANNOTATED BY AMINO ACID CHANGES</b>	<b>42</b>

## **Swine influenza A viruses: Acknowledgements and Methods**

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### **Brief Methods for Genetic and Antigenic Analyses**

Analyses were conducted by subtype and lineage or clade. Reference sequences and new data (deposited on or after January 1, 2024) downloaded from GISAID or GenBank incorporated into the USDA-ARS NADC octoFLUdb and were subsequently aligned with MAFFT (Katoh and Standley, 2013) using default settings. Alignments for each segment were inspected manually and trimmed to the start and stop codon. Phylogenetic inference was conducted with FastTree (Price et al., 2009) or IQ-Tree (Minh et al., 2020). Tabular comparisons between current CVVs or human seasonal vaccine strains and new swine data were generated using the NADC IAV bioinformatic toolkit flutile (<https://github.com/flu-crew>). A clade representative was selected using PARNAS (Markin et al., 2023: <https://github.com/flu-crew/parnas>) and the best matched available strain was selected for testing against reference ferret antisera in hemagglutination inhibition (HI) assays. All HI assays were performed with ferret anti-sera and guinea pig red blood cells. H3N2 assays were performed with the addition of oseltamivir. Phylogenies were subsampled and visualized using smot (Arendsee et al., 2022: <https://github.com/flu-crew/smot>).

## Global influenza A events in swine Epidemiology

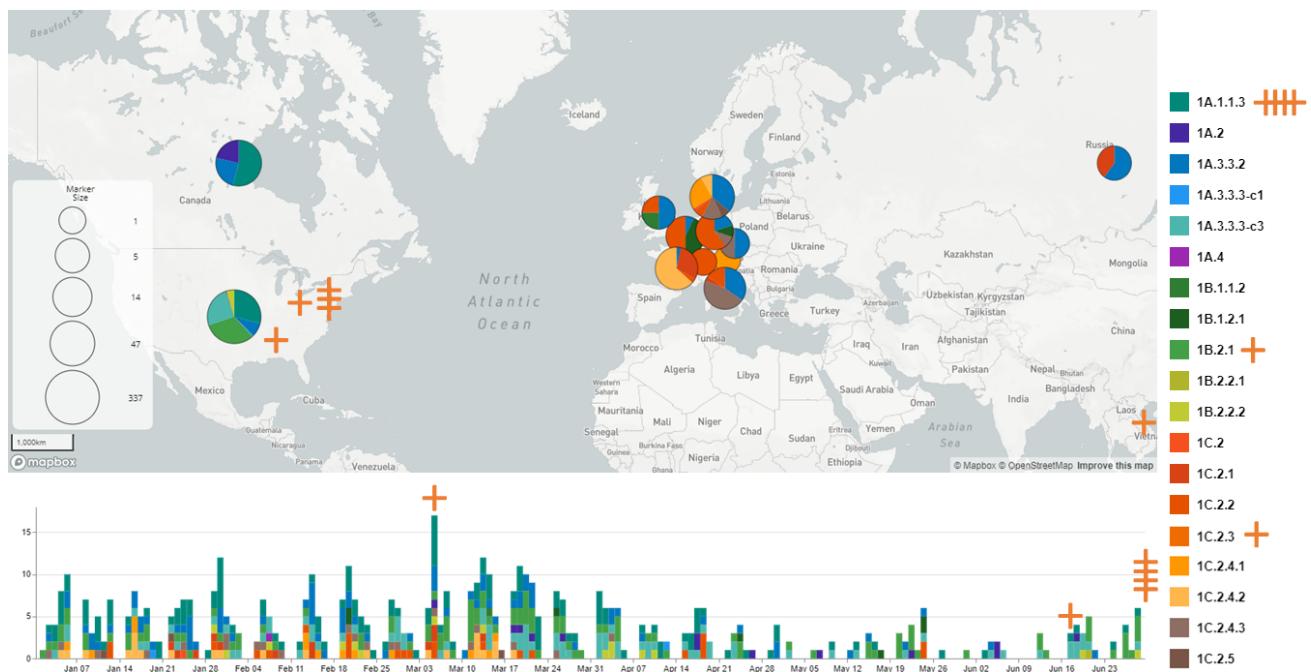


Figure 1. MicroReact map of swine IAV H1 HA genes colored by phylogenetic clade for sequences collected and deposited to GISAID or GenBank on or after January 1, 2024 (n=538); collection date is represented on bottom timeline. Strains submitted with only partial date were assigned a random date to preserve temporal clusters. Geographic nodes scaled to detection proportions. Clades containing variants, location, and date of detection are marked with orange crosses.

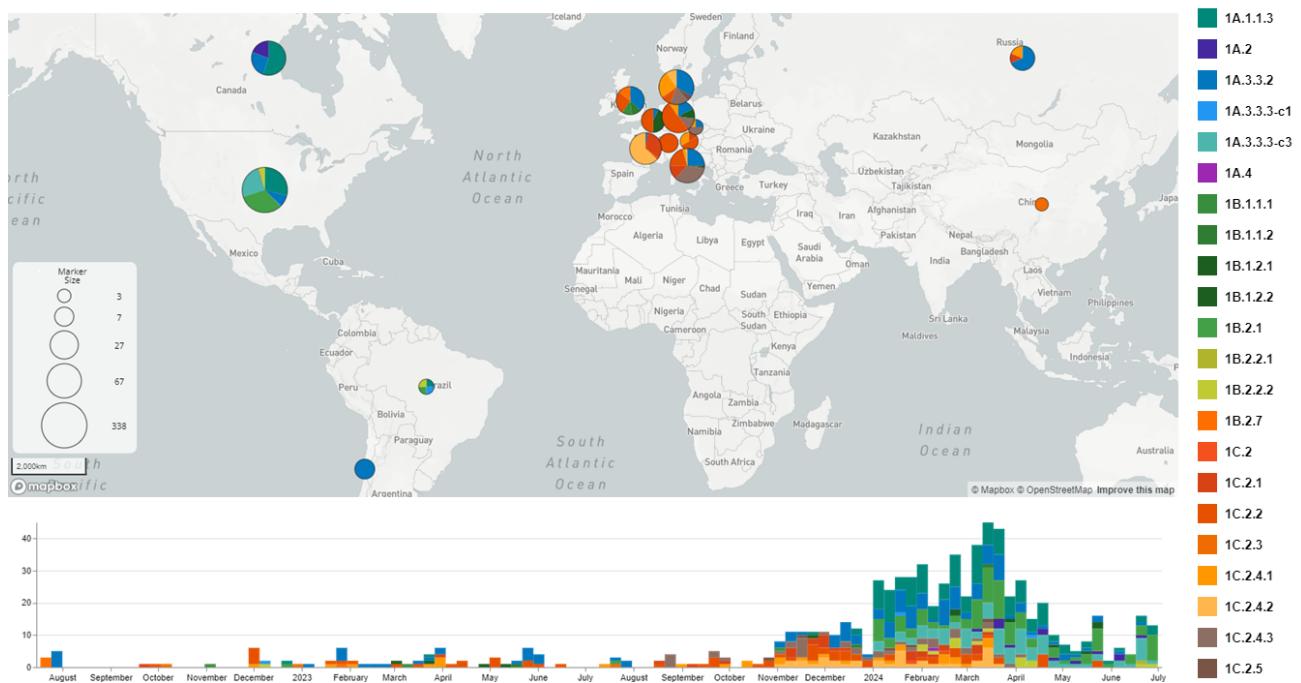


Figure 2. MicroReact map of swine IAV H1 HA genes colored by phylogenetic clade for sequences collected and deposited to GISAID or GenBank on or after July 1, 2022 (n=732); collection date is represented on bottom timeline. Strains submitted with only partial date were assigned a random date to preserve temporal clusters. Geographic nodes scaled to detection proportions.

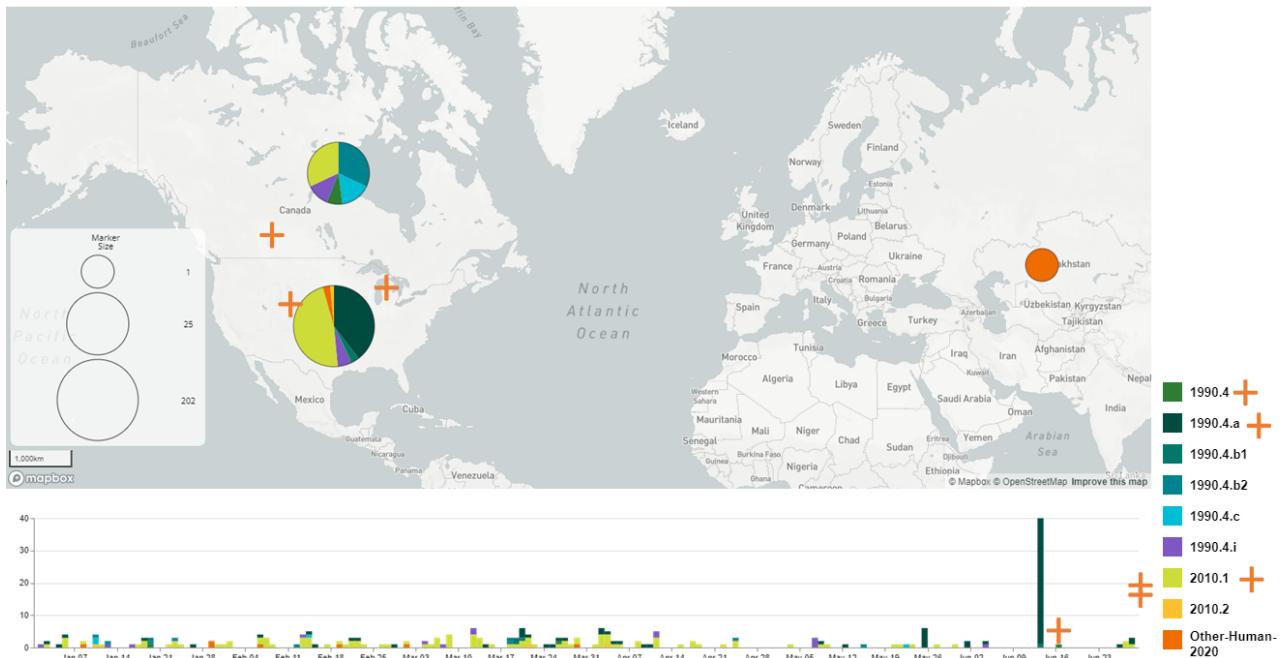


Figure 3. MicroReact map of swine IAV H3 HA genes colored by phylogenetic clade for sequences collected and deposited to GISAID or GenBank on or after January 1, 2024 (n=228). Strains submitted with only partial date were assigned a random date within the provided year to preserve temporal clusters. Geographic nodes scaled to detection proportions. Clades containing variants, location, and date of detection are marked with orange crosses.

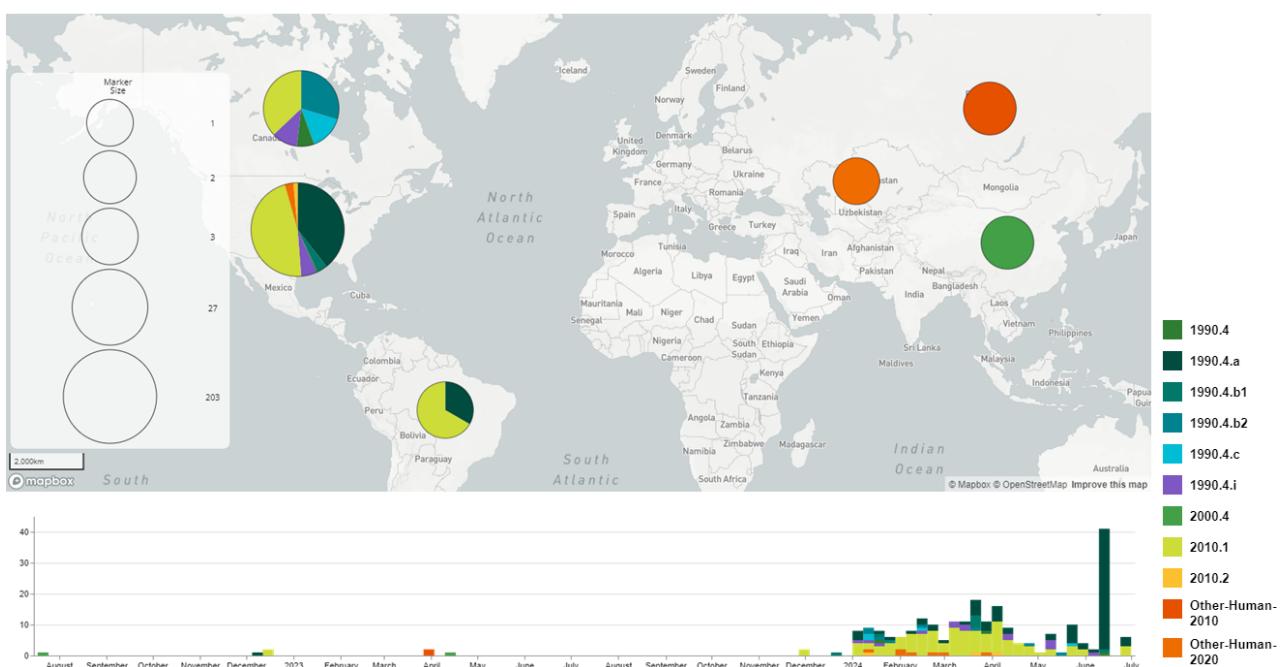
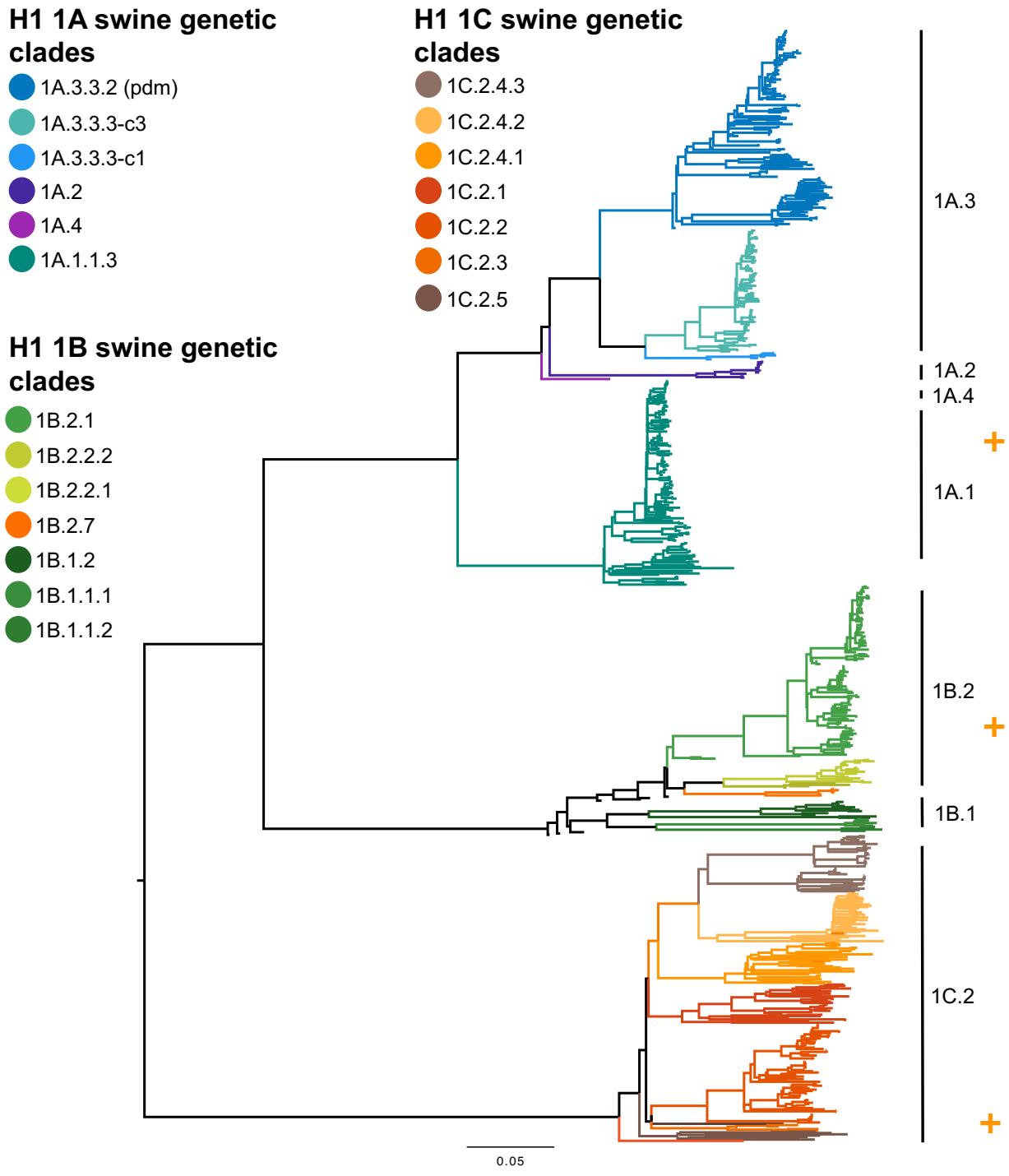


Figure 4. MicroReact map of swine IAV H3 HA genes colored by phylogenetic clade for sequences collected and deposited to GISAID or GenBank on or after July 1, 2022 (n=238). Strains submitted with only partial date were assigned a random date within the provided year to preserve temporal clusters. Geographic nodes scaled to detection proportions.

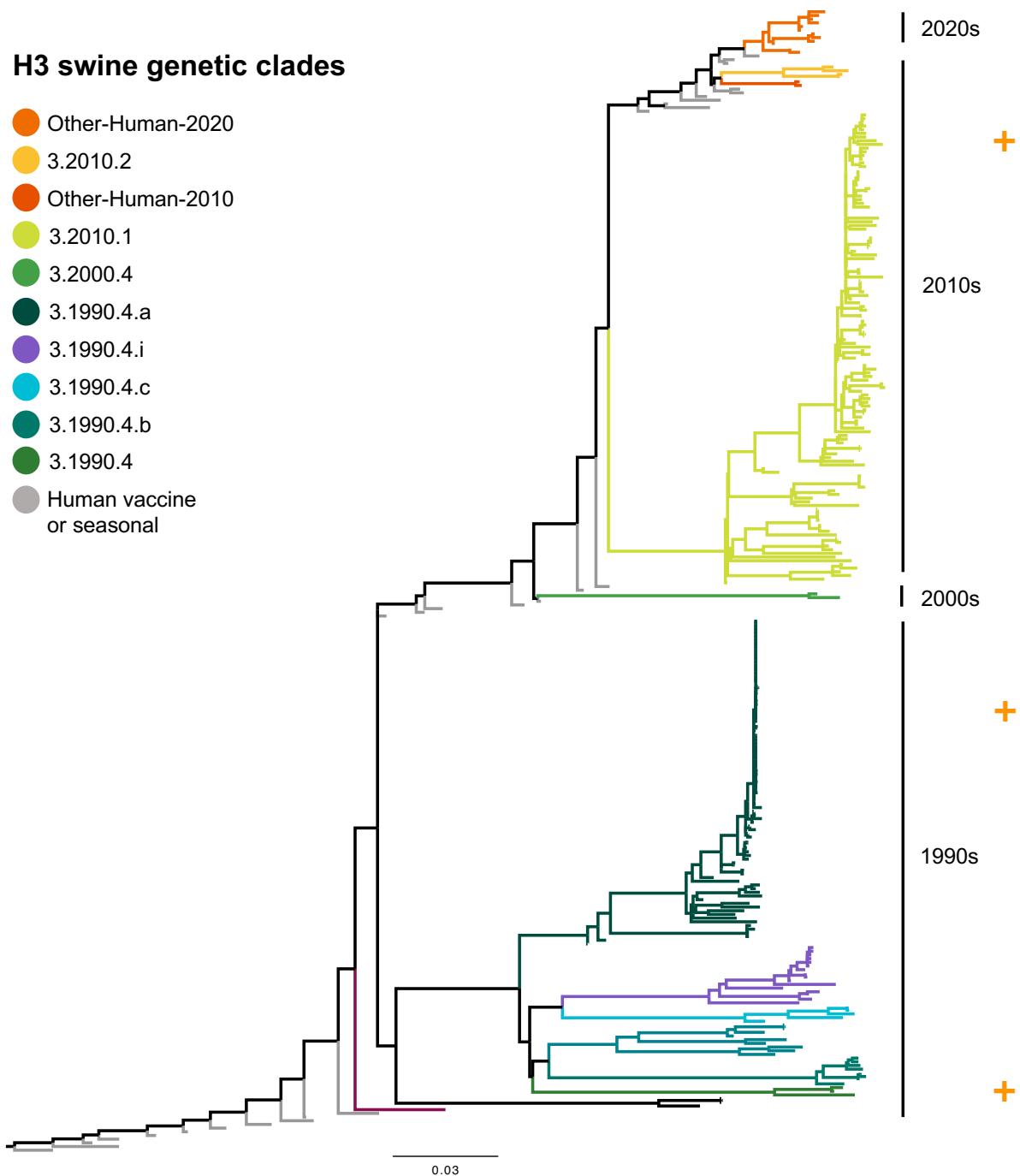
## Contemporary Global H1 swine IAV: genetic diversity



n=766, data deposited within last 6 months.

Figure 5. Global swine H1 phylogenetic tree (n=766) with reference strains (n=77) colored by clade and annotated by global H1 lineage nomenclature. Analyses were conducted with reference sequences and data (all data deposited on or after January 1, 2024) from GISAID or shared via the OFFLU swine IAV working group.

## Contemporary Global H3 swine IAV: genetic diversity



n=245, data deposited within last 6 months, and n=62 reference genes.

Figure 6. Global swine H3 phylogenetic tree (n=245) with reference strains (n=62) colored by clade and annotated by decade of introduction from human seasonal H3. Analyses were conducted with reference sequences and data (all data deposited on or after January 1, 2024) from GISAID or shared via the OFFLU swine IAV working group.

## **Regional geographic summary**

Phylogenetic analysis identified 32 genetic clades from H1 and H3 IAV in swine in sequence data deposited on or after January 1, 2024.

21 clades were H1 subtype, with detections from: 1A classical swine lineage (6 clades); 1B human-seasonal lineage (7 clades); and 1C Eurasian avian lineage (7 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. The 1A.3.3.2 (pdm09) circulated in all countries that deposited sequence data during this 6-month period (9 countries).
- 1B.1 human seasonal lineage was only in Europe, and the 1B.2 human seasonal lineage were detected in the Americas and Europe.
- The 1C.2 Eurasian avian lineage was detected in Europe and Asia.
- A new pre-2009 human-to-swine spillover was detected circulating in Northern Ireland: 1B.2.7.
- Diversity associated with unique amino acid deletion patterns and detection frequency in swine warranted new nomenclature: 1C.2.4.1, 1C.2.4.2, and 1C.2.4.3.

10 H3 clades were detected in swine within 5 distinct lineages derived from human seasonal H3 virus spillovers grouped by the decade of introduction (1990.4; 2000.4; 2010.1; 2010.2; 2020.1) an additional clade of novel human seasonal spillover was detected without evidence for onward circulation (Other-Human-2010). The 1990.4 lineage diversified into 6 co-circulating genetic clades.

- Most lineages exhibited regional circulation: the 2000.4 in China; and the 2010.2 and 2020.1 lineages were detected in the USA.
- The 1990.4 and the 2010.1 lineages were detected in the USA and Canada.
- Novel human-to-swine spillovers were detected in Russia (Other-Human-2010).
- A human-to-swine spillover was detected in the USA associated with the 2022-23 influenza season and demonstrated sustained transmission in pigs: 2020.1

### **Global Variant Cases:**

**During the reporting period (January 1 – June 30, 2024), 4 variant cases were reported and included with the swine analyses when sequence data were available:**

- **Canada: H3N2v (1990.4)**
- **USA: H1N2v (2x 1A.1.1.3)**
- **Vietnam: H1N1v (1C.2.3)**

**Additional variant cases were detected outside of this period, when sequence data were available these were included in analyses:**

- **USA: H1N2v (2x 1A.1.1.3 – August 5, August 7 2024; 1x 1B.2.1 – July 2023), H3N2v (1990.4.a – July 24 2024), H3N2v (2010.1 – July 9, 2024)**

## 1A classical swine lineage

★ H1v candidate vaccine virus

■ A/Victoria/4897/2022

A/Wisconsin/67/2022

H1N1pdm seasonal vaccines

Reported H1v cases

+ New variant(s)

# HI tested viruses

## H1 1A swine genetic clades

● 1A.3.3.2/pdm (n=132)

● 1A.3.3.3-c3 (n=89)

● 1A.3.3.3-c1 (n=3)

● 1A.2 (n=13)

● 1A.4 (n=1)

● 1A.1.1.3 (n=148)

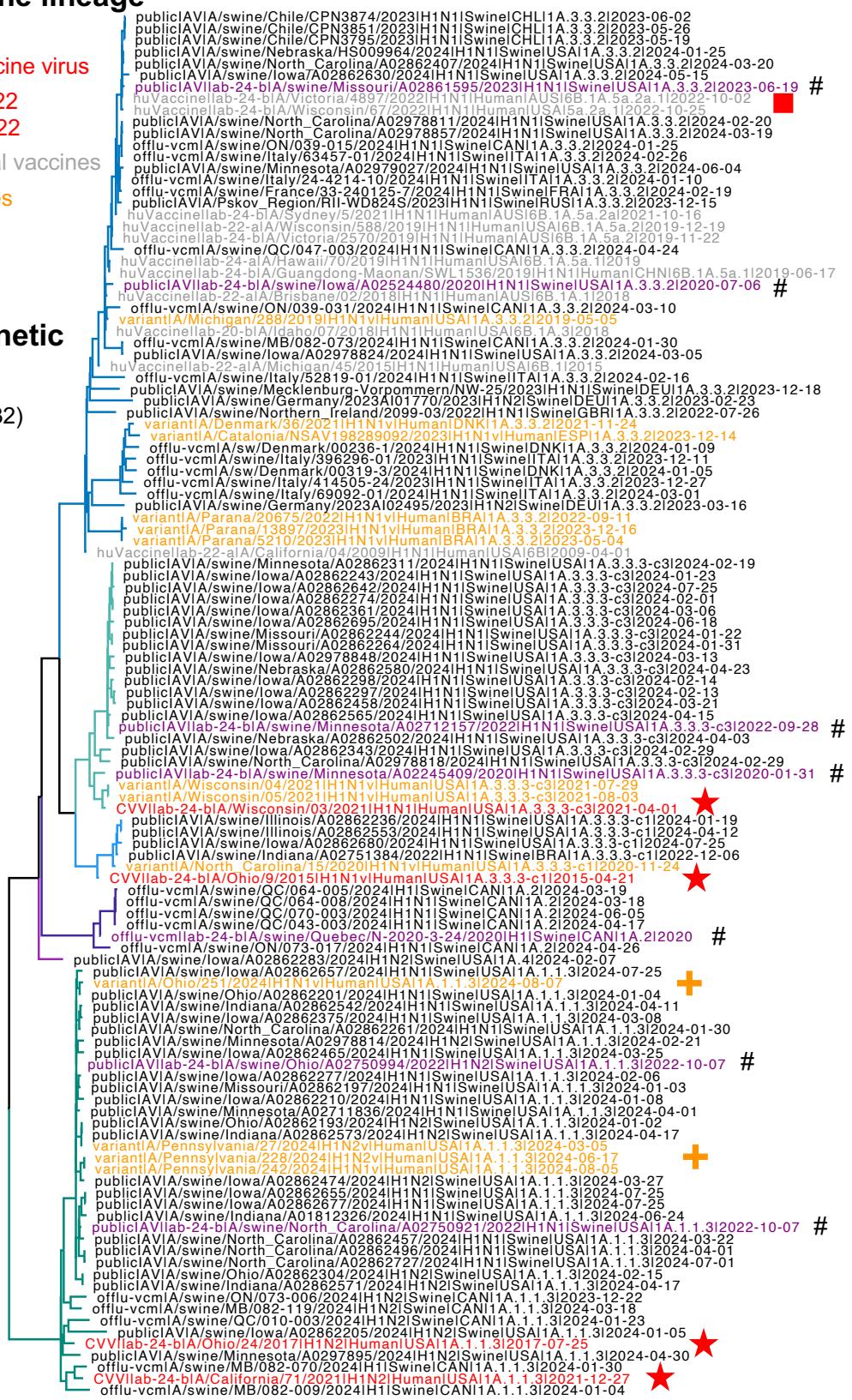


Figure 7. Swine H1 HA genes of the 1A lineage (tree was proportionally downsampled to 91 swine HA genes, excluding references). Number of detections of each clade from data deposited on or after January 1, 2024 are presented adjacent to the clade name in the figure key.

## Antigenic analysis: Swine 1A Lineage

Table 1. USA Data: Hemagglutination inhibition of CVV or human seasonal vaccine ferret antisera against contemporary swine 1A lineage strains selected to represent clade consensus.

- > 8 fold reduction
- 8 fold reduction
- 4 fold reduction

Global Clade			US Clade		IDCDC-RG59 A/Ohio/24/2017-like CVV	A/California/71/2021	A/swine/North_Carolina/A02750921/2022 #61	A/swine/North_Carolina/A02750921/2022 #61	A/Victoria/4897/2022	A/Wisconsin/67/2022	A/swine/Iowa/A02524480/2020 #30	A/swine/Iowa/A02524480/2020 #14	A/Wisconsin/3/2021-like CVV RG76C	A/swine/Minnesota/A02245409/2020 #28	A/swine/Minnesota/A02245409/2020 #12	Human Pooled Serum
+ IDCDC-RG59 A/Ohio/24/2017 CVV	1A.1.1.3	alpha-del	640	20	160	320	20	<10	160	320	20	20	20	20	80	
A/California/71/2021	1A.1.1.3	alpha-del	<10	5120	160	320	10	<10	<10	<10	<10	<10	<10	<10	160	
A/swine/North_Carolina/A02750921/2022	1A.1.1.3	alpha-del	<10	20	640	1280	<10	<10	<10	<10	20	<10	<10	80		
A/swine/Ohio/A02750994/2022	1A.1.1.3	alpha-del	20	80	640	1280	<10	<10	<10	<10	10	<10	<10	80		
A/Victoria/4897/2022	1A.3.3.2, 5a.2a.1	pdm09	<10	<10	<10	<10	2560	2560	10	20	40	<10	<10	320		
A/Wisconsin/67/2022	1A.3.3.2, 5a.2a	pdm09	<10	<10	<10	<10	<10	2560	320	40	80	<10	<10	160		
A/swine/Iowa/A02524480/2020*	1A.3.3.2	pdm09	20	<10	10	10	80	10	640	2560	40	20	20	160		
A/swine/Missouri/A02861595/2023	1A.3.3.2	pdm09	<10	<10	<10	<10	20	10	10	10	80	<10	<10	80		
IDCDC-RG76 A/Wisconsin/03/2021 CVV	1A.3.3.3-c3	gamma.3	<10	<10	<10	<10	20	<10	<10	10	5120	40	40	160		
A/swine/Minnesota/A02245409/2020*	1A.3.3.3-c3	gamma.3	<10	<10	40	80	40	<10	40	40	640	1280	1280	160		
A/swine/Minnesota/A02712157/2022*	1A.3.3.3-c3	gamma.3	<10	<10	20	40	20	<10	20	20	320	320	160	80		
A/swine/Quebec/N-2020-3-24/2020	1A.2	beta	<10	<10	<10	<10	<10	<10			80	<10	20	80		

Reference CVV in red, seasonal vaccines in dark red, new swine in bold. Homologous titers highlighted in gray. Human sera were collected in USA with titer relative to A/Wisconsin/67/2022, pool of 2 male and 2 female adults.

- The contemporary swine 1A.1.1.3 (alpha-del) had >8-fold decrease from 1A.1.1.3 CVV A/Ohio/24/2017 and A/California/71/2021 ferret anti-sera but retained reactivity to human pooled sera.
- The contemporary swine 1A.3.3.2 (pdm) with onward transmission in swine had >8-fold decrease to A/Victoria/4897/2022 5a.2a.1 and A/Wisconsin/67/2022 5a.2a vaccine strains but retained reactivity to human pooled sera.
- The contemporary swine 1A.3.3.3-c3 (gamma.3) virus had 4-8-fold decrease from the within-clade 1A.3.3.3-c3 CVV A/Wisconsin/2021 but retained reactivity to human pooled sera.
- The contemporary swine 1A.2 (beta) virus has no within clade CVV and >8-fold decrease to CVV and human seasonal vaccine ferret anti-sera but retained reactivity to human pooled sera.

Table 2. EU Study Design: Hemagglutination inhibition of CVV or human seasonal vaccine ferret antisera against contemporary swine 1A lineage strains.

- >8 fold reduction
- 8 fold reduction
- 4 fold reduction

Global Clade		A/California/71/21	A/California/7/2009	A/Guangdong-Maonan/SWL1536/2019	A/Victoria/2570/2019 (IVR-215)	A/Victoria/4897/2022 (IVR)-238	A/Ohio/9/2015 CVV
A/California/71/21	H1N1 1A.1.1.3	1280	20	160	160	0	40
A/California/7/2009	H1N1 1A.3.3.2	40	640	1280	320	320	0
A/Guangdong-Maonan/SWL1536/2019 (IVR-215)	1A.3.3.2, 1A.5a.1	40	2560	10240	1280	320	40
A/Victoria/2570/2019 (IVR-215)	1A.3.3.2, 1A.5a.2	80	160	640	10240	5120	160
A/Victoria/4897/2022 (IVR-238)	1A 3.3.2, 5a.2a.1	160	80	640	10240	10240	320
A/swine/Italy/63457-01/2024	1A.3.3.2	80	80	1280	10240	5120	80
A/Ohio/9/2015 CVV	H1N1 1A.3.3.3	20	40	160	80	20	320

Reference CVV in red, reference seasonal vaccine strains in dark red, new swine strains in bold.  
Homologous titers highlighted gray.

- The contemporary swine 1A.3.3.2 (pdm) with onward transmission in swine retained reactivity with A/Victoria/4897/2022 5a.2a.1 vaccine strain ferret anti-sera.

Table 3. Amino acid substitutions between representative swine 1A.1.1.3 clade strains compared to the within-clade CVVs (A/California/71/2021 and A/Ohio/24/2017) and recent 1A.1.1.3 variants.

site	A/California/71/2021	A/Ohio/24/2017	A/swine/Ohio/A02750994/2022	A/swine/North_Carolina/A02750921/2022	A/Ohio/25/1/2024	A/Pennsy/lyania/228/2024	A/Pennsy/lyania/242/2024	A/Pennsy/lyania/27/2024	annotations
48	A		S	S	S	S	S	S	
69	P	S	S	S	S	S	S	S	
70	I				T				Cb
71	P	L	L	L	L	L	L	L	Cb
84	N							S	
97	N				D	D			
103	V	E	E	E	E	E	E	E	
119	T	I	I	I	I	I	I	I	
124	S	P	P		P	P	P	A	Sa
126	H		Y	Y	Y	Y	Y	Y	
127	E	K	K	K	K	K	K	K	
128	T							K	
132	A	V	E	E	E	E	E	E	RBS
138	Y	D							
140	G			E					Ca2
141	K	A							
142	S			N			G		Ca2
143	S				G	G			
149	M	I		V					
155	G		A	A	A	A	A	A	Sa
156	D	N							Sb
157	S		L						Sa
160	M	R	R	K	R	R	R	R	Sa
166	A	V	V	V	V	V	V	V	Ca1
168	D	N	N	N	N	N	N	N	
170	G	R							Ca1
185	D	G	G		G	G	G	G	
186	S	N	N	N	N	N	N	N	
189	R	Q	Q	Q	Q	Q	Q	Q	Sb, RBS
195	T	A	A	A	A	A	A	A	Sb, RBS
209	K	E							
222	N	G	G	G	G	G	G		Ca2, RBS
224	A	T							RBS
232	A	T	T	T	T	T	T	T	
235	E			A					
252	R	K							
261	S			P					
272	I		T						
273	H						Y		
283	K			E					
286	L				I	I			
298	V						I		
308	R	K	K	K	K	K	K	K	
310	T		R	R	R	R	R	R	
311	R	K							
aadiff		26	21	22	26	24	24	26	

Reference CVVs in red, HI swine strains in purple.

Table 4. Amino acid substitutions between representative swine 1A.2 strain compared to the A/Wisconsin/67/2022, the nearest HI-tested human vaccine.

site	A/Wisconsin/67/2022	A/swine/Quebec/N-2020-3-24/2020	annotations
35	D	N	
54	Q	K	
61	I	L	
71	S	F	Cb
73	A	R	Cb
83	S	P	
85	S	P	
104	Q	H	
109	S	L	
120	T	A	
121	S	N	
128	S	T	
129	D	N	
130	N	K	
138	H	Y	
142	R	N	Ca2
156	K	N	Sb
161	I	L	
162	N	S	Sa
163	Q	K	Sa
164	T	S	Sa
168	D	N	
170	G	K	Ca1
176	L	I	
185	I	S	
189	E	Q	Sb, RBS
190	S	T	Sb, RBS
cont.			
site	A/Wisconsin/67/2022	A/swine/Quebec/N-2020-3-24/2020	annotations
195	A	E	Sb, RBS
203	T	S	
205	R	K	
216	T	A	
234	V	I	
235	E	D	
239	K	T	
250	A	V	
256	T	A	
259	K	R	
260	E	G	
261	A	S	
270	T	K	
273	H	Q	
274	D	N	
276	N	T	
277	A	T	
283	E	K	
285	A	S	
295	V	I	
298	I	V	
302	K	E	
308	R	K	
311	K	N	
314	L	M	
321	V	I	
aadiff		53	

Reference vaccine strain in gray, HI strain in purple.

Table 5. Amino acid substitutions between representative swine 1A.3.3.2 clade strains compared to two current WHO recommended human seasonal vaccines used in HI assays (A/Wisconsin/67/2022 and A/Victoria/4897/2022) and additional HI-tested seasonal vaccine strains and CVV.

site	A/Wisconsin/67/2022	A/Victoria/4897/2022	A/California/07/2009	A/Victoria/2570/2019	A/Guangdong-Maonan/SWL1536/2019	A/swine/Iowa/A02524480/2020	A/swine/Missouri/A02861595/2023	A/swine/Italy/63457-01/2024	annotations
47	V							I	
54	Q		K	K	K				
74	R		S						Cb
83	S		P						
84	N		S						
96	I						T		
97	N		D						
112	E					D			
113	R				K				
120	T						A		
127	D					N			
129	D		N			N			
130	N		K		K	K			
137	S		P	P	P		P	Ca2	
142	R		K	K	K	K	K	Ca2	
156	K		N		N	N	Q		Sb
161	I		L		L	L			
162	N		S					Sa	
163	Q		K					Sa	
164	T		S					Sa	
173	V				I				
183	P		S						
185	I		S			T			
186	T		A	A	A	A			
187	D				A			RBS	
189	E		Q	Q		Q		Sb, RBS	
203	T		S						
216	T	A	I			A			
217	R					X			
223	Q	R		R				RBS	
224	A		E	E	E	E		RBS	
250	A		V		V	V			
256	T		A						
259	K		R	R	R	R			
260	E		N	D	D	N		D	
277	A		T	T	T	T		T	
283	E		K						
295	V		I						
308	R		K	K	K	K			
321	V		I						
aadiff		2	30	11	14	17	5	7	

Reference vaccine strains in gray, HI strains in purple.

Table 6. Amino acid substitutions between representative 1A.3.3.3-c3 swine strains compared to nearest HI-tested CVVs (A/Wisconsin/03/2021 and A/Ohio/9/2015).

site	A/Wisconsin/03/2021	A/Ohio/9/2015	A/swine/Minnesota/A02245409/2020	A/swine/Minnesota/A02712157/2022	annotations
2	T	K			
3	L	I			
35	T	N	N	N	
36	R	K			
45	K	R	R	R	
48	A	X			
56	N			S	
71	S	A			Cb
74	S			R	Cb
83	S		P		
84	N	S		K	
86	E	N			
113	R	K			
120	T		A		
127	E		D	D	
129	D	N	N	N	
130	K		R		
137	P		S		Ca2
142	R	N	N	N	Ca2
146	R	K			
149	V	I			
153	Q	K			Sb
155	G	E			Sa
161	V	I		I	
163	T	I	K	K	Sa
166	I	T			Ca1
168	N			D	
169	K	R	R		
170	E	G			Ca1
171	K			R	
183	S	P			
186	A	T			
189	R	Q	Q	Q	Sb, RBS
193	K	Q			Sb, RBS
195	E	A	A	A	Sb, RBS
196	D	N			
197	A	S			
205	R		K	K	
222	D	G			Ca2, RBS
224	S	A	A	A	RBS
250	A	V			
252	R			I	
262	G			E	
269	D	E			
270	A	T	T	T	
271	S	P			
278	T			A	
295	I			V	
302	E			K	
326	S			T	
aadiff	34	16	23		

Reference CVVs in red, HI swine strains in purple.

## 1B human-like lineage

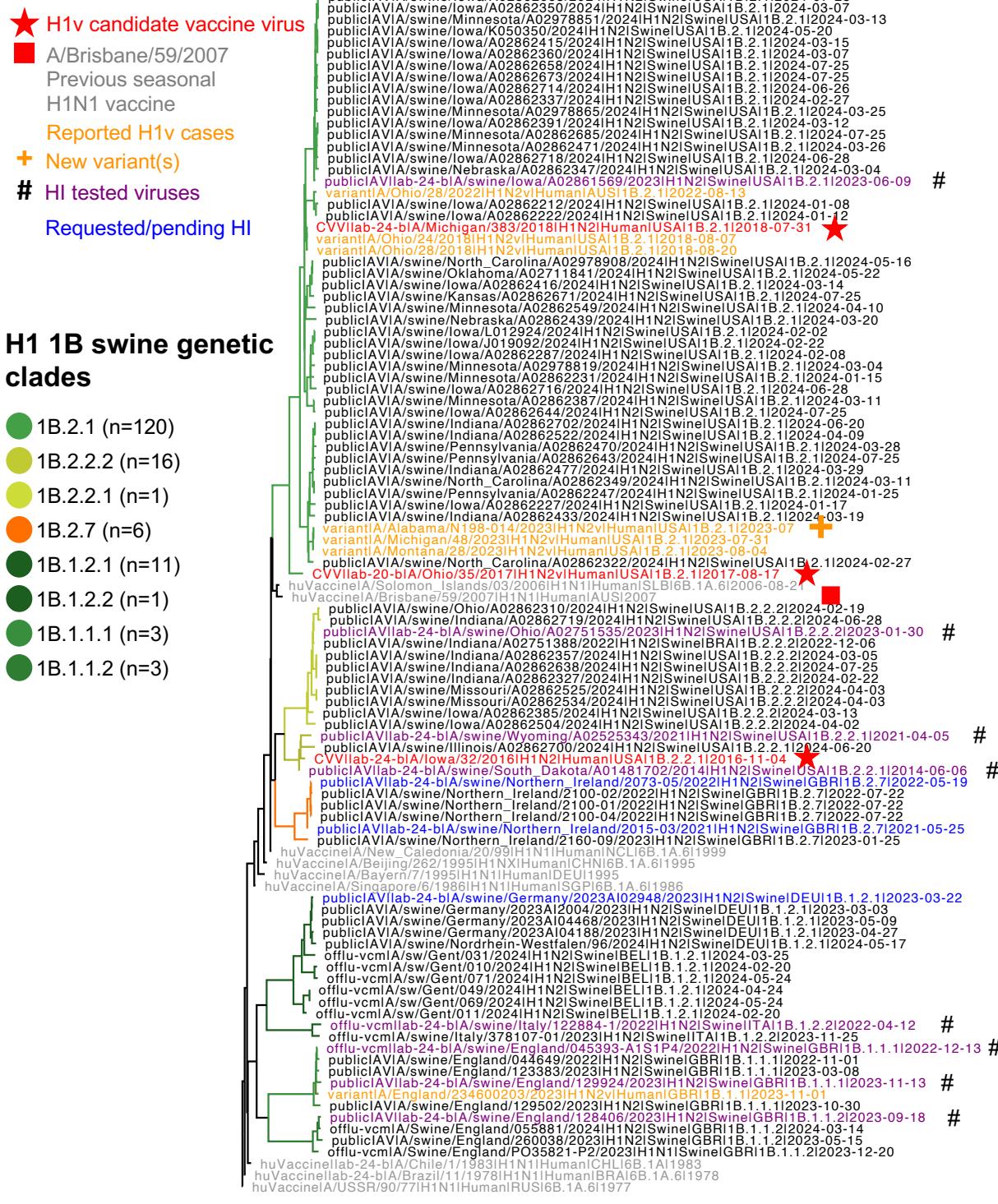


Figure 8. Swine H1 HA genes of the 1B lineage (tree was proportionally down sampled to 85 swine HA genes, excluding references). Number of detections of each clade from data deposited on or after January 1, 2024 are presented adjacent to the clade name in the figure key.

## Antigenic analysis: Swine 1B Lineage

Table 7. USA Data: Hemagglutination inhibition of CVV vaccine ferret antisera against contemporary swine 1B lineage strains selected to represent clade consensus.

- > 8 fold reduction
- 8 fold reduction
- 4 fold reduction

	Global Clade	US Clade	A/Michigan/383/2018 RG58A	A/Iowa/32/2016	A/swine/Wyoming/A02525343/2021** #15	A/swine/Wyoming/A02525343/2021* #16	Human Pooled Sera
A/Michigan/383/2018 RG58A	1B.2.1	delta-2	160	<10	<10	<10	80
+ A/swine/Iowa/A02861569/2023	1B.2.1	delta-2	160	40	10	10	40
A/Iowa/32/2016	1B.2.2.1	delta-1a	<10	160	40	20	80
A/swine/Wyoming/A02525343/2021	1B.2.2.1	delta-1a	<10	20	160	80	80
A/swine/South_Dakota/A01481702/2014	1B.2.2.1	delta-1a	<10	10	20	<10	80
A/swine/Ohio/A02751535/2023*	1B.2.2.2	delta-1b	<10	10	<10	<10	20

Reference CVV in red, new swine strains in bold. Homologous titers highlighted gray. Human sera were collected in USA with titer relative to A/Wisconsin/67/2022, pool of 2 male and 2 female adults.

- The 1B.2.1 (delta-2) clade swine representative had no loss of titer to the within clade CVV and had a 4-fold loss in cross-reactivity to human pooled sera.
- The 1B.2.2.1 (delta-1a) clade swine representative had 8-fold reduction from the within clade CVV A/Iowa/32/2016 but retained reactivity to human pooled sera.
- The contemporary swine 1B.2.2.2 (delta-1b) does not have a within-clade CVV and had a >8-fold decrease from CVV A/Iowa/32/2016 and had an 8-fold loss in cross-reactivity to human pooled sera.

Table 8. EU Study Design: Hemagglutination inhibition of CVV vaccine ferret antisera against contemporary swine 1B lineage strains selected to represent clade consensus.

	Global Clade	A/Chile/1/1983	A/Brazil/1/1978	A/Michigan/383/2018 CVV
A/Chile/1/1983	H1N1 1B	640	640	20
A/Brazil/11/1978	H1N1 1B	320	2560	40
A/swine/England/045393-A1S1P4/2022*	1B.1.1.1	10	80	40
A/Swine/England/129924/2023*	1B.1.1.1	20	320	80
A/Swine/England/128406/2023*	1B.1.1.2	320	5120	160
A/swine/Italy/122884-1/2022 H1N2*	1B.1.2.2	80	320	40
A/Michigan/383/2018 CVV	H1N2 1B.2.1	160	640	2560
A/swine/Northern Ireland/2015-03/2021	1B.2.7	40	40	80
A/swine/Northern Ireland/2073-05/2022	1B.2.7	40	40	80

- >8 fold reduction
- 8 fold reduction
- 4 fold reduction

\*Previously tested in report 2024a. Reference CVV in red, reference seasonal vaccine strains in dark red. New swine strains are bolded. Homologous titers highlighted gray.

- There are no within-clade CVVs for 1B lineages from Europe and the 1B.2.1 CVV has >8-fold loss in reactivity with 1B.1 representative swine strains.
- The swine 1B.1.1.1 had >8-fold loss in cross-reactivity with A/Chile/1/1983 and A/Brazil/11/1978.
- The swine 1B.1.1.2 strain retained cross-reactivity with the ancestral human seasonal reference strains.
- The contemporary swine 1B.1.2.2 had >8-fold loss in cross-reactivity against the human seasonal reference strains.
- The swine 1B.2.7 clade viruses had no within-clade CVV and >8-fold loss in cross-reactivity with A/Chile/1/1983 and A/Brazil/11/1978.

Table 9. Amino acid substitutions between representative swine 1B.1.x strains compared to most similar HI-tested vaccine strains (A/Chile/1/1983 and A/Brazil/11/1978).

site	A/Chile/1/1983	A/Brazil/11/1978	A/swine/England/045393-A1S1P4/2022	A/swine/England/128406/2023	A/swine/England/129924/2023	A/swine/Italy/122884-1/2022	annotations	site	A/Chile/1/1983	A/Brazil/11/1978	A/swine/England/045393-A1S1P4/2022	A/swine/England/128406/2023	A/swine/England/129924/2023	A/swine/Italy/122884-1/2022	annotations
14	D		E		E			176	L		I				
19	V			I				181	H		N				
35	D			N				185	I		M				
36	N	S	S	S	S			189	K		R		R	Sb, RBS	
43	K	R						190	T	A	A	A	A	Sb, RBS	
44	L			M				193	R	H		H		Sb, RBS	
47	I					V		194	K	N		N		RBS	
48	A		P		P			196	N		T		T		
54	K		T		T	R		197	A	T		T			
66	E		K		K			202	V				M		
70	L			S			Cb	205	H	N					
71	F					L	Cb	207	N				S		
73	K			R			Cb	208	R				K	K	
74	K		N		N		Cb	209	R		K		K	K	
82	T		L		S	A		215	A			E			
85	S		P	P	P	A		216	K		R		R		
89	T		I	I	I	L		220	V	I	I	I	I	RBS	
94	Y		H		H	H		222	N	G			D	Ca2, RBS	
96	A		S	S	S	S		237	G		D	S	D	Ca1	
111	F			I		I		238	D	E	E	E			
116	I			M				239	T	E	I	E			
120	E		D		D			248	L		F				
121	S	R						252	W	Q		L			
125	K		G	N	G		Sa	258	S				N		
127	N					S		260	G		S		S		
128	V	I			I			261	F		L				
129	T				-			262	G		R		E		
130	K	R		R		-		267	T	I	I	I	V		
132	V			K	L	A	RBS	270	A	T		T	V		
134	A			V			RBS	272	M		L				
135	A	S	S	S	S	S	RBS	273	D		G				
137	S		P		P	P	Ca2	276	D		N		N	N	
138	H					K		277	A	T	T	T	T		
139	K		D	N	D	Q		278	K		E		T		
141	K					R		283	Q				R		
146	R			K		T		287	N			T			
149	L	V		V				288	S		N		N		
153	E	G		G		Sb		295	V			I			
155	N		D		N		Sa	298	V			I			
156	G	N		N		Sb		299	T		A				
157	S	L	L	L		Sa		305	K		R				
161	L	V	I	V	M			307	V		I				
162	S	N		N	T	Sa		308	R	K	K	K	K		
163	K		N		M	Sa		310	T			K			
164	S		R			Sa		311	K		R				
166	V				M	Ca1		313	R			K			
168	N				D			315	V			A			
170	E			G	R	Ca1		324	I		V		V		
171	K				R			aadiff	9	39	49	44	50		

Reference human seasonal vaccines in gray, HI swine strains in purple.

Table 10. Amino acid substitutions between representative 1B.2.1 swine strain compared to the within-clade CVV (A/Michigan/383/2018 RG58A) and a recent 1B.2.1 variant.

site	A/Michigan/383/2018	A/swine/Iowa/A02861569/2023	A/Alabama/N198-014/2023	annotations
5	V		I	
16	V		I	
69	L		M	
71	N	T	I	Cb
82	T		K	
83	S	A	P	
89	T	I	A	
112	K	E		
113	K		R	
119	K		E	
120	K	E		
141	N	E		
168	K	N	T	
169	E		K	
170	G		E	Ca1
173	V	I	I	
185	M		I	
193	H	R	N	Sb, RBS
224	E		G	RBS
237	G		K	Ca1
256	E	K		
258	S	N		
260	S		G	
277	T		A	
310	A		T	
aadiff		11	20	

Reference CVV strain in red, HI swine strain in purple, variant in orange.

Table 11. Amino acid substitutions between representative swine 1B.2.2.1 strains compared to the within-clade CVV (A/Iowa/32/2016).

site	A/Iowa/32/2016	A/swine/Wyoming/A02525343/2021	A/swine/South_Dakota/A01481702/2014	annotations
19	L	V	V	
72	S	P		
74	K	E	E	Cb
96	T	A	A	
106	S	N		
130	T	D		
132	K	T	V	RBS
141	E		K	
157	L	R		Sa
166	K		E	Ca1
168	E	D	D	
175	I	V		
208	R	K		
215	T	A		
222	D	N		Ca2, RBS
241	I	V		
287	N	T		
310	T	R		
aadiff		16	7	

Reference CVV strain in red, HI swine strains in purple.

Table 12. Amino acid substitutions between representative swine 1B.2.2.2 strain compared to the nearest tested CVV (A/Iowa/32/2016) in USA HI assays and the most similar human vaccine (A/Michigan/2/2003).

Relative to HI				Relative to most similar vaccine			
site	A/Iowa/32/2016	A/swine/Ohio/A02751535/2023	annotations	site	A/Michigan/2/2003	A/swine/Ohio/A02751535/2023	annotations
19	L	V		36	S	N	
36	S	N		50	L	I	
50	L	I		69	L	S	
82	A	T		74	E	K	Cb
85	S	P		94	Y	D	
86	D	E		129	V	T	
94	Q	D		132	V	K	RBS
96	T	A		141	K	E	
119	R	K		146	R	K	
129	V	T		149	L	V	
142	G	S	Ca2	153	G	E	Sb
146	R	K		162	I	S	Sa
149	I	V		166	A	K	Ca1
153	V	E	Sb	168	N	D	
168	E	D		175	I	V	
170	G	E	Ca1	176	L	I	
175	I	V		184	N	D	
176	L	I		186	G	E	
183	S	P		187	D	N	RBS
184	N	D		193	H	R	Sb, RBS
186	G	E		194	T	K	RBS
187	D	N	RBS	202	V	A	
193	H	R	Sb, RBS	208	R	E	
194	T	K	RBS	222	D	N	Ca2, RBS
202	M	A		228	N	K	
208	R	E		236	P	A	
222	D	N	Ca2, RBS	244	A	S	
228	N	K		249	I	V	
236	P	A		256	A	T	
244	T	S		261	F	L	
249	I	V		271	P	S	
256	A	T		273	D	N	
269	K	N		274	E	Q	
271	P	S		277	A	T	
273	D	N		aadiff		34	
274	E	Q					
277	A	T					
283	K	Q					
289	N	S					
310	T	A					
aadiff		40					

Reference CVV in red, reference human seasonal vaccine in gray, HI swine strain in purple.

Table 13. Amino acid substitutions between representative swine 1B.2.7 strains compared to the nearest tested CVV (A/Iowa/32/2016) in HI assays and the most similar human vaccine (A/New\_Caledonia/20/99).

site	Relative to HI			Relative to most similar vaccine			annotations	
	A/Iowa/32/2016	A/swine/Northern_Ireland/2015-03/2021	A/swine/Northern_Ireland/2073-05/2022		A/New_Caledonia/20/99	A/swine/Northern_Ireland/2015-03/2021	A/swine/Northern_Ireland/2073-05/2022	
19	L	V	V					
24	V	I	I					
30	V	I						
43	L	S	S					
44	L	I	I					
68	E	K	K					
72	S	P	P					
73	K	Q	Q	Cb				
74	K	E	E	Cb				
82	A	T	T					
85	S	P	P					
86	D	K	K					
94	Q	H	H					
96	T	D	D					
112	E	K	K					
119	R	K	K					
132	K	V	V	RBS				
142	G	R	R	Ca2				
149	I	L	L					
153	V	E	E	Sb				
163	K	M	M	Sa				
166	K	S	S	Ca1				
168	E	N	N					
170	G	E	E	Ca1				
173	V		I					
183	S	P	P					
184	N	D	D					
186	G	Q	Q					
187	D	N	N	RBS				
197	A		T					
202	M	V	V					
237	G	E	E	Ca1				
244	T	A	A					
258	S	D	D					
261	L	F	F					
269	K	N	N					
271	P	S	S					
273	D	S	S					
277	A	T	T					
283	K	Q	Q					
289	N	R	R					
295	V	I	I					
306	Y	F	F					
310	T	A	A					
321	I	T	T					
aadiff		43	44					

Reference human seasonal vaccine strain in gray, HI swine strains in purple.

## 1C Eurasian avian lineage

★ H1v candidate vaccine virus

Reported H1v cases

+ New variant(s)

# HI tested viruses

Requested/pending HI

## H1 1C swine genetic clades

- 1C.2.4.3 (n=43)
- 1C.2.4.2 (n=37)
- 1C.2.4.1 (n=31)
- 1C.2.1 (n=28)
- 1C.2.2 (n=71)
- 1C.2.3 (n=3)
- 1C.2.5 (n=5)
- 1C.2 (n=1)

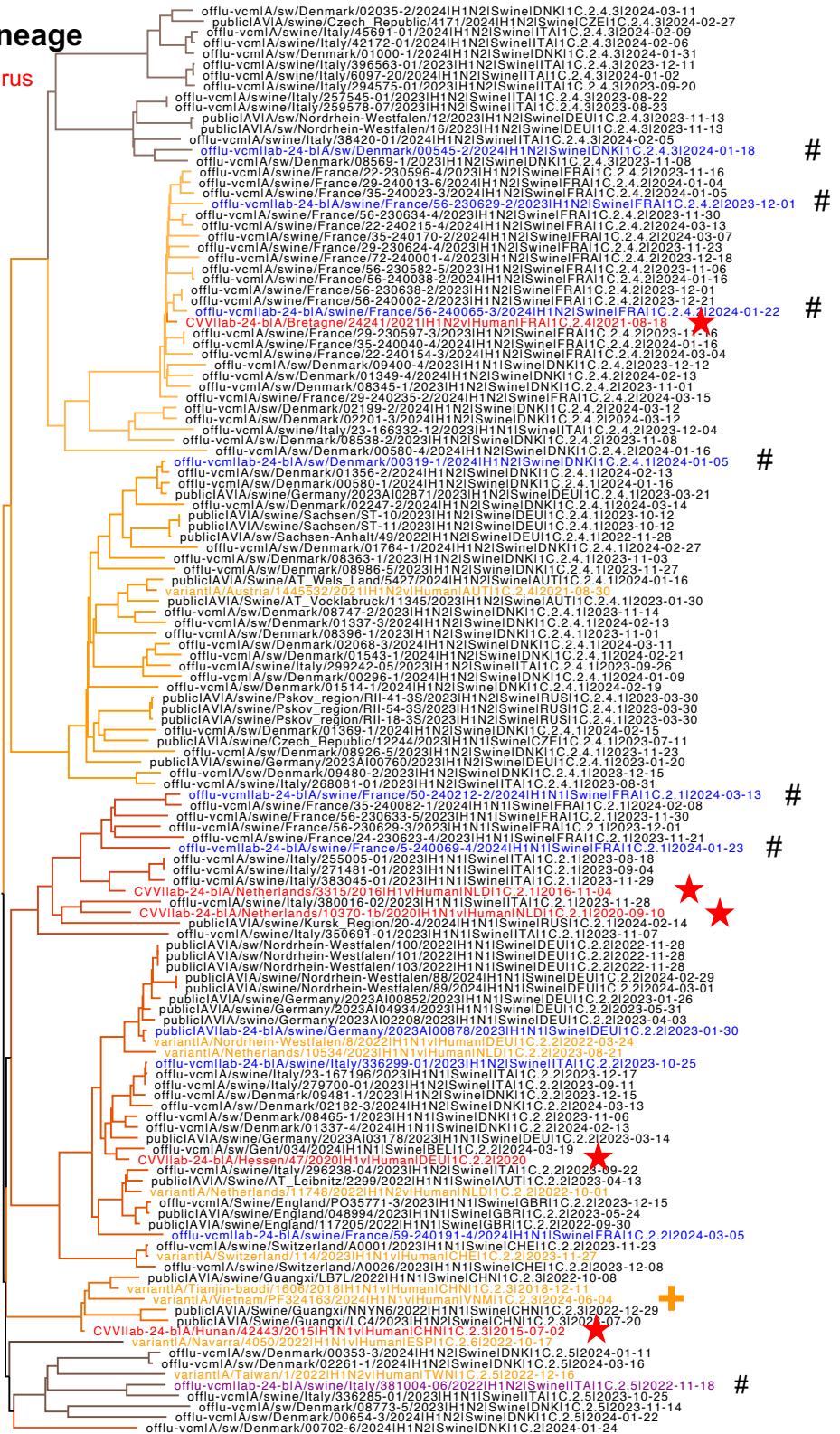


Figure 9. Swine H1 HA genes of the 1C lineage (tree was proportionately downsampled to 109 swine HA sequences, excluding references). Number of detections of each clade from data deposited on or after January 1, 2024 are presented adjacent to the clade name in the figure key.

## Antigenic analysis: Swine 1C Lineage

Table 14. UK & EU Study Design: Hemagglutination inhibition of CVV vaccine ferret antisera against contemporary swine 1C lineage strains selected to represent clade consensus.

			A/Netherlands/3315/2016 CVV	A/Netherlands/10370-1b/2020 CVV	A/Hessen/47/2020-like CVV	A/Hunan/42443/2015 CNIC-1601 CVV	A/Bretagne/24241/2021 CVV
		Global Clade					
A/Netherlands/3315/2016 CVV	1C.2.1		640	640	1280	20	80
A/Netherlands/10370-1b/2020 CVV	1C.2.1		40	640	640	80	20
A/swine/France/5-240069-4/2024	1C.2.1		160	320	320	20	160
A/swine/France/50-240212-2/2024	1C.2.1		160	320	320	20	20
A/Hessen/47/2020-like CVV	1C.2.2		40	160	5120	640	20
A/Hunan/42443/2015 CNIC-1601 CVV	1C.2.3		160	320	5120	1280	40
A/swine/Denmark/00319-1/2024	1C.2.4.1		80	640	320	40	320
A/Bretagne/24241/2021 CVV	1C.2.4.2		160	160	160	40	10240
A/swine/France/56-230629-2/2023	1C.2.4.2		80	160	1280	40	10240
A/swine/France/50-2400122-4/2024	1C.2.4.2		80	320	320	40	2560
A/swine/France/56-240065-3/2024	1C.2.4.2		80	160	640	40	5120
A/swine/Denmark/00545-2/2023	1C.2.4.3		20	160	640	20	40

Reference CVV in red, new swine strains in bold. Homologous titers highlighted in gray. \*Previously tested in report 2024a.

- The 1C.2.1 strain retained cross-reactivity to the 1C.2.1 CVV A/Netherlands/10370-1b/2020.
- The 1C.2.4.1 swine strain from Denmark retained cross-reactivity with a different clade CVV strain (1C.2.1: A/Netherlands/10370-1b/2020).
- The 1C.2.4.2 swine strains retained reactivity to the within-clade CVV A/Bretagne/24241/2021.
- The representative swine 1C.2.4.3 had no within-clade CVV and demonstrated a range of 4- to >8-fold loss to available 1C CVV strains.

Table 15. Amino acid substitutions between representative swine 1C.2.1 strains compared to within-clade CVVs (A/Netherlands/3315/2016 and A/Netherlands/10370-1b/2020).

site	A/Netherlands/3315/2016	A/Netherlands/10370-1b/2020	A/swine/France/15-240069-4/2024	A/swine/France/50-240212-2/2024	annotations
20	M		L	L	
31	N	D			
44	L	M			
51	Q			H	
69	L		S	S	
71	I	L		L	Cb
74	N	K			Cb
80	I			V	
83	S	P			
84	N		K	K	
96	A		T	T	
97	D	N	N		
120	E	A	A	A	
125	N		S		Sa
132	S	T			RBS
134	V		I		RBS
136	C			X	
137	S	P	T	T	Ca2
141	I	A	V	V	
142	K	N	N	X	Ca2
152	V		I		
155	E	G	A	A	Sa
161	I	L			
162	S			N	Sa
163	T	K	K	E	Sa
169	K			R	
175	I	V	V	V	
179	V		I		
190	T			A	Sb, RBS
199	V	I			
202	G	E	E	E	
204	S		P		Ca1
208	K	Q			
214	I			V	
215	V	A	I		
220	V		I		RBS
236	Q			K	
253	Y	H			
258	N	D			
262	N			S	
266	M			V	
267	M	I			
271	N	H		S	
272	V			I	
273	H			Q	
288	S			G	
298	I			L	
311	Q	R			
321	T	I	V	I	
324	V	I	I	I	
aadiff		26	22	30	

Reference CVVs in red, HI swine strains in purple.

Table 16. Amino acid substitutions between recent 1C.2.3 variant compared to within-clade CVV (A/Hunan/42443/2015).

site	A/Hunan/42443/2015	A/Vietnam/PF324/163/2024	annotations
31	N	D	
47	K	Q	
54	N	K	
56	S	N	
66	K	E	
86	K	T	
107	T	A	
108	V	I	
171	K	R	
253	H	Y	
258	K	R	
302	E	K	
314	M	L	
aadiff		13	

Reference CVV in red, new variant detection in orange.

Table 17. Amino acid substitutions between representative swine 1C.2.4.x strains compared to the within-clade CVV (A/Bretagne/24241/2021) and similar 1C.2.3 CVV (A/Hunan/42443/2015).

cont.

site	A/Bretagne/24241/2021	A/Hunan/42443/2015	A/sw/Denmark/00319-1/2024	A/swine/France/56-230629-2/2023	A/swine/France/56-240065-3/2024	A/sw/Denmark/00545-2/2024	A/swine/France/50-240122-4/2024	annotations	site	A/Bretagne/24241/2021	A/Hunan/42443/2015	A/sw/Denmark/00319-1/2024	A/swine/France/56-230629-2/2023	A/swine/France/56-240065-3/2024	A/sw/Denmark/00545-2/2024	A/swine/France/50-240122-4/2024	annotations
5	I	V	V			V			157	P	S	S			S	Sa	
20	M	L	L			L	T		159	S	P	P			P	Sa	
31	N					D			161	L					I		
35	T	N							162	S		N				Sa	
36	N	S	S						163	K		G		E		Sa	
39	G		E						166	K	T	T	R	T		Ca1	
40	K					R			168	N					D		
43	S					N			169	K					R		
48	A	I							172	E					K		
56	D	S	N	N	N	N	N	N	185	Y	D						
57	V			I					186	S		R					
66	E	K							194	N		H	S		RBS		
69	L				I	M			200	S					L		
71	V	L	L		L		Cb		201	V					I		
74	N		S				Cb		202	V	G	E			R		
80	I			V					203	S					T		
83	S		P						208	Q	K	R			R		
84	N		S						216	P	A	T	S	D			
86	K		E						218	P		Q			RBS		
89	T	A			I				219	E	K	R			K	RBS	
96	A		S		S				220	I	V				RBS		
99	E				G				222	E			K		K	Ca2, RBS	
102	R	K							224	R	A	A	A		RBS		
104	L	Q	R						236	Q			K				
105	L					I			237	E	G	G	G		Ca1		
111	F		L						239	T			N				
119	K				G	E			252	R	W	W					
120	-	A	A		A				253	Y	H						
121	N	T	T		T				258	E	K	D	D	D	D		
124	P				K		Sa		259	K					M		
125	S	N	D		N		Sa		260	G					S		
127	E	D			K				261	S		L	Y	P			
128	A	T	T		T				262	N	S			S	S		
129	-	T	T						266	M		V					
130	-	R	Q		D				267	K	R	I	E				
134	V		I				RBS		269	D		E					
135	S	A	A				RBS		271	H	Q			R			
138	K	H	H	R	R				288	S	G	G					
141	A				T				289	D	N	N		N	G		
142	N		K	S	P	X	Ca2		290	R	L	L					
146	R				Q				298	I	V						
152	T	V	V						307	V				I			
153	S	K			K		Sb		311	Q		R	K				
155	G				-		Sa		313	R			K				
156	K	N	G		S		Sb		aadiff	44	49	8	5	52	12		

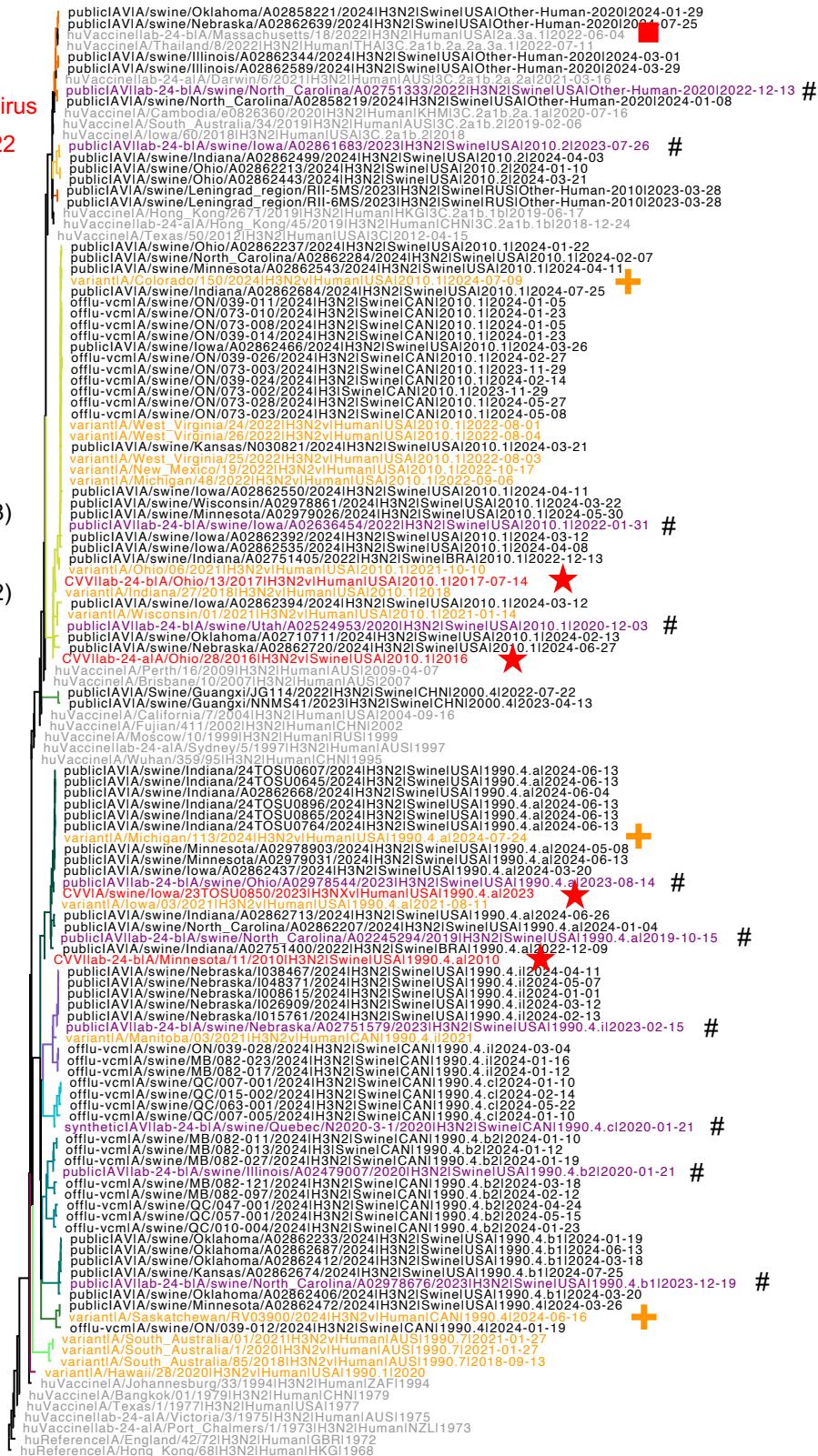
Reference CVVs in red, HI swine strains in purple.

## H3 swine lineage

- ★ H3v candidate vaccine virus
- A/Massachusetts/18/2022
- Previous H3N2 seasonal vaccines
- Reported H3N2v cases
- + New variant(s)
- # HI tested viruses

## H3 swine genetic clades

- Other-Human-2020 (n=8)
- 3.2010.2 (n=3)
- Other-Human-2010 (n=2)
- 3.2010.1 (n=113)
- 3.2000.4 (n=2)
- 3.1990.4.a (n=81)
- 3.1990.4.i (n=14)
- 3.1990.4.c (n=4)
- 3.1990.4.b2 (n=8)
- 3.1990.4.b1 (n=8)
- 3.1990.4 (n=2)
- Human vaccine or seasonal



0.03

Figure 10. Swine H3 HA genes (tree was proportionally down sampled to 85 swine HA genes, excluding references). Number of detections of each clade from data deposited on or after January 1, 2024 are presented adjacent to the clade name in the figure key.

## Antigenic analysis: Swine H3

Table 18. USA Data: Hemagglutination inhibition of CVV or human seasonal vaccine ferret antisera against contemporary swine H3 strains selected to represent clade consensus.

- > 8 fold reduction
- 8 fold reduction
- 4 fold reduction

Global Clade		A/Minnesota/11/2010 x 203	A/swine/Iowa/23TOSU0850/2023	A/swine/North_Carolina/A02245294/2019 (H3N2) #32	A/swine/North_Carolina/A02245294/2019 (H3N2) #18	IDCDC-RG60A A/Ohio/13/2017 CVV	A/swine/Utah/A02524953/2020 (H3N2) #19	A/swine/Utah/A02524953/2020 (H3N2) #20	A/Massachusetts/18/2022	Human pooled sera
A/Minnesota/11/2010 x 203	1990.4.a	1280	40	80	160	20	40	80	nt	40
A/swine/Iowa/23TOSU0850/2023	1990.4.a	20	1280	40	40	<10	<10	<10	<10	160
A/swine/North_Carolina/A02245294/2019	1990.4.a	80	160	640	640	20	20	40	20	40
+ A/swine/Ohio/A02978544/2023	1990.4.a	40	320	320	320	10	10	20	20	80
A/swine/North_Carolina/A02978676/2023	1990.4.b1	40	20	40	40	20	40	40	20	80
A/swine/Illinois/A02479007/2020	1990.4.b2	20	640	640	640	40	20	20	20	40
A/swine/Quebec/N2020-3-1/2020	1990.4.c	40	80	40	40	20	40	40	20	10
A/swine/Nebraska/A02751579/2023	1990.4.i	<10	40	10	10	<10	10	10	20	40
IDCDC-RG60A A/Ohio/13/2017 CVV	2010.1	<10	80	20	80	1280	160	160	20	320
A/swine/Utah/A02524953/2020	2010.1	10	20	40	40	160	640	640	40	80
+ A/swine/Iowa/A02636454/2022	2010.1	10	<10	20	40	160	320	320	10	160
A/swine/Iowa/A02861683/2023	2010.2	10	<10	10	10	<10	10	20	80	80
A/swine/North_Carolina/A02751333/2022	2020.1	<10	<10	10	10	<10	<10	<10	160	320
A/Massachusetts/18/2022	2a.3a.1	<10	<10	10	10	10	<10	10	1280	160
A/Darwin/6/2021										640

Reference CVV in red, seasonal vaccine strains in dark red, new swine strains in bold. Homologous titers highlighted in gray. Human sera were collected in USA with titer relative to A/Darwin/6/2021, pool of 2 male and 2 female adults. nt=not tested.

- The contemporary swine 1990.4.a had a 4-fold decrease from CVV A/swine/Iowa/23TOSU0850/2023 and had > 8-fold reduction in reactivity in adult human pooled sera.
- The contemporary swine 1990.4.b1 does not have a CVV contained within clade and demonstrated a >8-fold decrease from CVV and had >8-fold reduction in reactivity in adult human pooled sera.
- The contemporary swine 1990.4.i does not contain a within clade CVV and demonstrated a >8-fold decrease from CVV A/Minnesota/11/2010 and had >8-fold reduction in reactivity in adult human sera.
- The contemporary swine 2010.1 representative strain had an 8-fold loss to A/Ohio/13/2017 and an 8-fold loss in reactivity with adult human sera.
- The contemporary swine 2010.2 and 2020.1 representative strains do not contain CVV and demonstrated 8-fold or greater loss to the human vaccine strain. The 2010.2 strain had 8-fold loss in reactivity against adult human high responder sera.

Table 19. Amino acid substitutions between representative swine 1990.4.x strains compared to within-lineage CVVs (A/swine/Iowa/23TOSU0850/2023 and A/Minnesota/11/2010 x 203) and recent variants.

site	A/swine/Iowa/23TOSU0850/2023	A/Minnesota/11/2010	A/swine/Ohio/A02978544/2023	A/swine/North_Carolina/A02245294/2019	A/swine/Nebraska/A02751579/2023	A/swine/North_Carolina/A02978676/2023	A/swine/Illinois/A02479007/2020	A/swine/Quebec/N2020-3-1/2020	A/Saskatchewan/RV03900/2024	A/Michigan/113/2024	annotations
1	Q			K				R			
2	K			N							
5	G					E					
6	N	S	S	S	S	S	D	S			
8	N		K								
9	S					N	N				
10	M		T								
21	P					S					
27	K				R						
46	S			T							
48	T			K							
49	G		D								
50	R			E							
53	N			S	S						Site C
54	S						G				Site C
56	H				Y						
57	Q			K	K	K		K			
58	I		V				V				
62	K		G								
78	D					G					
80	Q		E								
81	N			D		D					
82	K			R							
83	E			T	K				K		
96	S	N	N	D	N	N	N	N			
101	Y						F				
103	P					R					
104	D		E								
105	Y						H				
106	A				T						
107	T		S	S	S	S	S				
117	N		T	T	T	T	T	T			
119	E		K				Q				
121	T		N		N						
122	Q		P			P					Site A
124	I	S	N	N	S	N	V				
131	A		T	G	D		N				
133	D		N								Site A
135	S			A							
137	Y		F		I	F	L				Site A
138	S	A			A		A				
140	R		K		K		K				
142	G		N			K					
144	V			E	D		N				Site A
145	N		K		S	K					Site A
155	Y		H	H			H				Site B
156	H	N		S			N				
158	N		E			D					

cont.

Reference CVVs in red, HI swine strains in purple, new variant detection in orange.

Table 20. Amino acid substitutions between representative swine 2010.1 strains compared to the within-clade CVVs (A/Ohio/28/2016) and recent variant.

site	A/Ohio/13/2017	A/swine/Utah/A02524953/2020	A/swine/Iowa/A02636454/2022	A/Colorado/150/2024	annotations
25	I			M	
30	T			M	
31	N		D	D	
45	S		N	N	
56	Y	H			
62	E		G	G	
88	V	I			
92	K	R			
96	N		D	D	
106	A		V		
112	V	A			
122	N		K	K	Site A
142	R			K	
144	S	T			Site A
156	H	Q			
158	N			D	
167	T	A			
202	I		T	T	
209	N	G			
212	A		T	T	
216	N			I	
223	V		I	I	
238	R		K	K	
264	K		R	R	
312	N	K			
aadiff		9	11	15	

Reference CVV in red, HI swine strains in purple, new variant detection in orange.

Table 21. Amino acid substitutions between representative swine 2010.2 strain compared to current WHO recommended human seasonal vaccine and used in HI assays (A/Massachusetts/18/2022) and HI-tested CVV (A/Ohio/13/2017). A separate comparison was also made against the most similar human vaccine (A/Kansas/14/2017).

Relative to A/Massachusetts/18/2022				Relative to most similar vaccine			
site	A/Massachusetts/18/2022	A/Ohio/13/2017	A/swine/Iowa/A02861683/2023	site	A/Kansas/14/2017	A/swine/Iowa/A02861683/2023	annotations
3	I	L					
9	S	N	G				
10	T	M					
31	N		D				
33	R	Q					
45	N	S					
46	S	F					
48	I	T					
50	K	E	E				
56	H	Y					
58	I		V				
62	G	E	E				
67	I		V				
82	K	N					
83	E	K	Q				
92	R	K					
94	N	H	Y				
96	S	N	N				
106	A		V				
121	K	N					
131	K	T	T				
133	N	D		Site A			
135	T	A	I				
138	A	S	S				
142	G	R					
144	S		K	Site A			
145	S	N		Site A			
156	S	H	Q				
158	N		D				
159	N	F	Y				
160	I	K	K				
164	Q	L	L				
165	N	E					
167	T		I				
171	K	N	N				
174	F		X				
186	D	A	G	Site B			
189	K		S	Site B			
190	N	D	D				
192	F	I	T				
195	F	Y	Y				
197	Q		R				
198	S	A					
199	S	A					
203	T	I	I				
209	S	N					
223	V		I				
238	K	R					
242	I		T				
278	K	N		Site C			
280	E	A					
291	D		N				
312	S	N					
323	V	I					
aadiff		41	32				

Reference vaccine strain in gray, CVV in red, HI swine strain in purple.

Table 22. Amino acid substitutions between representative swine 2020.1 strain compared to the A/Massachusetts/18/2022, the nearest HI-tested human vaccine and most similar human vaccine.

site	A/Massachusetts/18/2022	A/swine/North_Carolina/A02751333/2022	annotations
53	N	D	Site C
79	F	V	
96	S	N	
156	S	H	
192	F	I	
223	V	I	
aadiff		6	

Reference vaccine in gray, HI swine strain in purple.

## **Summary and Risk Assessment**

### **Global Variant Cases:**

During the reporting period (January 1 – June 30, 2024), 4 variant cases were reported and included with the swine analyses when sequence data were available:

- Canada: H3N2v (1990.4)
- USA: H1N2v (2x 1A.1.1.3)
- Vietnam: H1N1v (1C.2.3)

Additional variant cases were detected outside of this period, when sequence data were available these were included in analyses:

- USA: H1N2v (2x 1A.1.1.3 – August 5, August 7 2024; 1x 1B.2.1 – July 2023), H3N2v (1990.4.a – July 24 2024), H3N2v (2010.1 – July 9, 2024)

### **Europe Swine:**

- H1 1A: The contemporary swine 1A.3.3.2 retained cross-reactivity with recent human seasonal H1 vaccines.
- H1 1B: There were no within-clade CVVs tested for 1B lineages from Europe and the 1B.2.1 CVV has significant loss in reactivity with the 1B.1 representative swine strains. The swine 1B.1.1.1 had significant loss in cross-reactivity with A/Chile/1/1983 and A/Brazil/11/1978. The swine 1B.1.1.2 strain retained cross-reactivity with the ancestral human seasonal reference strains. The contemporary swine 1B.1.2.2 had significant decrease in cross reactivity against the human seasonal reference strains. A newly detected group of viruses, 1B.2.7, had no within-clade CVV and >8-fold loss in cross reactivity to ancestral human seasonal reference strains.
- The 1C.2.1 strain retained cross-reactivity to the 1C.2.1 CVV A/Netherlands/10370-1b/2020. The 1C.2.4.1 swine strain retained cross-reactivity with a different clade CVV strain (1C.2.1: A/Netherlands/10370-1b/2020). The 1C.2.4.2 swine strains retained reactivity to the within-clade CVV A/Bretagne/24241/2021. The representative swine 1C.2.4.3 had no within-clade CVV and demonstrated a range of 4- to >8-fold loss to available 1C CVV strains.

### **North America Swine:**

- H1 1A: The contemporary swine 1A.1.1.3 had >8-fold decrease from within clade CVVs but retained reactivity to human pooled sera. The contemporary swine 1A.3.3.2 had >8-fold decrease to seasonal vaccine strains but retained reactivity to human pooled sera. The contemporary swine 1A.3.3.3-c3 virus had 4-8-fold decrease from the within-clade CVV but retained reactivity to human pooled sera. The contemporary swine 1A.2 virus has no within clade CVV and >8-fold decrease to CVV and human seasonal vaccine ferret anti-sera but retained reactivity to human pooled sera.
- H1 1B: The 1B.2.1 swine representative had no loss of titer to the within clade CVV and had a 4-fold loss in cross-reactivity to human pooled sera. The 1B.2.2.1 clade swine representative had 8-fold reduction from the within clade CVV but retained reactivity to human pooled sera. The contemporary swine 1B.2.2.2 does not have a within-clade CVV and had a >8-fold decrease from the 1B.2.2.1 CVV and had an 8-fold loss in cross-reactivity to human pooled sera.
- H3: The contemporary swine 1990.4.a had a 4-fold decrease from the new CVV and had > 8-fold reduction in reactivity in adult human pooled sera. The contemporary swine 1990.4.b1 does not have a within clade CVV and demonstrated a >8-fold decrease from 1990.4.a CVV and had >8-fold reduction in reactivity in adult human pooled sera. The contemporary swine 1990.4.i does not contain a within clade CVV and demonstrated a >8-fold decrease from 1990.4.a CVV and had >8-fold reduction in reactivity in adult human sera. The contemporary swine 2010.1 representative strain had an 8-fold loss to the 2010.1 CVV and an 8-fold loss in reactivity with adult human sera. The contemporary swine 2010.2 and 2020.1 representative strains do not contain CVV and demonstrated ≥8-fold loss to the human vaccine strain. The 2010.2 strain had 8-fold loss in reactivity against adult human high responder sera.

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

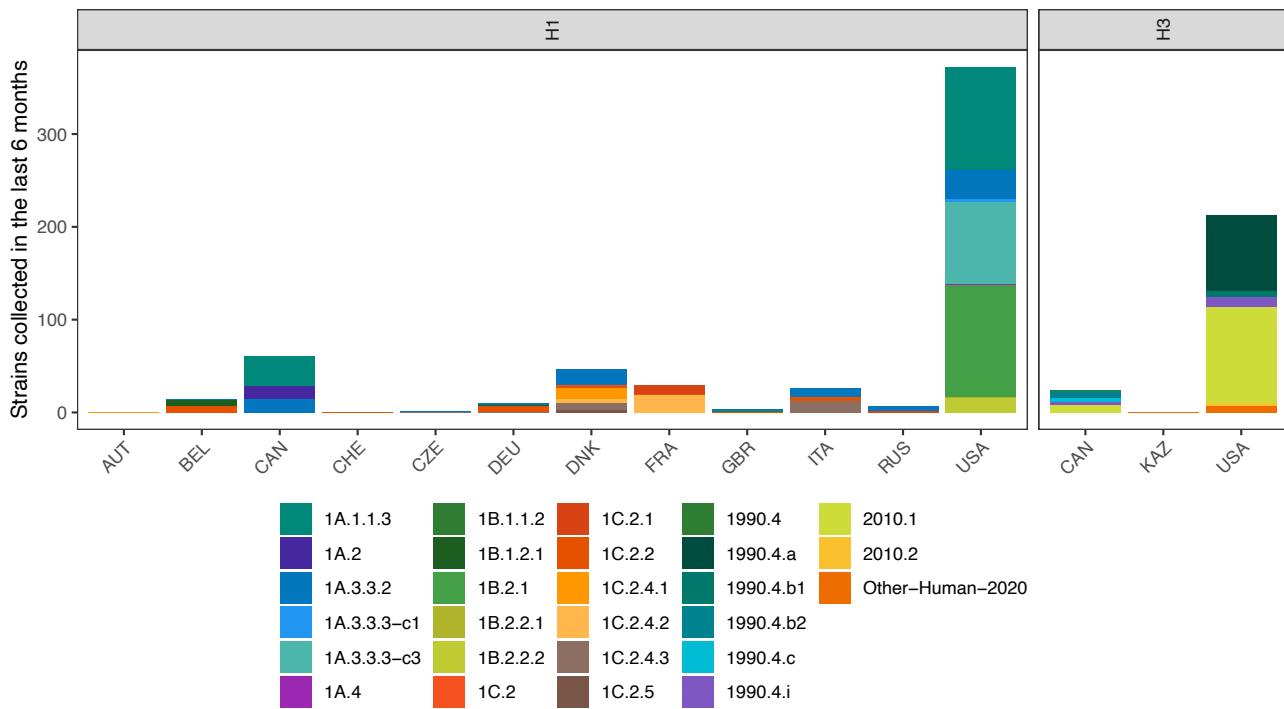


Figure A1. Summary of swine HA genes colored by phylogenetic clade for sequences deposited on or after January 2024 and truncated to those collected within the last 6 months (n = 813).

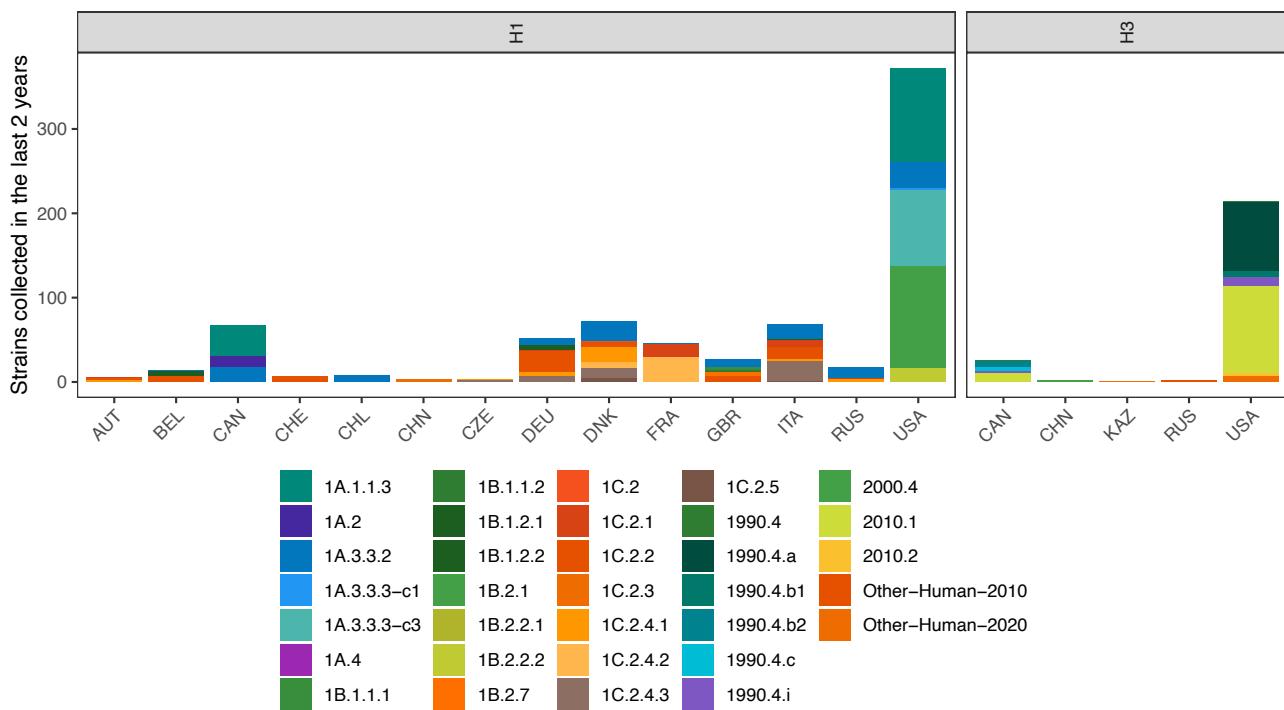


Figure A2. Summary of swine HA genes colored by phylogenetic clade. Expanded collection date criteria for non-USA sequences to a 24-month window, post June 2022 (n = 1009).

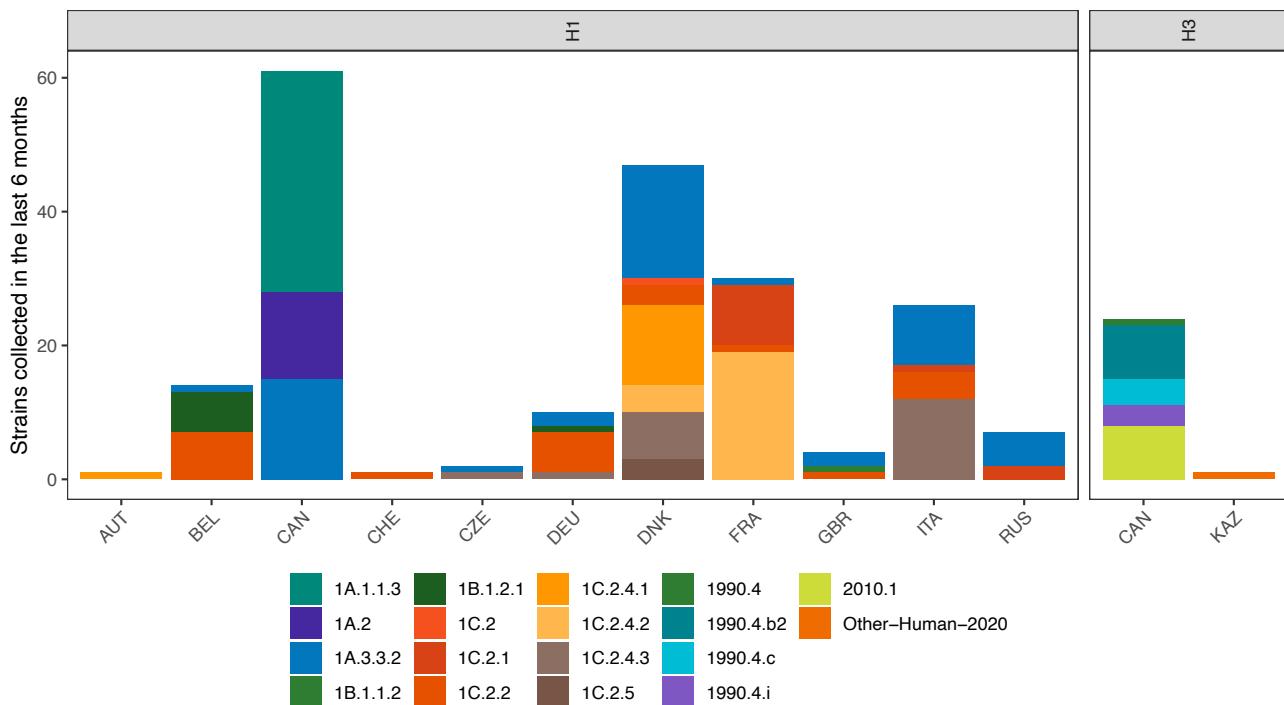


Figure A3. Summary of swine HA genes colored by phylogenetic clade for sequences deposited on or after January 2024 and truncated to those collected within the last 6 months ( $n = 228$ ) in any country other than the United States of America.

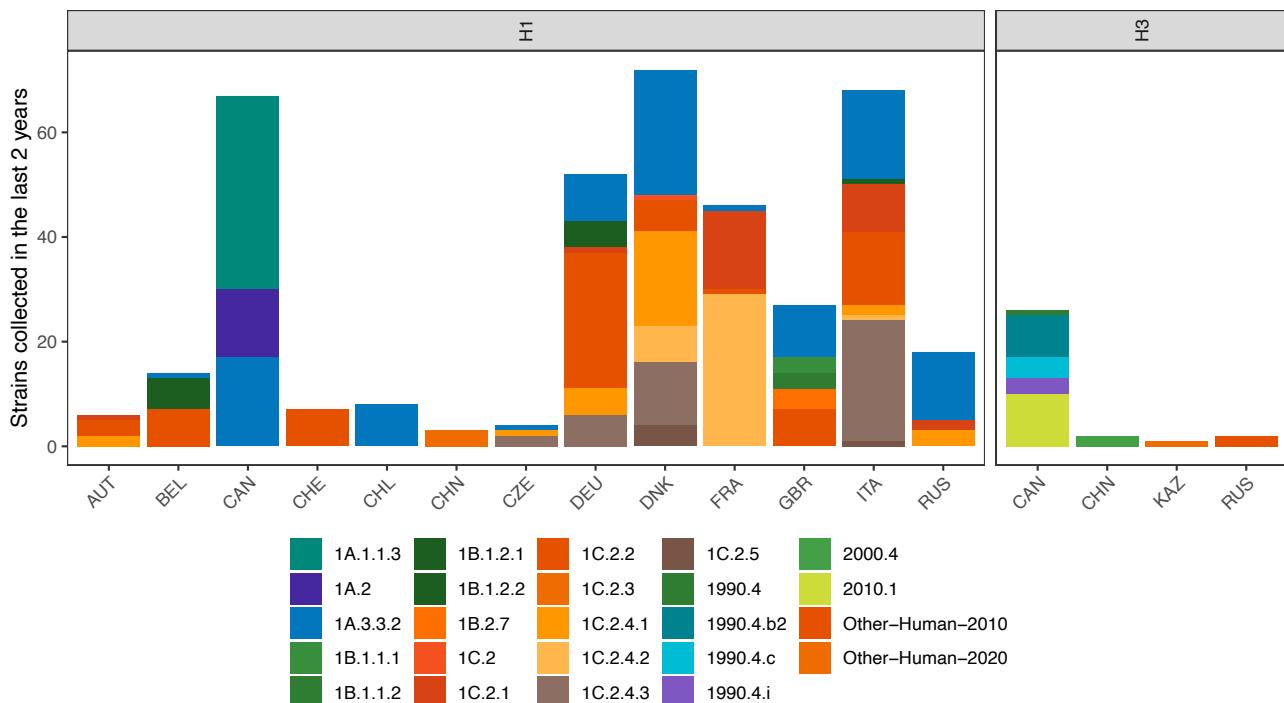


Figure A4. Summary of swine HA genes colored by phylogenetic clade. Expanded collection date criteria for non-USA sequences to a 24-month window, post June 2022 ( $n = 423$ ). Note that USA data has been excluded.

Table A1a. Summary of swine H1 clades by country collected in the past 6 months and deposited on or after January 2024.

<b>clade</b>	<b>Country</b>	<b>count</b>
1C.2.4.1	AUT	1
1A.3.3.2	BEL	1
1B.1.2.1	BEL	6
1C.2.2	BEL	7
1A.1.1.3	CAN	33
1A.2	CAN	13
1A.3.3.2	CAN	15
1C.2.2	CHE	1
1A.3.3.2	CZE	1
1C.2.4.3	CZE	1
1A.3.3.2	DEU	2
1B.1.2.1	DEU	1
1C.2.2	DEU	6
1C.2.4.3	DEU	1
1A.3.3.2	DNK	17
1C.2	DNK	1
1C.2.2	DNK	3
1C.2.4.1	DNK	12
1C.2.4.2	DNK	4
1C.2.4.3	DNK	7
1C.2.5	DNK	3
1A.3.3.2	FRA	1
1C.2.1	FRA	9
1C.2.2	FRA	1
1C.2.4.2	FRA	19
1A.3.3.2	GBR	2
1B.1.1.2	GBR	1
1C.2.2	GBR	1
1A.3.3.2	ITA	9
1C.2.1	ITA	1
1C.2.2	ITA	4
1C.2.4.3	ITA	12
1A.3.3.2	RUS	5
1C.2.1	RUS	2
1A.1.1.3	USA	111
1A.3.3.2	USA	31
1A.3.3.3-c1	USA	3
1A.3.3.3-c3	USA	89
1A.4	USA	1
1B.2.1	USA	120
1B.2.2.1	USA	1
1B.2.2.2	USA	16

Table A1b. Summary of swine H1 clades by country collected in the past 24 months and deposited on or after July 2022.

cont.

<b>clade</b>	<b>country</b>	<b>count</b>
1C.2.1	AUT	1
1C.2.2	AUT	3
1C.2.4.1	AUT	2
1A.3.3.2	BEL	1
1B.1.2.1	BEL	6
1C.2.2	BEL	7
1A.1.1.3	CAN	37
1A.2	CAN	13
1A.3.3.2	CAN	17
1C.2.2	CHE	7
1A.3.3.2	CHL	8
1C.2.3	CHN	3
1A.3.3.2	CZE	1
1C.2.4.1	CZE	1
1C.2.4.3	CZE	2
1A.3.3.2	DEU	9
1B.1.2.1	DEU	5
1C.2.1	DEU	1
1C.2.2	DEU	26
1C.2.4.1	DEU	5
1C.2.4.3	DEU	6
1A.3.3.2	DNK	24
1C.2	DNK	1
1C.2.2	DNK	6
1C.2.4.1	DNK	18
1C.2.4.2	DNK	7
1C.2.4.3	DNK	12
1C.2.5	DNK	4

<b>clade</b>	<b>country</b>	<b>count</b>
1A.3.3.2	FRA	1
1C.2.1	FRA	15
1C.2.2	FRA	1
1C.2.4.2	FRA	29
1A.3.3.2	GBR	10
1B.1.1.1	GBR	3
1B.1.1.2	GBR	3
1B.2.7	GBR	4
1C.2.2	GBR	7
1A.3.3.2	ITA	17
1B.1.2.2	ITA	1
1C.2.1	ITA	9
1C.2.2	ITA	14
1C.2.4.1	ITA	2
1C.2.4.2	ITA	1
1C.2.4.3	ITA	23
1C.2.5	ITA	1
1A.3.3.2	RUS	13
1C.2.1	RUS	2
1C.2.4.1	RUS	3
1A.1.1.3	USA	111
1A.3.3.2	USA	31
1A.3.3.3-c1	USA	3
1A.3.3.3-c3	USA	89
1A.4	USA	1
1B.2.1	USA	120
1B.2.2.1	USA	1
1B.2.2.2	USA	16

Table A2a. Summary of swine H3 clades by country collected in the past 6 months and deposited on or after January 2024.

<b>clade</b>	<b>country</b>	<b>count</b>
1990.4	CAN	1
1990.4.b2	CAN	8
1990.4.c	CAN	4
1990.4.i	CAN	3
2010.1	CAN	8
Other-Human-2020	KAZ	1
1990.4	USA	1
1990.4.a	USA	81
1990.4.b1	USA	7
1990.4.i	USA	11
2010.1	USA	103
2010.2	USA	3
Other-Human-2020	USA	7

Table A2b. Summary of swine H3 clades by country collected in the past 24 months and deposited on or after July 2022.

<b>clade</b>	<b>country</b>	<b>count</b>
1990.4	CAN	1
1990.4.b2	CAN	8
1990.4.c	CAN	4
1990.4.i	CAN	3
2010.1	CAN	10
2000.4	CHN	2
Other-Human-2020	KAZ	1
Other-Human-2010	RUS	2
1990.4	USA	1
1990.4.a	USA	81
1990.4.b1	USA	8
1990.4.i	USA	11
2010.1	USA	103
2010.2	USA	3
Other-Human-2020	USA	7

Table A3a. Recent swine and variant A(H1) activity shared with international agencies and collected from sequence repositories.

Country, area or territory	Host#	Genetic clade
Austria	Swine	1C.2.4.1
Belgium	Swine	1A.3.3.2; 1B.1.2.1; 1C.2.2
Canada	Swine	1A.1.1.3; 1A.2; 1A.3.3.2
Czech Republic	Swine	1A.3.3.2; 1C.2.4.3
Denmark	Swine	1A.3.3.2; 1C.2; 1C.2.2; 1C.2.4.1; 1C.2.4.2; 1C.2.4.3; 1C.2.5
France	Swine	1A.3.3.2; 1C.2.1; 1C.2.2; 1C.2.4.2
Germany	Swine	1A.3.3.2; 1B.1.2.1; 1C.2.2; 1C.2.4.3
Italy	Swine	1A.3.3.2; 1C.2.1; 1C.2.2; 1C.2.4.3
Russia	Swine	1A.3.3.2; 1C.2.1
Switzerland	Swine	1C.2.2
United Kingdom of Great Britain and Northern Ireland	Swine	1A.3.3.2; 1B.1.1.2; 1C.2.2
United States of America	Human (5)	1A.1.1.3; 1B.2.1
United States of America	Swine	1A.1.1.3; 1A.3.3.2; 1A.3.3.3-c1; 1A.3.3.3-c3; 1A.4; 1B.2.1; 1B.2.2.1; 1B.2.2.2
Vietnam	Human (1)	1C.2.3

#Swine H1 clades by country collected in the past 6 months and deposited on or after January 2024. \*Number of cases and/or detections.

Table A3b. Recent swine and variant A(H3) activity shared with international agencies and collected from sequence repositories.

Country, area or territory	Host#	Genetic clade
Canada	Human (1)	1990.4
Canada	Swine	1990.4; 1990.4.b2; 1990.4.c; 1990.4.i; 2010.1
Kazakhstan	Swine	2020.1
United States of America	Human (2)	1990.4.a; 2010.1
United States of America	Swine	1990.4; 1990.4.a; 1990.4.b1; 1990.4.i; 2010.1; 2010.2; 2020.1

#Swine H3 clades by country collected in the past 6 months and deposited on or after January 1, 2024. \*Number of cases and/or detections.



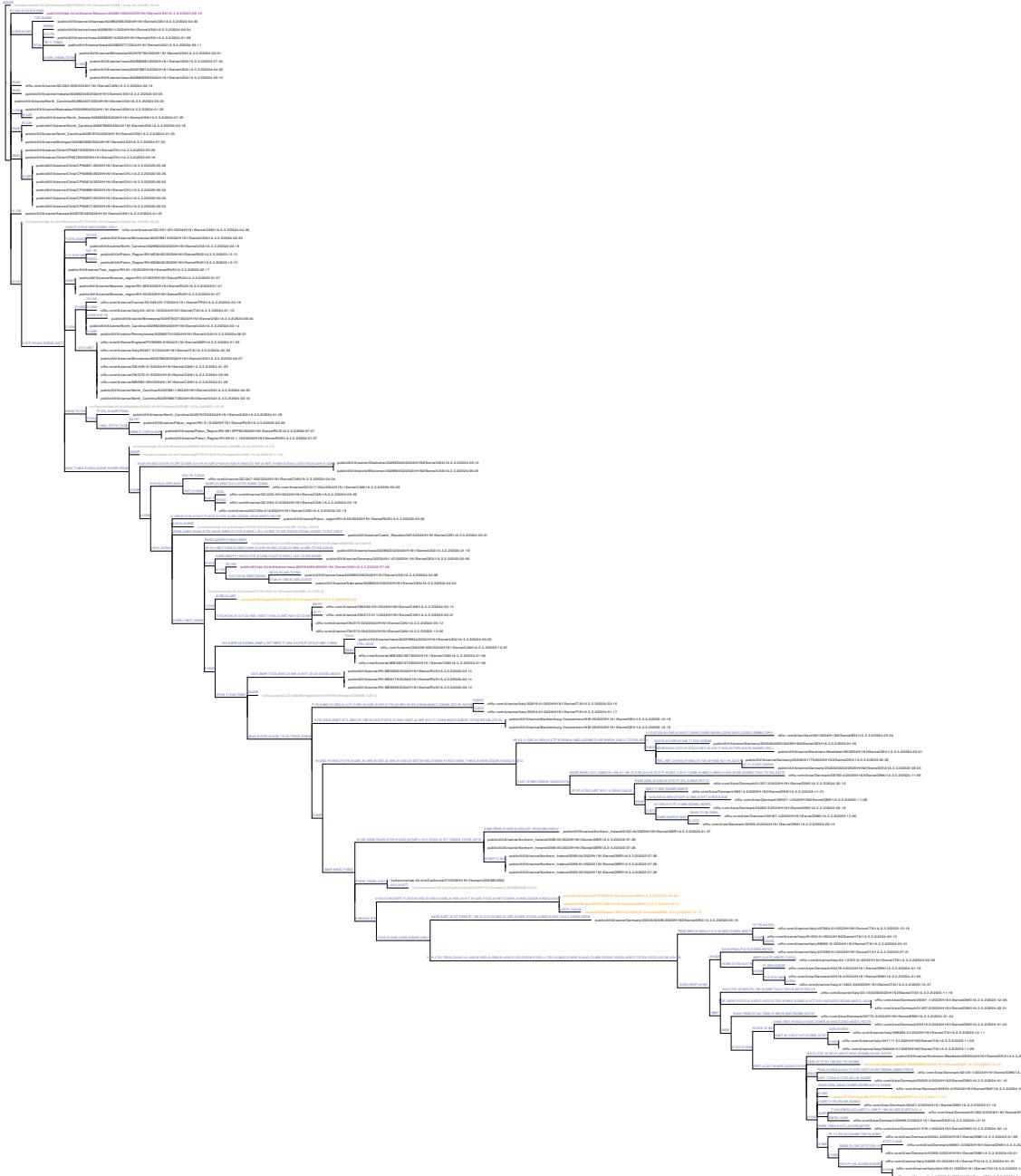


Figure A10. A phylogeny of the **1A.3.3.2 (pdm)** clade displaying n=130 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=17 reference genes. The clade is rooted relative to the most recent human vaccine strain (A/Victoria/4897/2022) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 7.

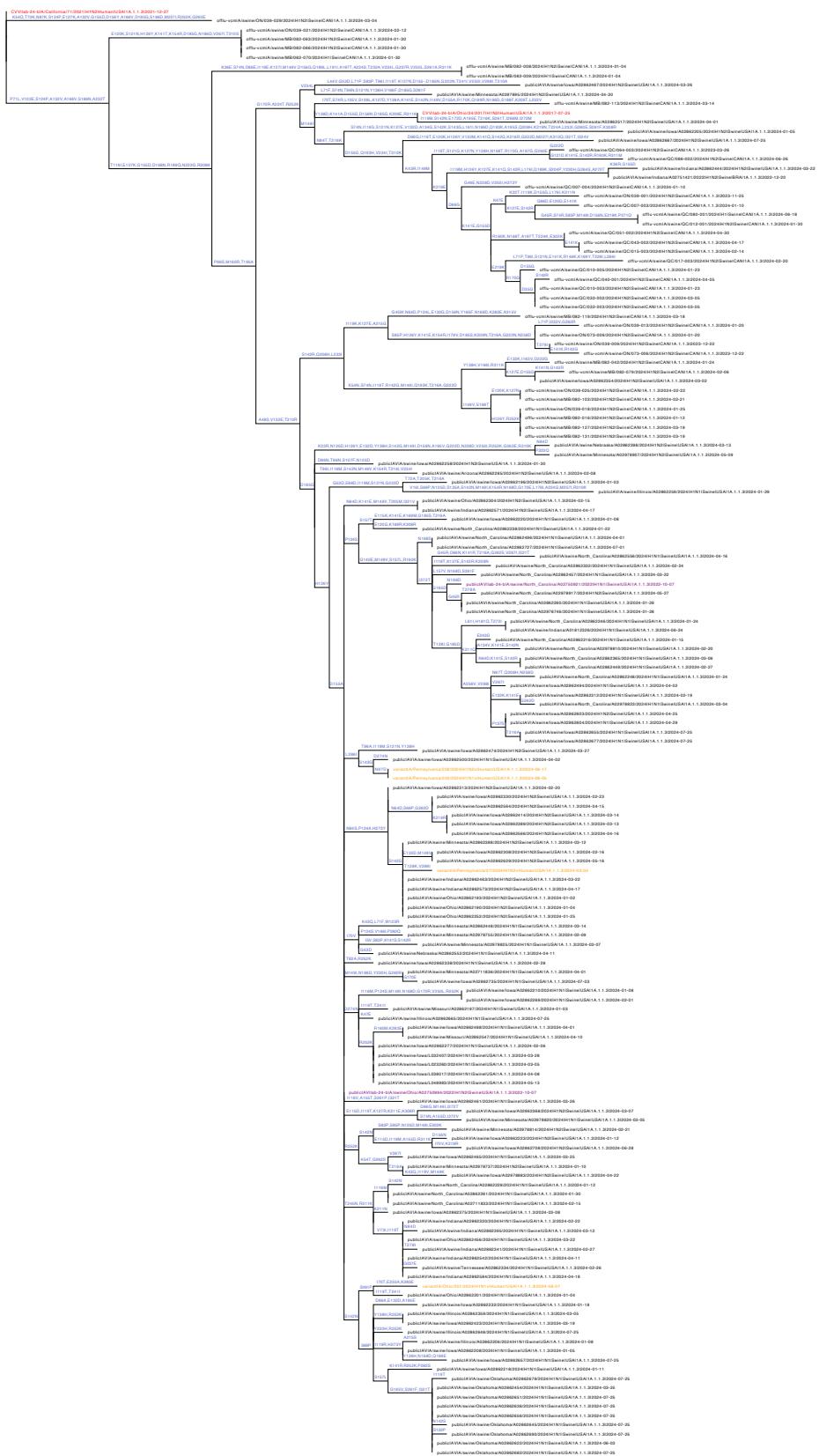


Figure A11. A phylogeny of the **1A.1.1.3** clade displaying n=151 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=6 reference genes. The clade is rooted relative to the most recent in-clade CVV (A/California/71/2021) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 7.

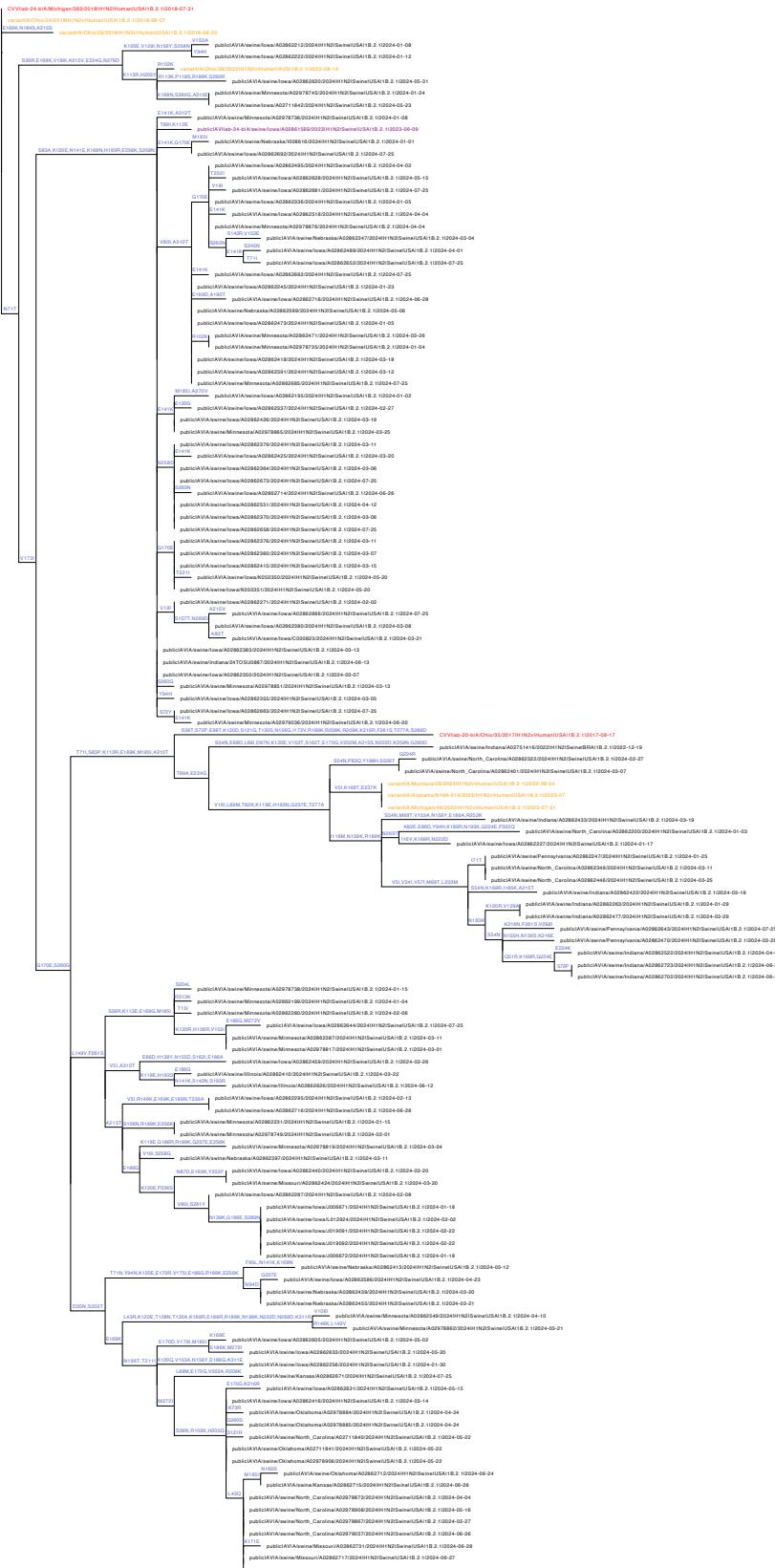


Figure A12. A phylogeny of the 1B.2.1 clade displaying n=122 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=8 reference genes. The clade is rooted relative to the most recent in-clade CVV (A/Michigan/383/2018) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 8.

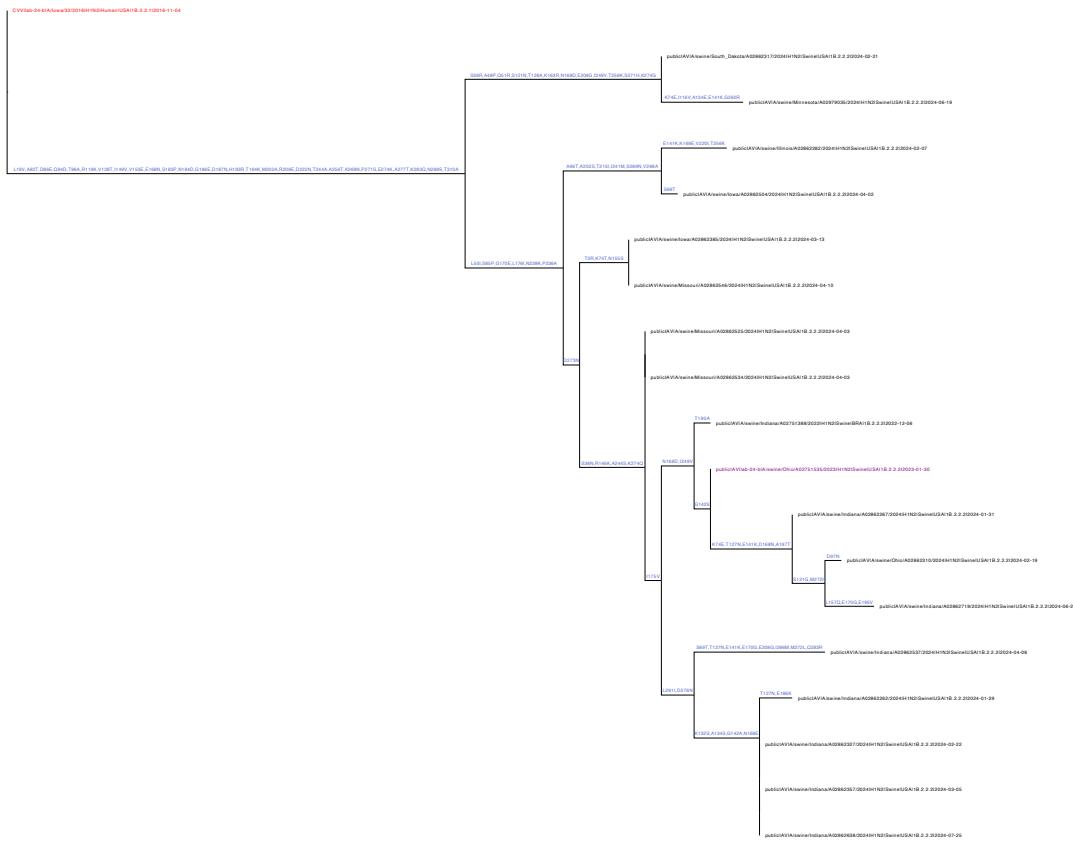


Figure A13. A phylogeny of the **1B.2.2.2** clade displaying n=18 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=1 reference genes. The clade is rooted relative to the closest CVV (A/Iowa/32/2016) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 8.

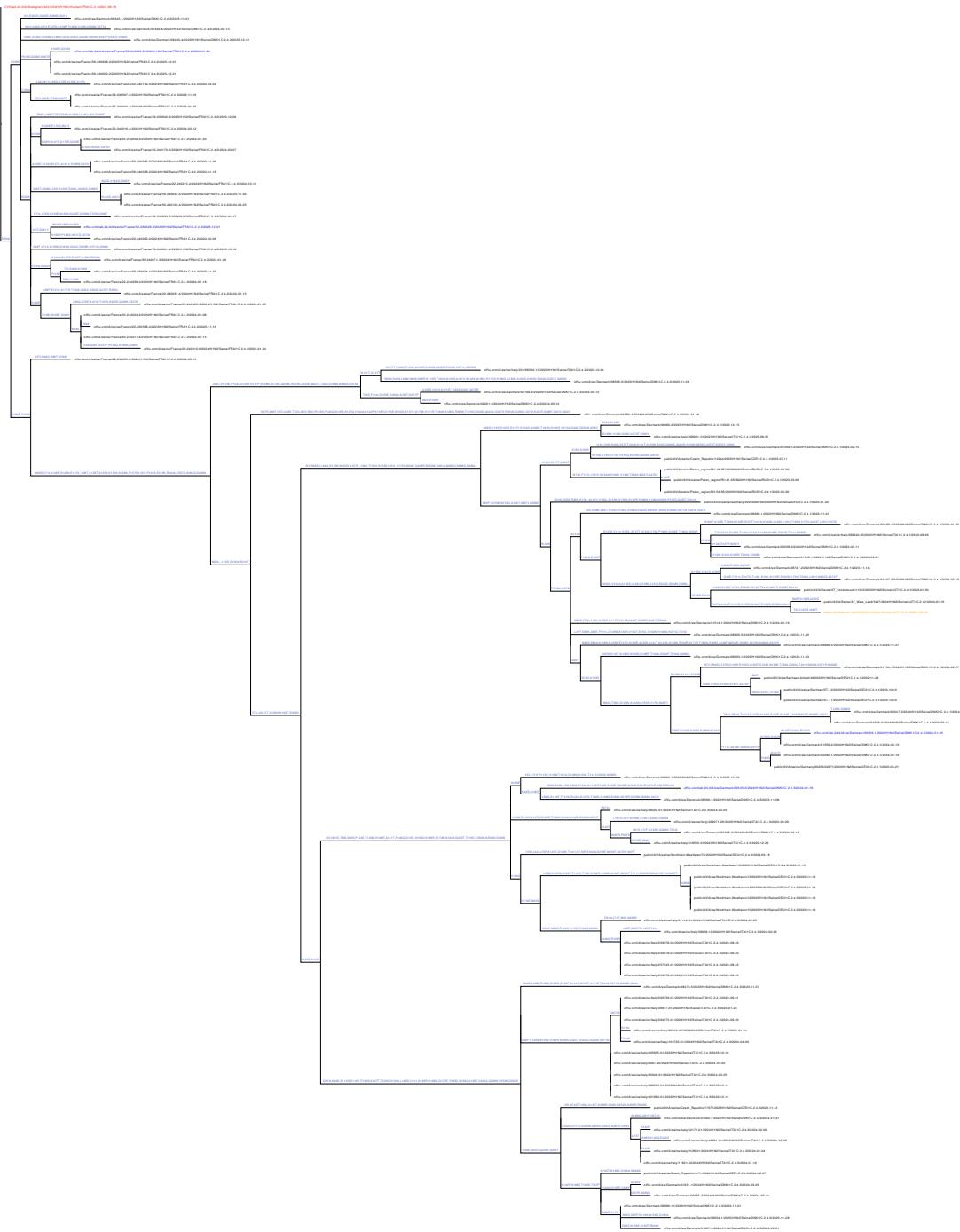


Figure A14. A phylogeny of the **1C.2.4** clade displaying n=110 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=2 reference genes. The clade is rooted relative to the closest CVV (A/Bretagne/24241/2021) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 9.

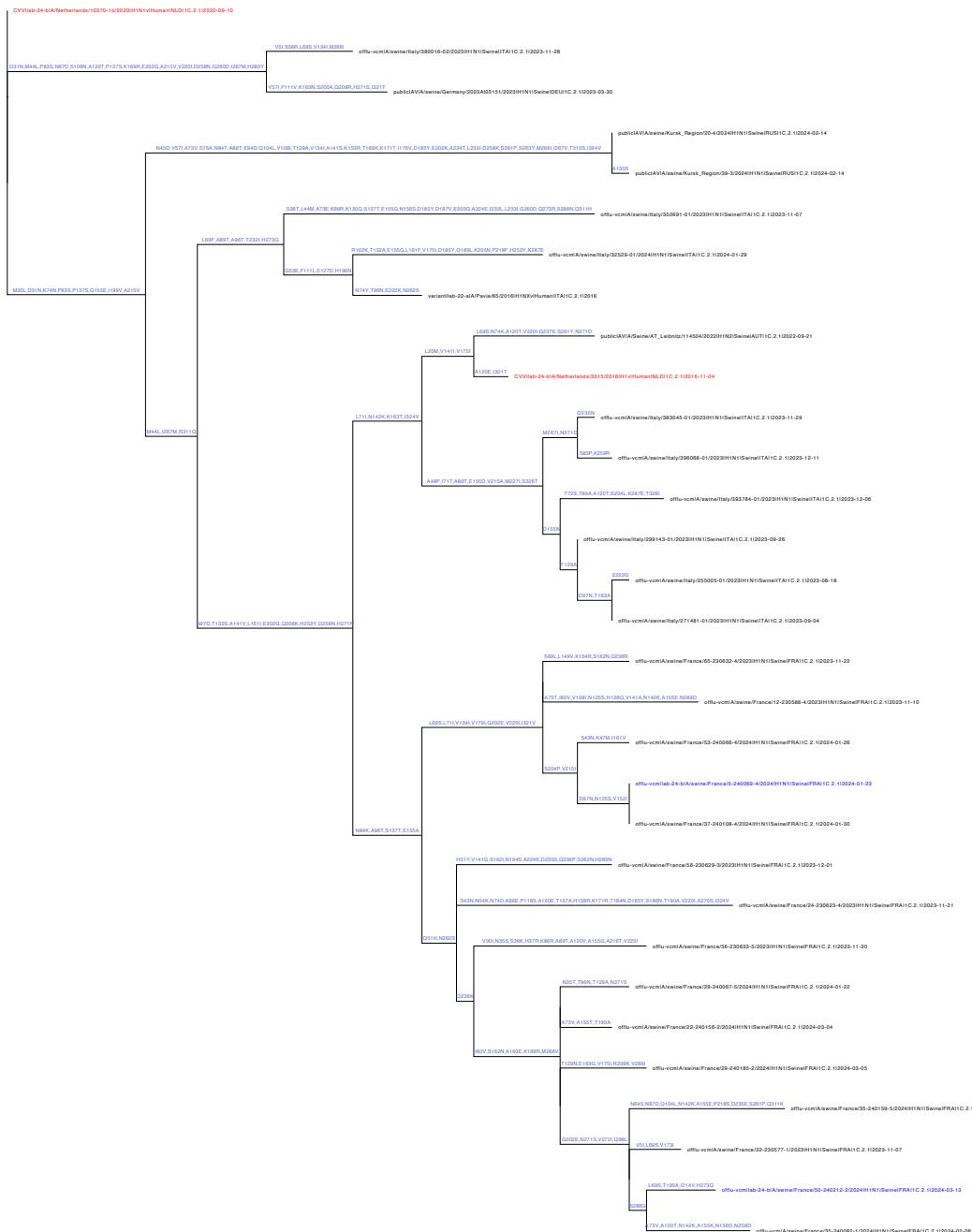


Figure A15. A phylogeny of the 1C.2.1 clade displaying n=28 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=3 reference genes. The clade is rooted relative to the closest CVV (A/Netherlands/10370-1b/2020) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 9.

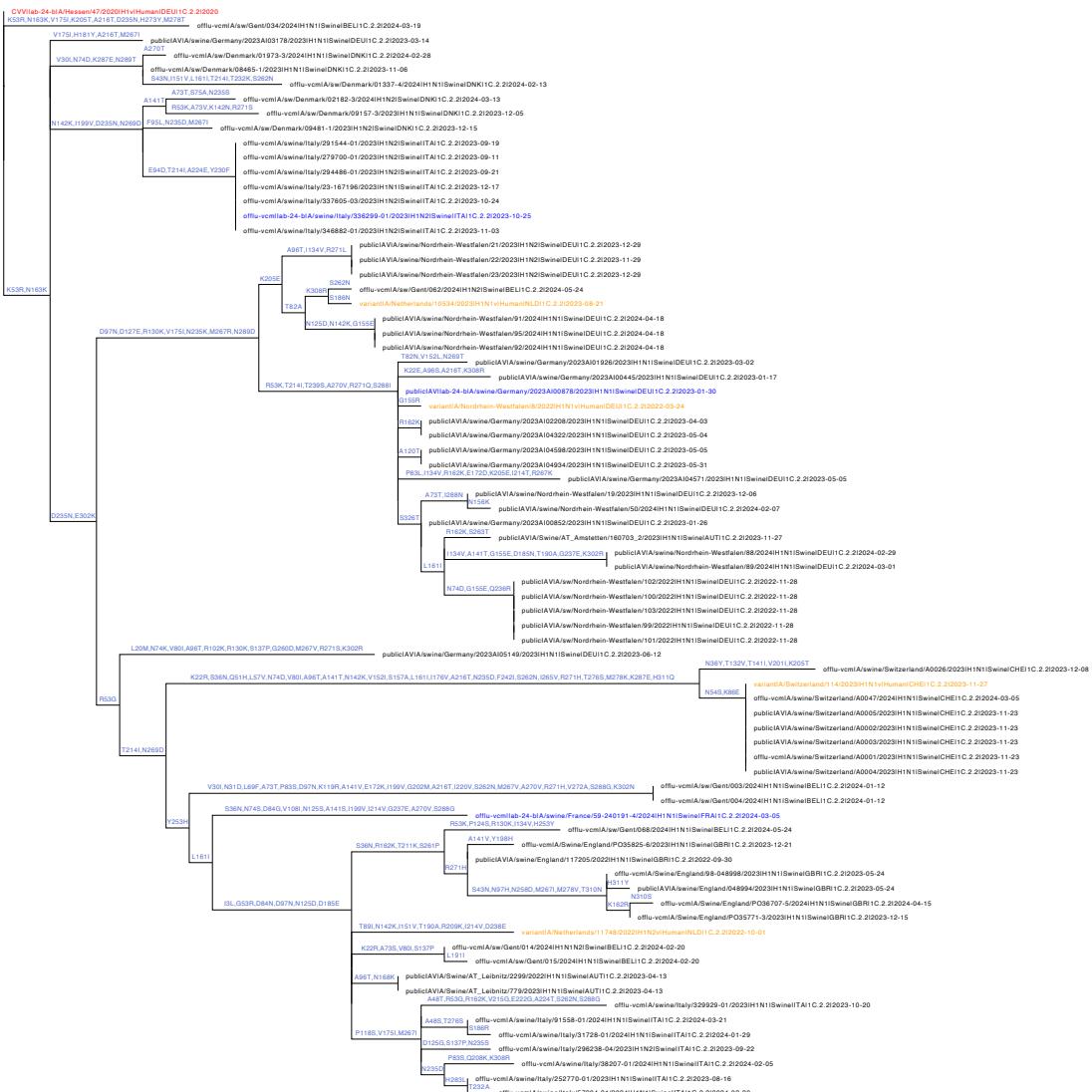


Figure A16. A phylogeny of the **1C.2.2** clade displaying n=70 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=5 reference genes. The clade is rooted relative to the in-clade CVV (A/Hessen/47/2020) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 9.

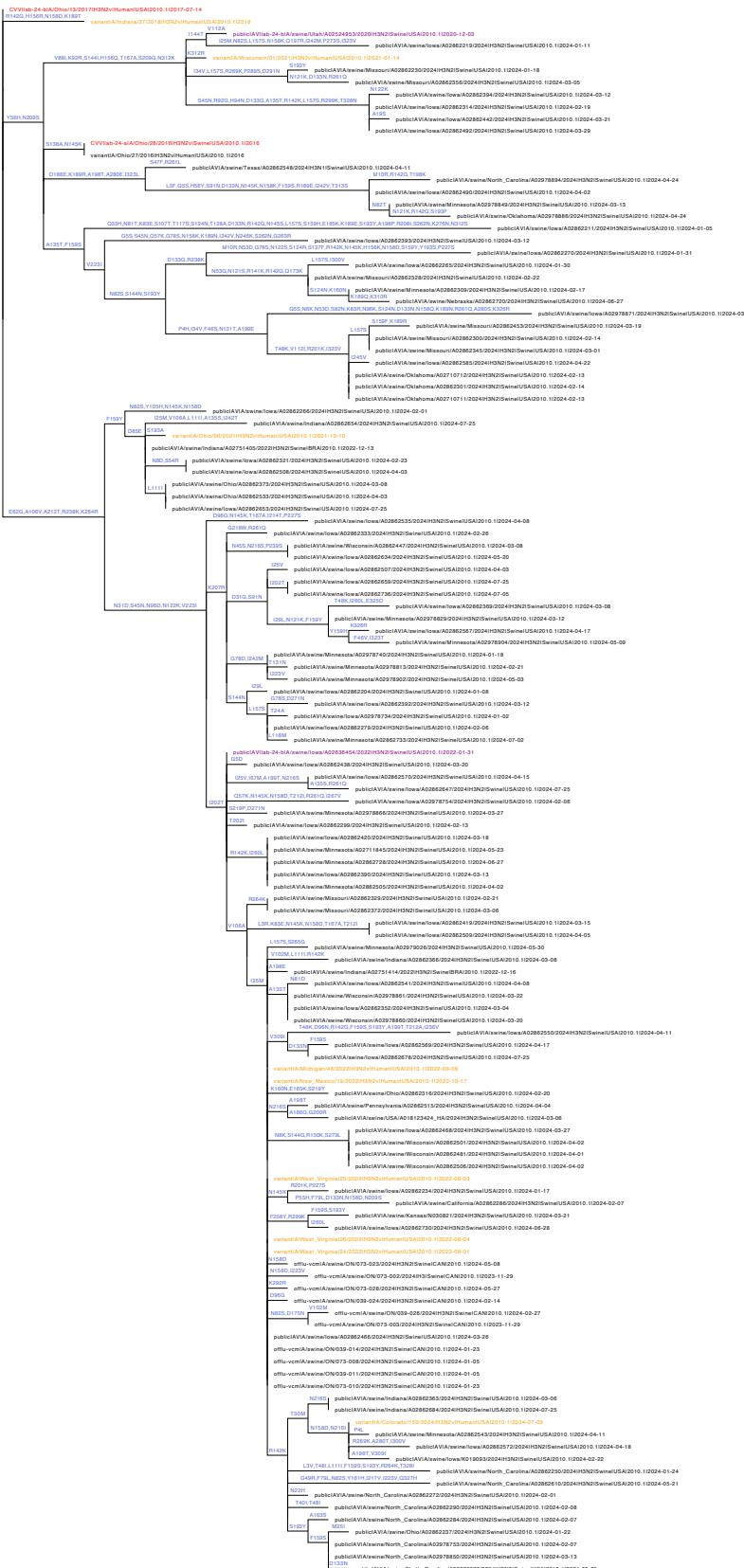


Figure A17. A phylogeny of the **3.2010.1** clade displaying n=117 sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=12 reference genes. The clade is rooted relative to the most representative in-clade CVV (A/Ohio/13/2017) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 10.

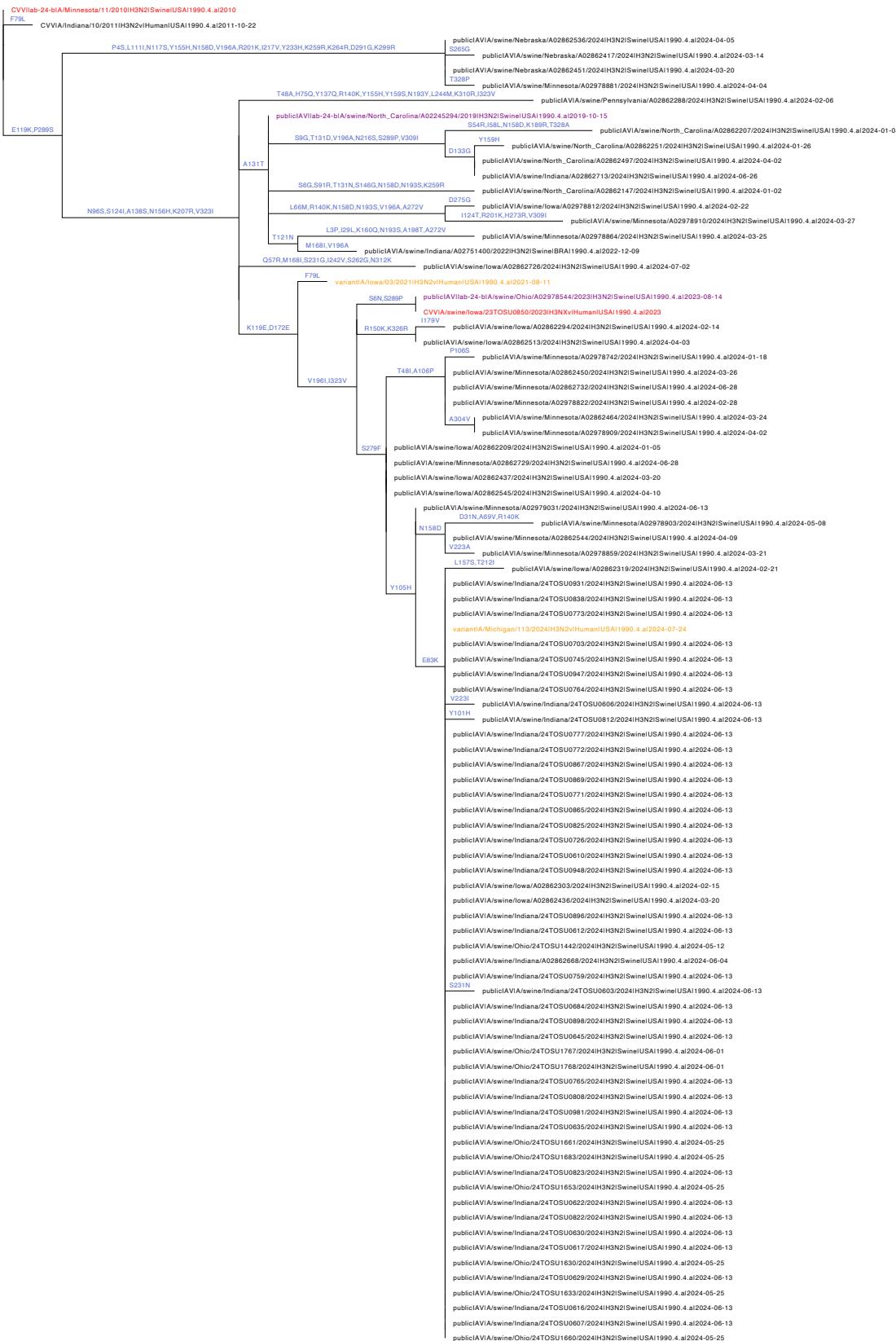


Figure A18. A phylogeny of the **3.1990.4.a** clade displaying n=84 swine sequences deposited on or after January 1, 2024 and collected in 2022-2024, and n=5 reference genes. The clade is rooted relative to the most representative in-clade CVV (A/Minnesota/11/2010) and all branches are annotated by the respective amino acid mutations in the HA1 region. The strains are colored to be consistent with Figure 10.