2024 - OFFLU Swine Influenza virus Technical Meeting

WHO VCM Discussion

- Amy Baker and Amelia Coggon

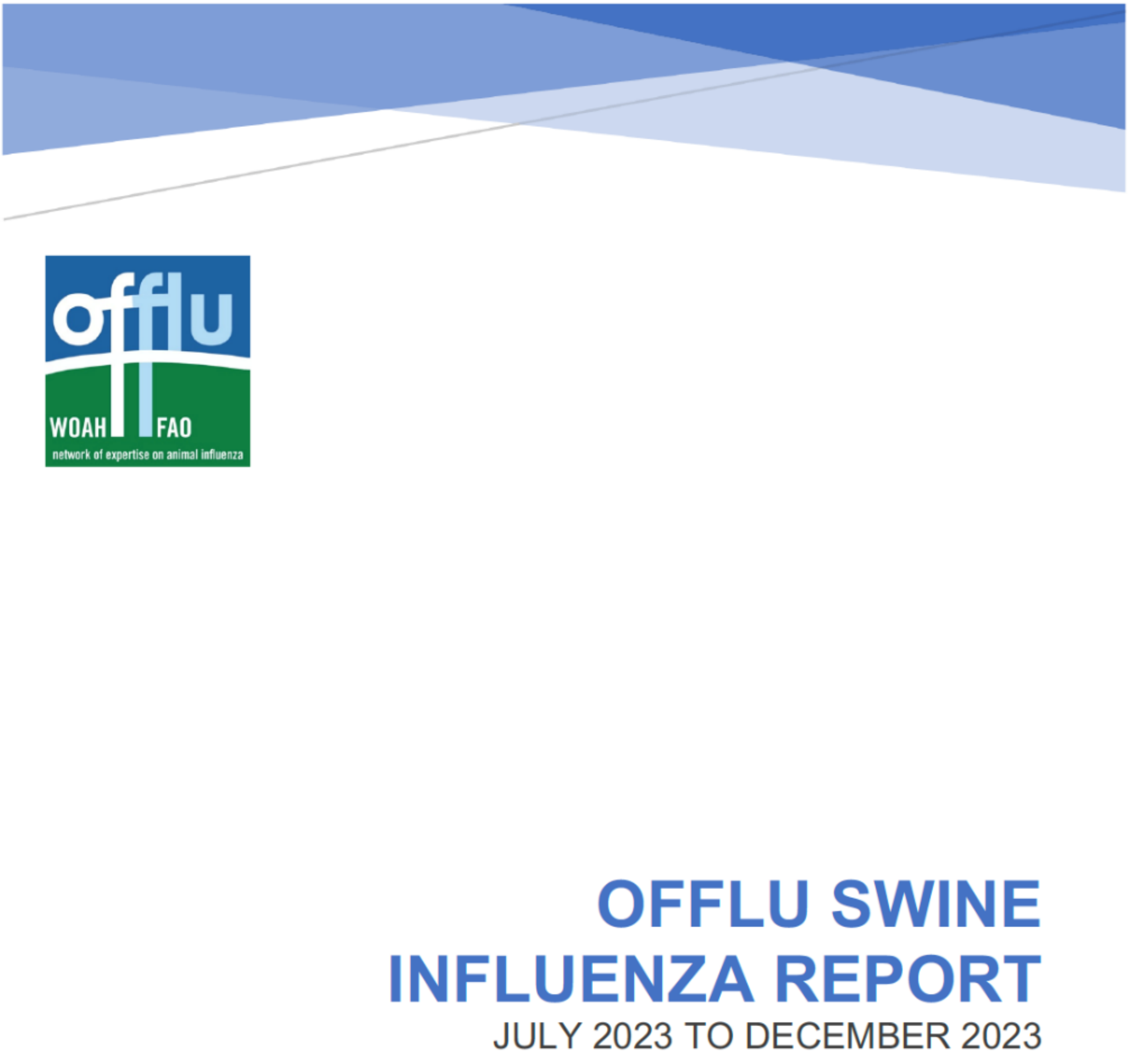
3 - 4 April 2024

World Health Organization

WHO Consultation on the Composition of Influenza Virus Vaccines for Use in the 2024 Northern Hemisphere Influenza Season

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

February 2024



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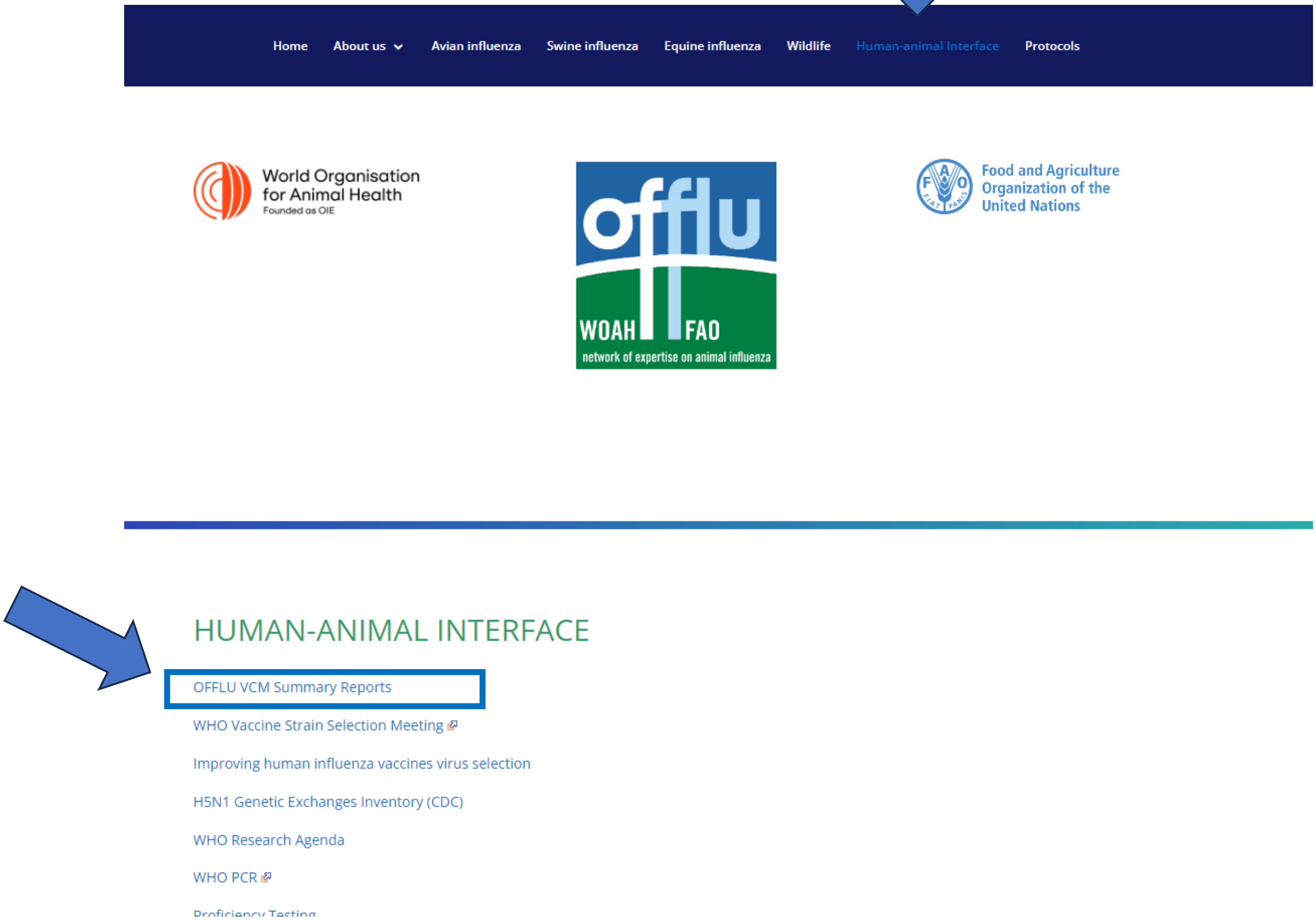
OFFLU SWINE INFLUENZA REPORT

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

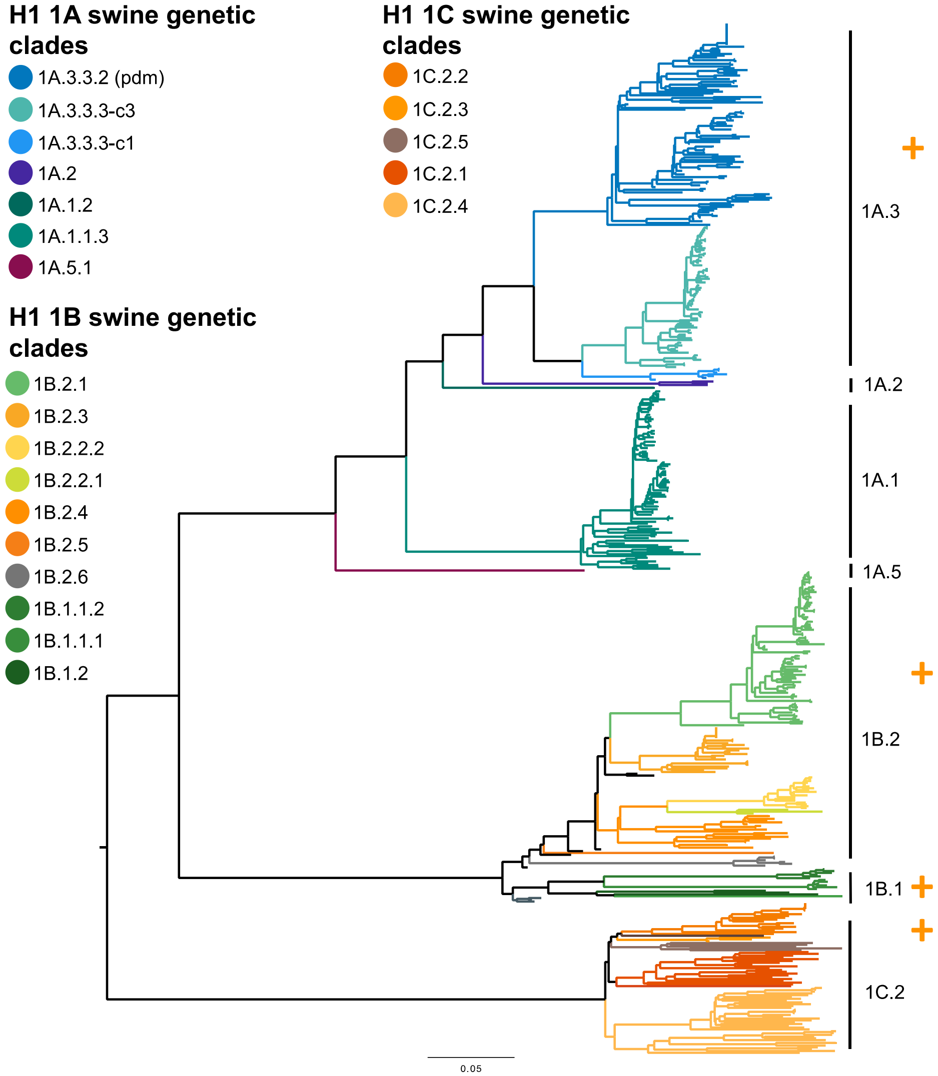
H5N1 Genetic Exchanges Inventory (CDC)

WHO Research Agenda

WHO PCR

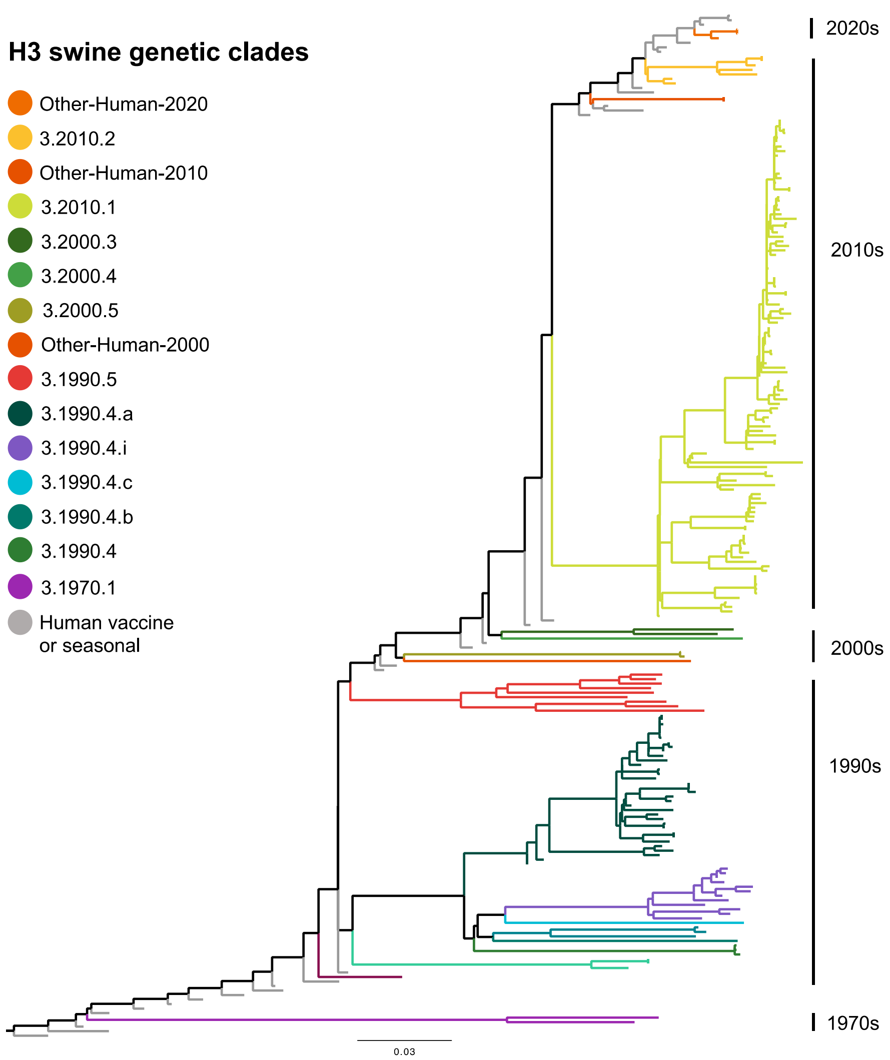
Proficiency Testing

Contemporary Global H1 swine IAV: genetic diversity



n=512, data deposited within last 6 months.

Contemporary Global H3 swine IAV: genetic diversity

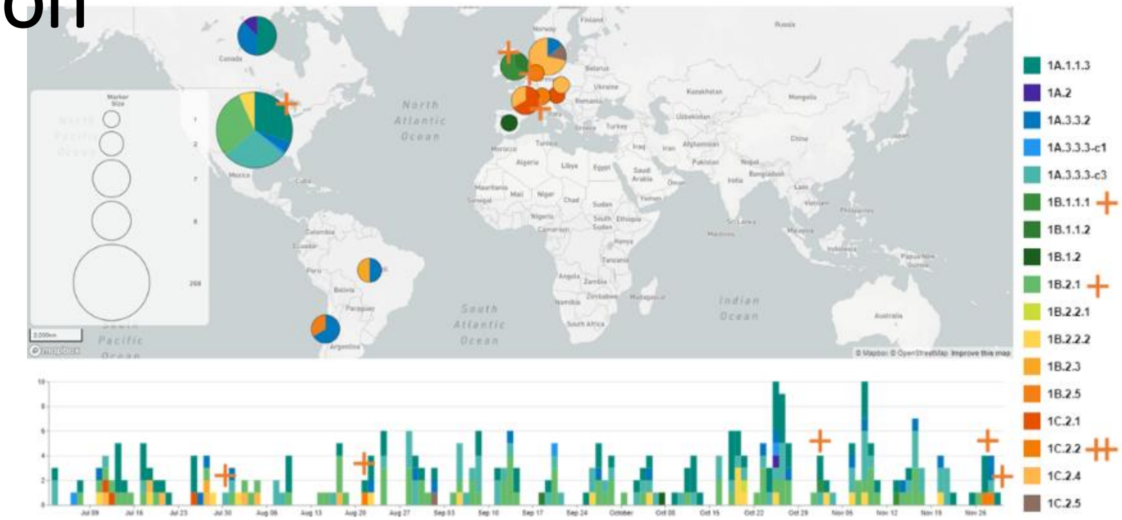


n=173, data deposited within last 6 months, and n=55 reference genes.

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

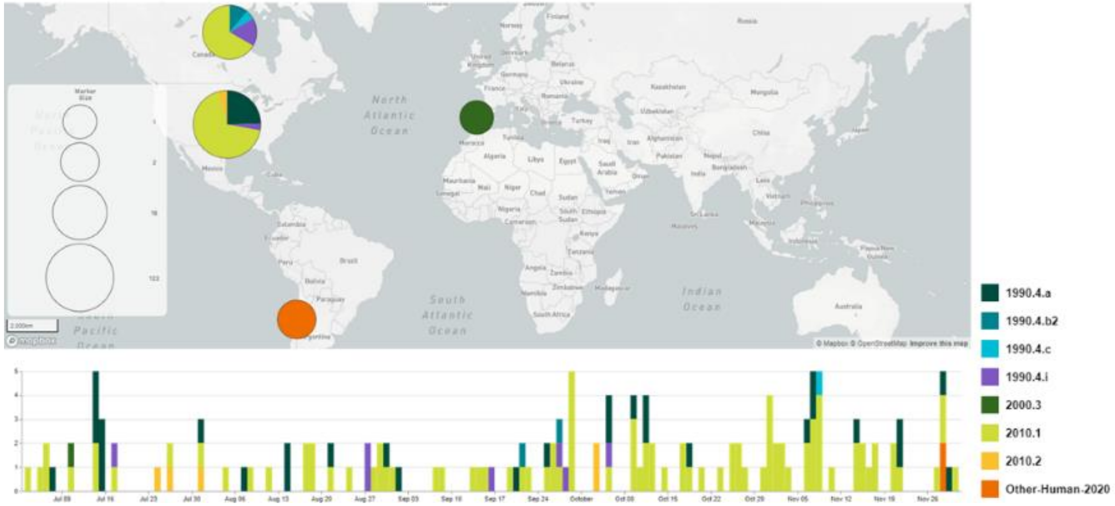
Swine H1 geographic distribution

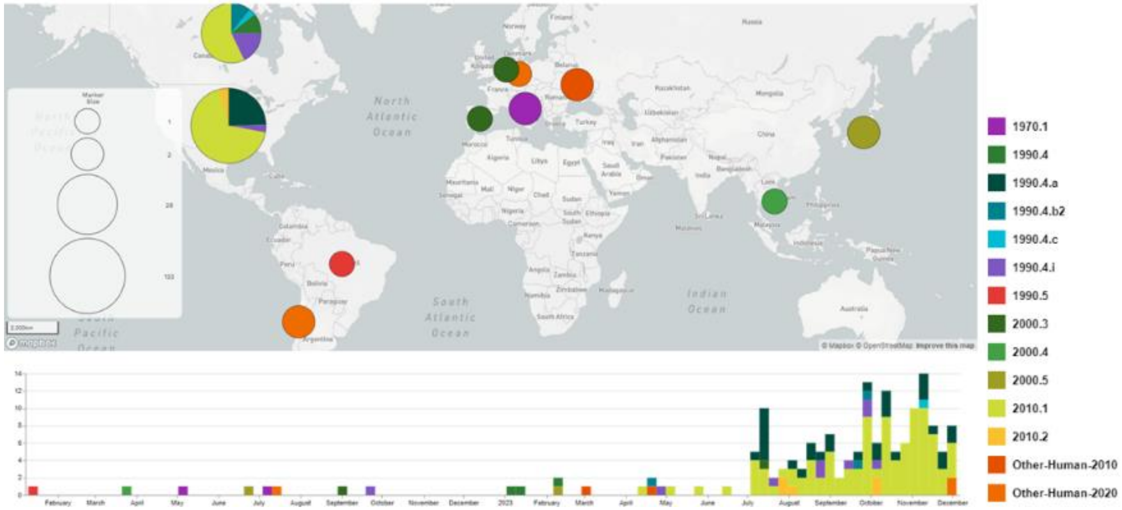
- 22 clades were H1 subtype, with detections from: 1A classical swine lineage (7 clades); 1B human-seasonal lineage (10 clades); and 1C Eurasian avian lineage (5 clades).
  - The 1A classical swine lineage viruses have global detection: 1A.1.1.3 in USA and Canada; 1A.2 in Canada; 1A.3.3.3-c1 in USA; 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

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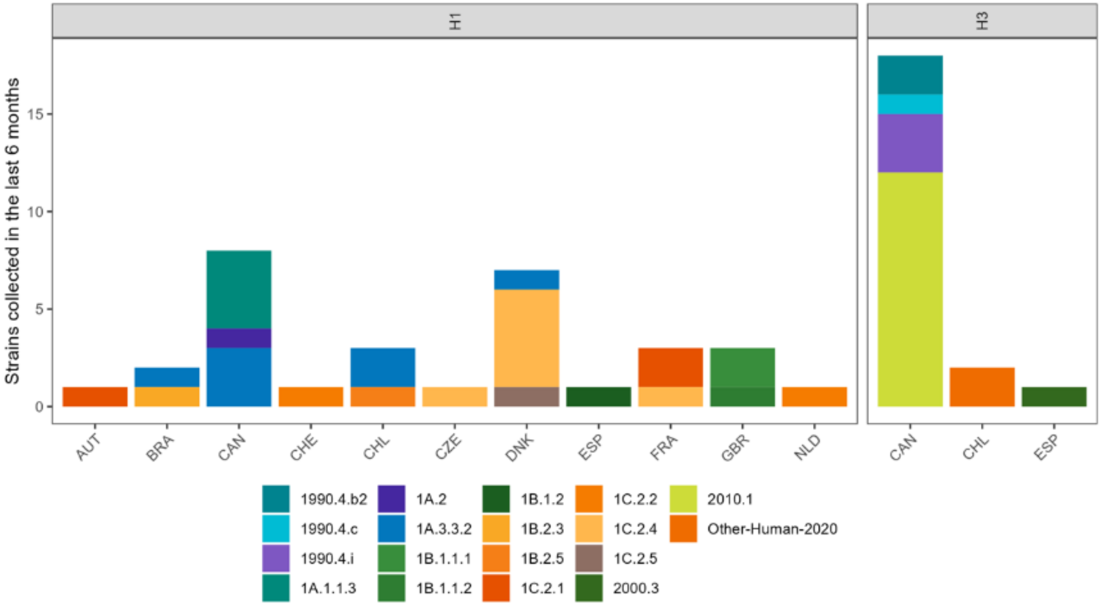
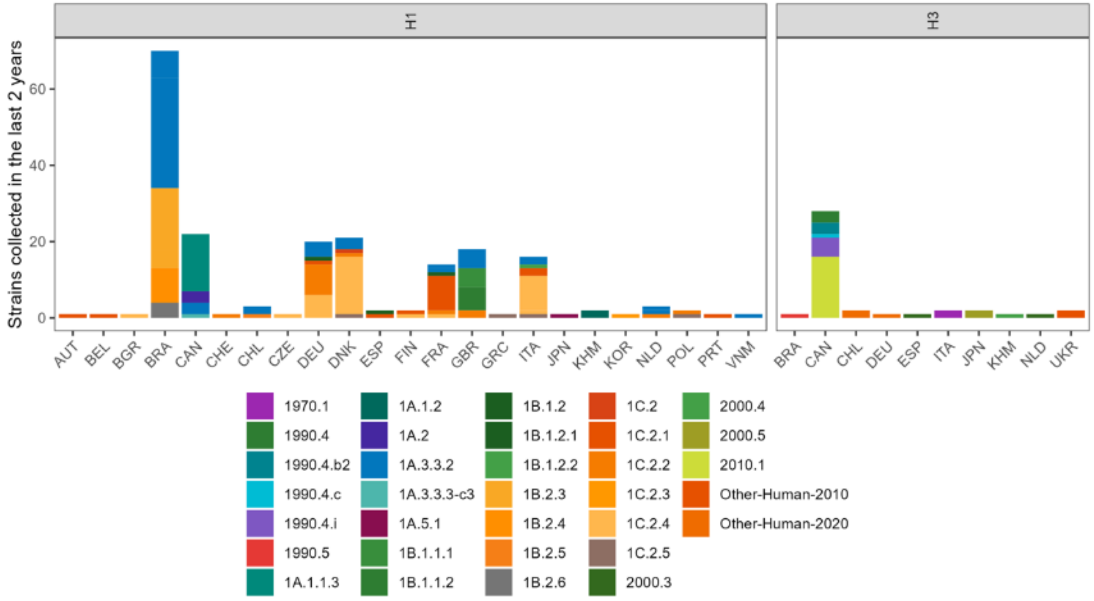
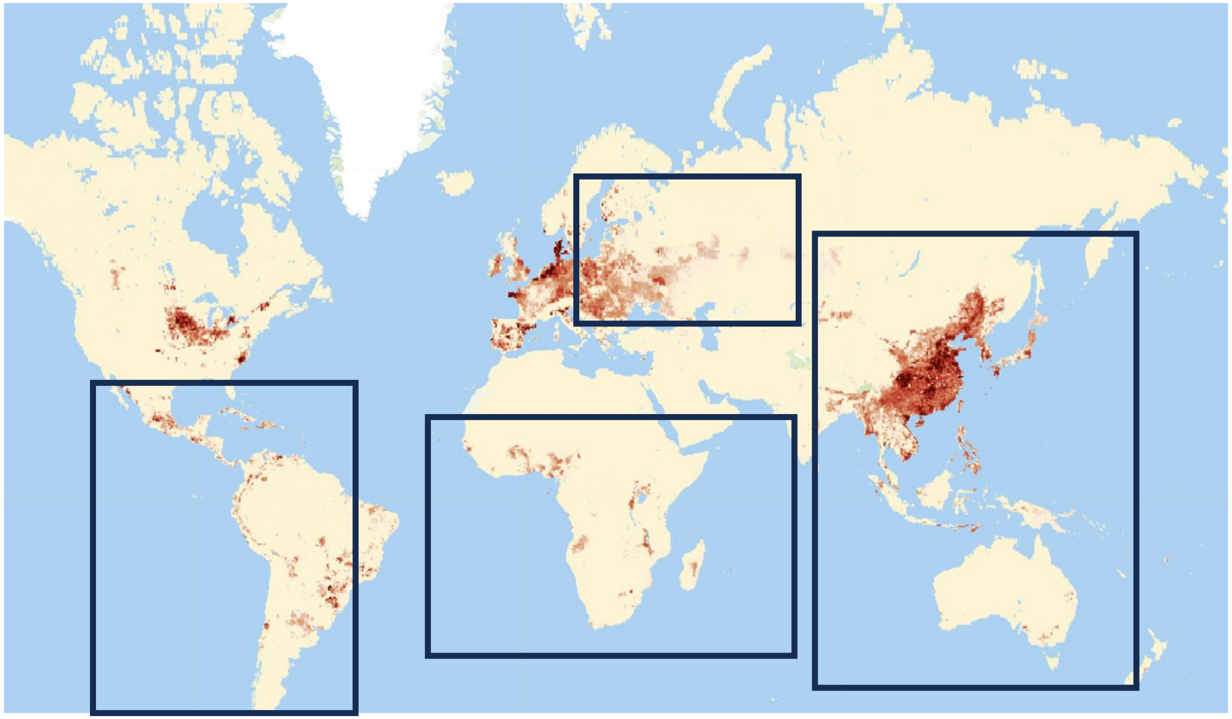
ESFLU
European Swine Influenza Network





Swine density 2015



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Contributions to Swine datapackage: **United Kingdom Canada, USA, Hungary, Brazil, Finland, France, Germany, Belgium, Italy, Denmark**

No sequence data from boxed regions

Novel Swine H1 & H3 Clades 2022-2024

1A Classical swine lineage:

- 1A.1.1.x
  - 1A.1.1.1/1A.1.1.2 (Canada)
  - 1A.1.1.3 (alpha-del)
- 1A.1.3 (Hong Kong, China)
- 1A.1.4 (Taiwan)
- 1A.3.3.3.x (USA)
- 1A.3.3.4 (Vietnam)
- 1A.5.x
  - 1A.5.1/1A.5.2/1A.5.3 (Japan)

1B Human seasonal lineage:

- 1B.1.1.x
  - *1B.1.1.1 (GB)*
  - *1B.1.1.2/1B.1.1.3*
- 1B.2.3 (Brazil)
- 1B.2.4 (Brazil)
- 1B.2.5 (Chile)
- *1B.2.6 (Brazil)*
- 1B.3 (Australia)
- *1B.x (Northern Ireland, pending)*

1C Eurasian avian lineage:

- 1C.2.4.x
  - *1C.2.4.1/1C.2.4.2/1C.2.4.3*
- 1C.2.6 (Spain)

H3 lineages:

- 1990.5.x
  - *1990.5.1/1990.5.2 (Brazil)*
- 1990.6 (Australia)
- 2000.5 (Japan)
- 2020? (USA)

Italics = BV-BRC tool and reference sets pending.
Require public data, i.e., preferable non-GISAID

Global Variant Cases

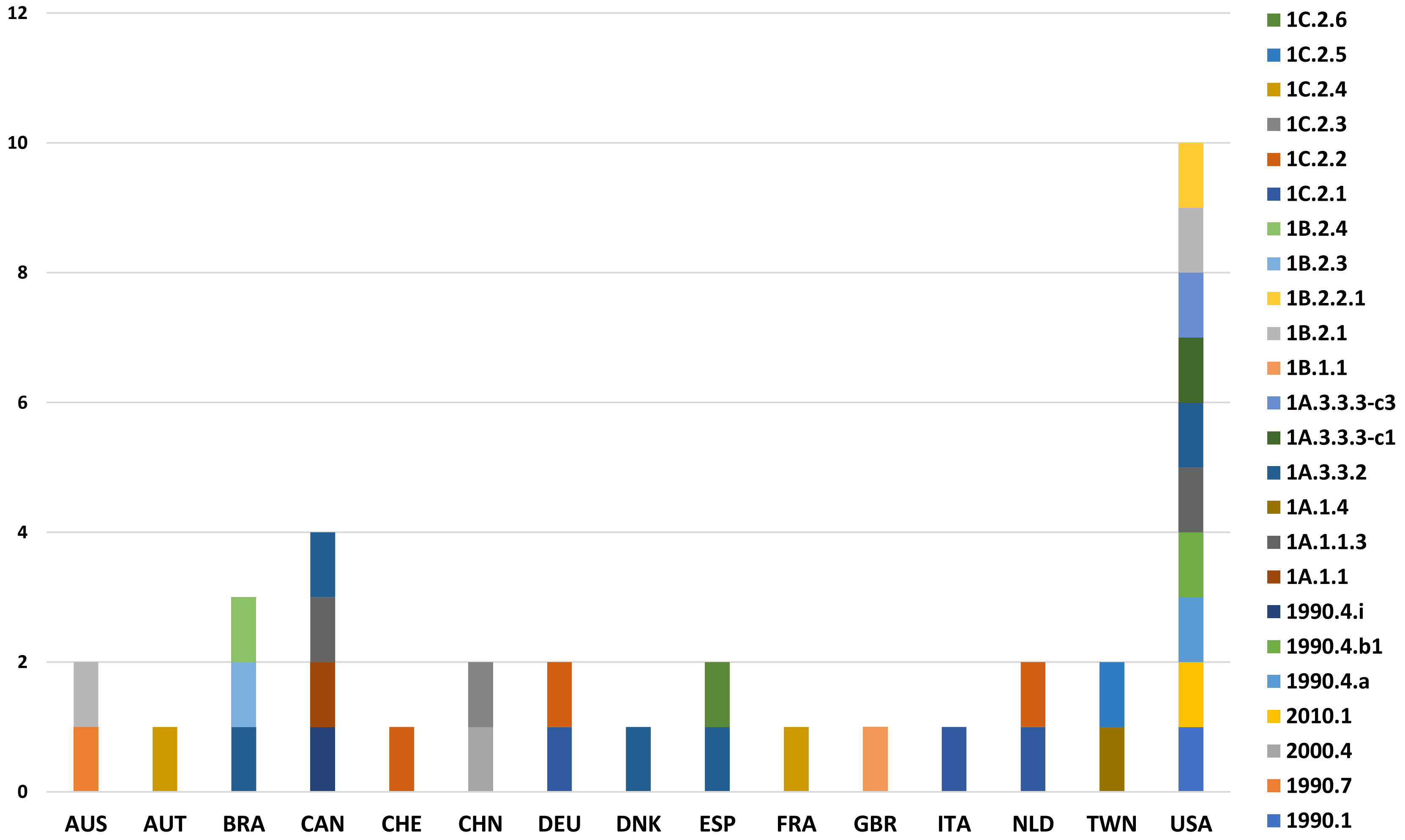
- 6 variant cases were reported (July 1 – December 31, 2023) and included with the swine analyses when sequence were available:
  - Brazil H1N1v (1A.3.3.2)
  - United Kingdom: H1N2v (1B.1.1.1)*
  - Netherlands: H1N1v (1C.2.2)
  - Switzerland: H1N1v (1C.2.2)
  - USA: H1N2v (1B.2.1), H1N2v (no sequence data), H3v (no sequence data)

*(1B.1.1.1 characterization: https://doi.org/10.2807/1560-7917.ES.2024.29.3.2400002)

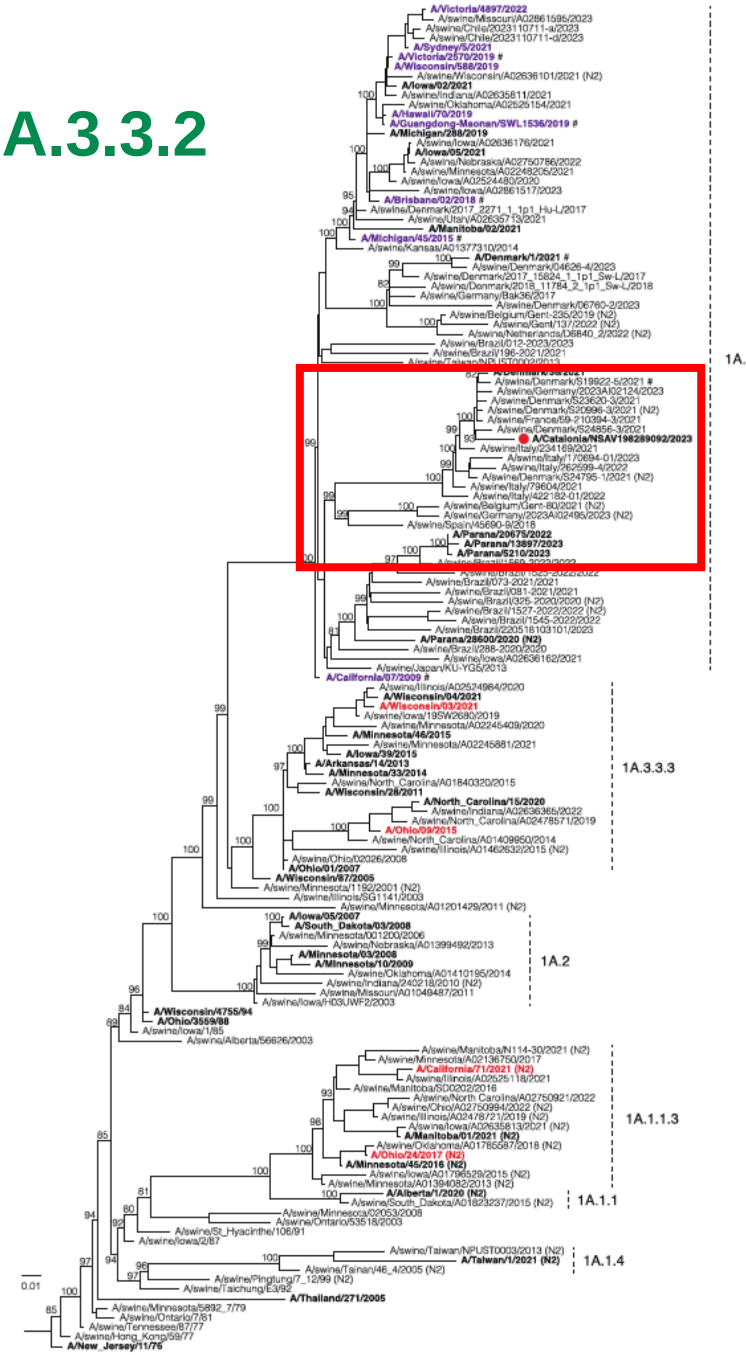
- Additional recent variant cases:
  - Brazil: H1N1v (1A.3.3.2)
  - Spain: H1N1v (1A.3.3.2)
  - USA Pennsylvania: H1N2v (1A.1.1.2)

Global Variants 2014-2024

2024 - OFFLU Swine Influenza virus Technical Meeting



1A.3.3.2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A/swine/Missouri/A02861595/2023
A/swine/Chile/2023110711-a/2023
A/swine/Chile/2023110711-d/2023
A/Sydney/5/2021
A/Victoria/2570/2019 #
A/Wisconsin/588/2019
A/swine/Wisconsin/A02636101/2021 (N2)
A/Iowa/02/2021
A/swine/Indiana/A02635811/2021
A/swine/Oklahoma/A02525154/2021
A/Hawaii/70/2019
A/Guangdong-Maonan/SWL1536/2019 #
A/Michigan/288/2019
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A/Iowa/05/2021
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A/swine/Iowa/A02524480/2020
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A/Michigan/45/2015 #
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A/Denmark/1/2021 #
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A/swine/Germany/Bak36/2017
A/swine/Denmark/06760-2/2023
A/swine/Belgium/Gent-235/2019 (N2)
A/swine/Gent/137/2022 (N2)
A/swine/Netherlands/D6840_2/2022 (N2)
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A/swine/Taiwan/NPUST0002/2013
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● A/Catalonia/NSAV198289092/2023
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pre-2009 seasonal A(H1N1) vaccine reference viruses
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A(H1N1)pdm09 vaccine reference viruses
0.01

WHO CVV from swine origin variant IAV

H1

Candidate vaccine viruses (like viruses)	Clade	Type	Institution*	Available
CNIC-1601 (A/Hunan/42443/2015) (H1N1)v	1C.2.3	Conventional	CCDC	Yes
IDCDC-RG48A (A/Ohio/9/2015) (H1N1)v	1A.3.3.3	Reverse genetics	CDC	Yes
IDCDC-RG58A (A/Michigan/383/2018) (H1N2)v	1B.2.1	Reverse genetics	CDC	Yes
IDCDC-RG59 (A/Ohio/24/2017) (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Yes
Candidate vaccine viruses in preparation	**Clade**	**Type**	**Institution**	**Availability**
A/Iowa/32/2016-like (H1N2)v	1B.2.2.1	Reverse genetics	CDC	Pending
A/Netherlands/3315/2016-like (H1N1)v	1C.2.1	Reverse genetics	MHRA	Pending
A/Ohio/35/2017-like (H1N2)v	1B.2.1	Reverse genetics	MHRA	Pending
A/Netherlands/10370-1b/2020 (H1N1)v	1C.2.1	Reverse genetics	MHRA	Pending
NIB-124 (A/Hessen/47/2020) (H1N1)v	1C.2.2	Conventional	MHRA	Pending
A/Bretagne/24241/2021 (H1N2)v NIB-131 (A/Bretagne/24241/2021 (H1N2)v	1C.2.4	Reverse genetics Conventional	SJCRH MHRA	Pending Pending
A/Wisconsin/03/2021 (H1N1)v	1A.3.3.3	Reverse genetics	CDC	Pending
A/California/71/2021 (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Pending

H3

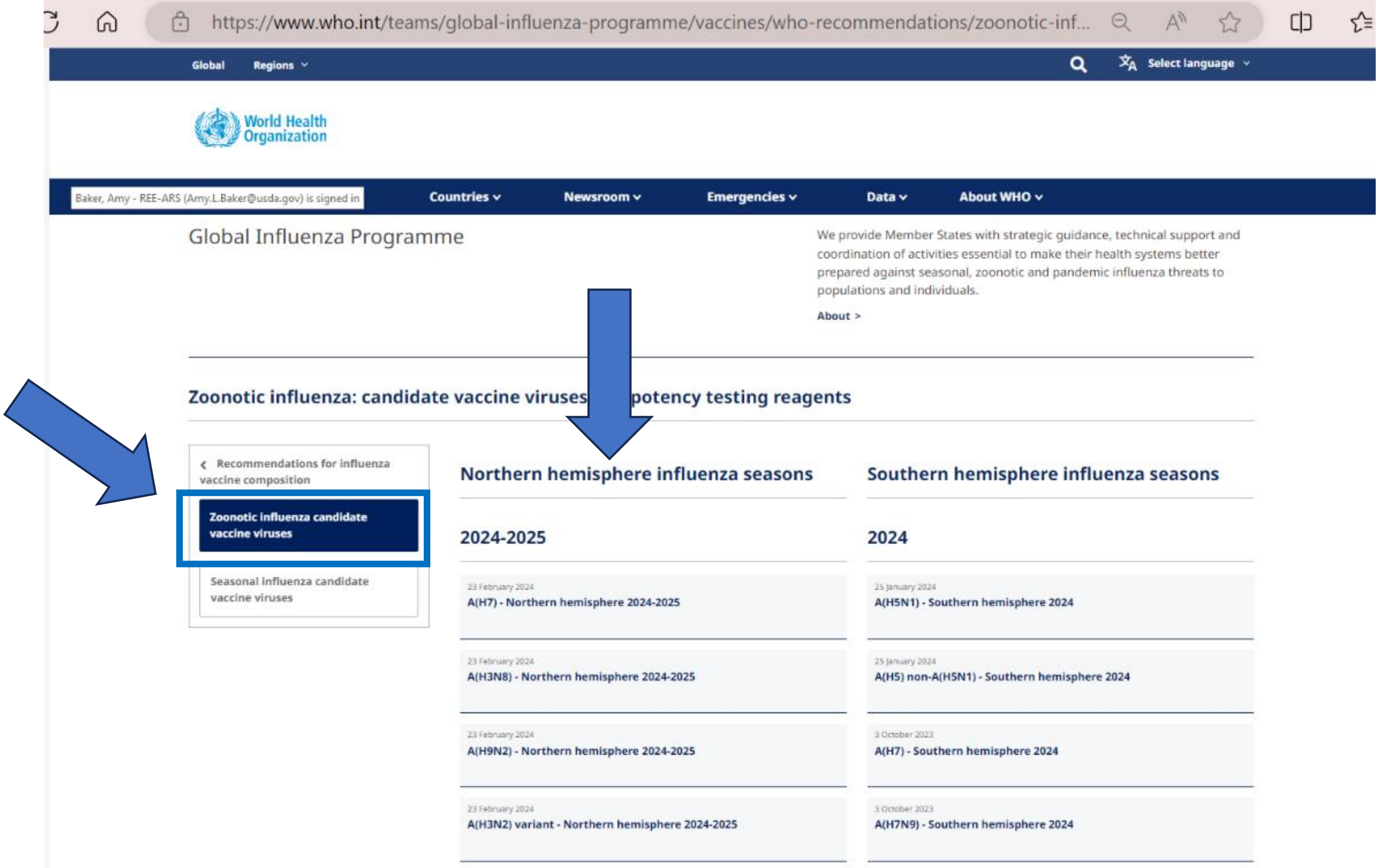
Candidate vaccine viruses (like viruses)	Clade	Type	Institution	Available
NYMC X-203 (A/Minnesota/11/2010)	1990.4.A	Conventional	CDC	Yes
NYMC X-213 (A/Indiana/10/2011)	1990.4.A	Conventional	CDC	Yes
IDCDC-RG55C (A/Ohio/28/2016)	2010.1	Reverse genetics	CDC	Yes
Candidate vaccine viruses in preparation		**Type**	**Institution**	**Availability**
A/Ohio/13/2017-like	2010.1	Reverse genetics	CDC	Pending
A/Ohio/28/2016-like	2010.1	Conventional	MHRA	Pending
A/swine/Iowa/23TOSU0850/2023	1990.4.a	Pending	CDC	Pending

- **Based on the current genetic, antigenic, and epidemiologic data, new CVVs that are antigenically like A/Catalonia/NSAV198289092/2023 and A/England/234600203/2023 are proposed. The available and pending A(H1)v CVVs are listed in Table 7.**
- **No new H3N2 CVV were proposed.**

Table 7. Status of influenza A(H1)v candidate vaccine virus development

Candidate vaccine viruses (like viruses)	Clade	Type	Institution*	Available
CNIC-1601 (A/Hunan/42443/2015) (H1N1)v	1C.2.3	Conventional	CCDC	Yes
IDCDC-RG48A (A/Ohio/9/2015) (H1N1)v	1A.3.3.3	Reverse genetics	CDC	Yes
IDCDC-RG58A (A/Michigan/383/2018) (H1N2)v	1B.2.1	Reverse genetics	CDC	Yes
IDCDC-RG59 (A/Ohio/24/2017) (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Yes
Candidate vaccine viruses in preparation	**Clade**	**Type**	**Institution**	**Availability**
A/Catalonia/NSAV198289092/2023-like (H1N1)v	1A.3.3.2	Pending	MHRA	Pending
A/England/234600203/2023-like (H1N2)v	1B.1.1.1	Reverse genetics	MHRA	Pending
A/Iowa/32/2016-like (H1N2)v	1B.2.2.1	Reverse genetics	CDC	Pending
A/Netherlands/3315/2016-like (H1N1)v	1C.2.1	Reverse genetics	MHRA	Pending
A/Ohio/35/2017-like (H1N2)v	1B.2.1	Reverse genetics	MHRA	Pending
A/Netherlands/10370-1b/2020 (H1N1)v	1C.2.1	Reverse genetics	MHRA	Pending
NIB-124 (A/Hessen/47/2020) (H1N1)v	1C.2.2	Conventional	MHRA	Pending
A/Bretagne/24241/2021 (H1N2)v NIB-131 (A/Bretagne/24241/2021 (H1N2)v	1C.2.4	Reverse genetics Conventional	SJCRH MHRA	Pending Pending
A/Wisconsin/03/2021 (H1N1)v	1A.3.3.3	Reverse genetics	CDC	Pending
A/California/71/2021 (H1N2)v	1A.1.1.3	Reverse genetics	CDC	Pending

Global Influenza Programme (who.int)



Global Influenza Programme

We provide Member States with strategic guidance, technical support and coordination of activities essential to make their health systems better prepared against seasonal, zoonotic and pandemic influenza threats to populations and individuals.

About >

Zoonotic influenza: candidate vaccine viruses potency testing reagents

Northern hemisphere influenza seasons

2024-2025

23 February 2024
A(H7) - Northern hemisphere 2024-2025

23 February 2024
A(H3N8) - Northern hemisphere 2024-2025

23 February 2024
A(H9N2) - Northern hemisphere 2024-2025

23 February 2024
A(H3N2) variant - Northern hemisphere 2024-2025

Southern hemisphere influenza seasons

2024

25 January 2024
A(H5N1) - Southern hemisphere 2024

25 January 2024
A(H5) non-A(H5N1) - Southern hemisphere 2024

3 October 2023
A(H7) - Southern hemisphere 2024

3 October 2023
A(H7N9) - Southern hemisphere 2024

Discussion topics

- Virus MTA and shipping to APHA or USDA
  - Permits, using the WHO Influenza CC to receive (St. Jude, Crick,) Nagoya (Bryan Charleston review on FMD)
  - Synthesizing viruses that can’t be shipped (GISAID and Nagoya issues)
  - Bacculovirus expressing HA
- Timelines for September (June sequence request) and February
- Undersurveilled regions
- Timeliness of data release or unpublished sharing through OFFLU
- Issues with GISAID only sequences availability to be used in other resources
  - BV-BRC, octoFLU, Nextclade, etc.
  - Uploading is an issue for moving to GenBank (can BV-BRC assist?)
- To discriminate between zoonotic variant cases and seasonal viruses detected in humans:
  - Sequencing (around 10% of samples received by CCs from NICs)
  - Swine influenza expertise (via OFFLU) engage with public health labs on regional diversity of IAV-S. Activity for tripartite? Regional one-page brief on current IAV-S diversity to share with public health via WHO regions.
- What are global reassortment patterns in Swine? Will this affect fitness for purpose of public health diagnostic PCR assays?
  - Detection of seasonal pdm09 NP gene (in US); continual contribution of seasonal M gene vs. sustained M in IAV-S
  - Include in regional briefs for bullet above
- OFFLU develop a point of contact list with visualization for WHO, FAO and WOAH ref labs with influenza expertise for website (explore how to include smaller labs)

Discussion topics, cont.

- Barriers to updating vaccine antigens: licensing authorities, biologics companies, market, antigenic selection
- Surveillance algorithm: detection by PCR (M or NP target), subtyping assays, commercial reagents
    - FAO has guidelines from 2010
    - OFFLU swine recommendations?
    - Ref lab proficiency panels (which labs can provide?)
- Regional swine influenza meetings to increase contributions from local and regional labs
    - Presentations or side group meetings at societies or professional meetings on behalf of OFFLU
    - Webinars from OFFLU experts: hot topics, research updates, techniques. Send topics/speaker names to OFFLU secretariat. Send registration for other organized webinars to OFFLU secretariat.

Action Items – Technical group membership

- New Co-chair
  - Chiara Chiapponi
- Suggestions for new members:
  - Latin America
    - (Chile) Victor Niera, Rodrigo Tapia; (Latin America) Daniel Perez; (Brazil) Rejane Schaffer, Helena Lage; (Colombia) Gloria Ramirez; (Central) Montse Torremorell
  - Asia
    - (Cambodia) Erik Karlson; (Vietnam); (Korea) Choi, UK suggestions?; (Taiwan) Tommy suggestion?; (Thailand) Taweewat Deemagan NIH;
  - South Asia
  - Eastern Europe
    - ESFLU coverage (Russia) Sharshor Kirill; (Ukraine)
- Leverage other swine virus expertise (ASFV, PRRSV…); test samples collected for other disease for FLU; sequencing services through FAO/International Atomic Energy Agency;
- Nomenclature for HA and NA clades (contact Tavis Anderson)

Workplan

- Develop one-page summaries on regional IAV-S diversity to share with public health
    - OFFLU scientist work with tripartite to create a template
    - OFFLU will formalize a plan for distribution
- Increase visibility of OFFLU to increase regional coverage
    - Send secretariat links when giving public webinars
    - Represent OFFLU at professional/society meetings
- WOAH/OFFLU post a statement on HPAI in cattle (already posted link to USDA APHIS and CDC websites)
- Training opportunities: FAO intern program, CEIRR & ref lab and university programs. Send info to secretariat

offlu

WOAH FAO

network of expertise on animal influenza

Thank you